SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	nucleotide		
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	1 -	\=possible nucleotide insertion) .
			:RKLEGHHDVVACDFSPDGALLATASYDTRVYIWDPHNGDILM
			EFGHLFPPPTP1FAGGANDRWVRSVSFSHDGLHVASLADDKMVR
	l		FWRIDEDYPVOVAPLSNGLCCAFSTDGSVLAAGTHDGSVYFWAT
	į		
			PRQVPSLQHLCRMSIRRVMPTQEVQKLPIPSKLLEFLSYRI
5906	146	2038	REGAGSGRMASGA\YNPYIKIIEQPRQRGMRFRYKCEGRSAGSI
ı			PGEHSTDNNRTYPSIQIMNYYGKGKV\RITLVTK\NDPYKPHPH
1 .		<b>!</b>	DLVGKDCRD\GYYEAEFGQE\RRP\LFFQN\LGIRCVKKKEVKE
l		1	A\IITR\IKAGINPFDVP*KQLNDIEDCDLDVVRLWFRVFLPDG
	ì	1	HGNL\TTALPPV\VSSPIYDNRAPNTAELRVCRVNKNCGSVRGG
{	1		DEIFLLCDKVQKDDIEVRFVLNDWBAKGIFSQADVHRQVAIVFK
I	Ī	ĺ	TPPYCKAITEPVTVKMQLRRPSDQEVSESMDFRYLPDEKDTYGN
1	[	1	KAKKOKTTLLFOKLCODHVETGFRHVDQDGLELLTSGDPPTLAS
1	1	l	OSAGITVNFPERPREGLIGSIGEGRYFKKEPNLFSHDAVVREMP
	Í	l	
	ł	1	TGVSSQAESYYPSPGPISSGLSHHASMAPLPSSSWSSVAHPTPR
	1	l	SGNTNPLSSFSTRTLPSNSQGIPPFLRIPVGNDLNASNACIYNN
j	1		ADDIVGMEASSMPSADLYGISDPNMLSNCSVNMMTTSSDSMGET
1	1	ł	DNPRLLSMNLENPSCNSVLDPRDLRQLHQMSSSSMSAGANSNTT
1	Ī	1	VFVSQSDAFEGSDFSCADNSMINESGPSNSTNPNSHVFVQDSQY
j			SGIGSMQNEQLSDSFPYEFFQV
5907	99	1873	TYLLSSWSS**NLDTKIKSQVKV/RKGHKKISWPYPQPAKQNGK
ì	ŀ	1	KATSKVPSAPHFVHPNDHANREAELKKKWVBEMREKQQAAREQE
	į.		ROKRRTIESYCODVLRROBEFEHKEEVLQBLNMFPQLDDBATRK
i			AYYKEFRKVVEYSDVILEVLDARDPLGCRCPOMBEAVLRAQGNK
l			KLVLVLNKIDLVPKEVVBKWLDYLRNELPTVAFKASTOHQVKNL
l			NRCSVPVDQASEBLLKSKACFGAKNLMRVLGNYCRLGEVRTHIR
I			VOVVGLPNVGKSSLINSLKRSRACSVGAVPGITKFMQEVYLDKF
ł	]		1
1			IRLIDAPGIVPGPNSEVGTILRNCVHVQKLADPVTPVETILQRC
		1	NLBEISNYYGVSGFQTTBHFLTAVAHRLGKKKKGGLYSQEQAAK
1		}	AVLADWVSGKISFYIPPPATHTLPTHLSAEIVKEMTEVFDIEDT
j		1	EQANEDTMECLATGESDELLGDTDPLEMBIKLLHSPMTKIADAI
1			ENKTTVYKIGDLTGYCTNPNRHQMGWAKRNVDHRPKSNSMVDVC
1			SVDRRSVLQRIMETDPLQQGQALASALKNKKKMQKRADKIASKL
ļ			SDSMMSALDLSGNADDGVGD
5908	247	975	HCGIKKRGEGSGSPSPASGGFQLGCQIP3PSLPSEEETHPHTRA
			HTRTLRATLTRRPPRSHSTRLRFFMPLDGDGGLASWK/PMRER*
	1	1	GWRRPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI
i		1	VTLWGKVVSSANHHKAHHVKTGTCBVVALHRCCNKNKI BERSQT
l		I	VKCSCFPGQVAGTTRAAPSCVDASIVEQKWWCHNQPCLEGEECK
1	1	l .	VLPDRKGWSCSSGNKVKTTRVTH
5909	1	5002	PAIPGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP
2009	1 -	3002	SSNLRADRSMICAOARAGKNLYHNRFLGLAAMAFPSRNSQSLRR
		ŀ	CKBPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR
1	I	l .	
j	ļ.	1	STIMGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS
l		l	ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV
1	]		SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS
1	I	1	DFQAMGLKKGMFFNPDPYLKISIQPGKHSIPPALPHHGQKRRSK
1	1	ĺ	IIGNTVNPIWQABQFSFVSLPTDVLBIEVKDKFAKSRPIIKRFL
	Ì		GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFBI
1	[		TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE
1	Į.	!	SSESWKPEQLGEGSVPDRPGNQSIELSRPAKEAAVITEAGDQGM
1			VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGREASALLLE
I	1		<u> </u>
1	[	Í	DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG
	1	l	EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR
i	1	ł	IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV
	ŀ		AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT
		l	
			HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS
			HPSTGSESDSSPRQGGDHSCKGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD
			SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER
			SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEBENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT
			SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER

* *		111	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide .
NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence ·	"	\=possible nucleotide insertion)
			GGGGSDSEABSSQSSLDLRREGSLSPVNSQKITLLLQSPAVKFI
J	j	)	TNPEFFTVLHANYSAYRVFTSSTCLKHMILKVRRDARNFERYOH
ł		İ	NRDLVNFINMFADTRLELPRGWEIKTDOOGKSFFVDHNSRATTF
1	1		IDPRIPLONGRLPNHLTHROHLORLRSYSAGEASEVSRNRGASL
		1	LARPGHSLVAAIRSQHQHESLPLAYNDKIVAFLRQPNIFEMLQE
1			RQPSLARNHTLREKIHYIRTEGNHGLEKLSCDADLVILLSLPEE
I			eimsyvplqaafhpgysfsprcspcsspqnspglqrasarapsp
ì	}		YRRDFEAKLRNFYRKLEAKGFGQGPGKIKLIIRRDHLLEGTFNQ
			VMAYSRKELQRNKLYVTFVGEEGLDYSGPSRBPPFLLSQELFNP
Ì			YYGLFBYSANDTYTVQISPMSAFVENHLEWFRFSGRILG\LALI HQYLLDAFFT\RPFYKALL\RLPC\D\LSDLBYLDEEFHQSLQW
1	<b>,</b>		MKDNNITDILDETFTVNEKVFGQVTERELKSGGANTQVTEKNKK
}			EYIBRMVKWRVERGVVQQTEALVRGFYEVVDSRLVSVFDARELE
1	1		LVIAGTAEIDLNDWRNNTBYRGGYHDGHLVIRWFWAAVERFNNE
i	1		QRLRLLQFVTGTSSVPYEGFAAPPWBPMGLRRFLP+KKWGKITS
L			LPPRG\HTCLQPDWDLPTVSPRTPMLYEK\LLTA\VEBTSTFGT
5910	1526	446	VAEFAAMBPGRTQIKLDPRYTADLLEVLKTNYGIPSACFSQP2T
1			AAQLLRALGPVELALTSILTLLALGSIAIFLEDAVYLYKNTLCP
1			IKRRTLLWKSSAPTVVSVLCCFGLWIPRSLVLVEMTITSFYAVC
1	1		FYLLMLVMVEGFGGKEAVLRTLRDTPMMVHTGPCCCCCPCCPRL
1			LLTRKKLQ\R*CWALSNTPS*R*R*PWWACFSSPTASMTQQTFL
1			RGAÇLYGSTLSSA/CSTLLALNTIGIISRQARLHLGEQNMGAKP ALFQVLLILTALQPSIFSVLANGGQIACSPPYSSKTRSQVMNCH
			LLILBTPLMTVLTRMYYRRKDIKVGYRTFSSPDLDLNLKALRNM
l			AWTMRGCCTH
5911	109	595	QLPLAPCIQGKGLKMRSPKPQSFIIRSSHSGAGLLVKNPSTPVF
1	,		CGHRRGGAAFKYKPTPVVGPEQRPTGQKHMRGGVSLLSPRLECS
	r		GTISAHCNLRLPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET
			GFHHVGQAGLELL/NVVIHLPRPPKVLGLQA
5912	924	277	MILNKALMLGALALTTVMSPCGGEDIVADHVASYGVNLYQSYGP
i .			SGQYSHBPDGDERFYVDLERKETVWQLPLFRRFRRFDPQFALTN
1			IAVLKHNLNIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNTLI CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFILODQ
1			VTSPSFPFE**DL*TAKVEQLGAWFEPLLKHWGARIPTTL
5913	46	1198	QLRMAGAEGAAGRQSELEPVVSLVDVLEEDERLENEACAVLGGS
1			DSEKCSYSQGSVKRQALYACSTCTPBGKEPAGICLACSYBCHGS
			HKLFKLYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN
1			FFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE
			SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM
1			B*/DDQEVIKPENGRHQDSTLKEDVPEQGKDDVREVKVEQNSKP
	·		CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT
			YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKCKI
5914	960	124	AQATORSDPLMDTLSSMNRVQQVELIC/GIQ*FED
	, ,	144	NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN BNGALSEVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG
	, , , , , , , , , , , , , , , , , , ,		GHDYQIGPYRKNLLCYDHRTDVWBERRPMTTARGWHSMCSLGDS
]	1		IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE
1			SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP
1			KATAGGSACPIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH
[			PHRHLPGLCRPAATS
5915	1604	703	FPGRPTRPLKLGRRRKRARI I QAPHCHSPRPRTCPPGALQAPEA
	]		PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT
	ŀ		PORDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS
			KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS
	ľ		PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS
L			PVLQELPGPAGGEFPEGL**AAGPAAH
. 5916	256	633	SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR
) i	Į		TVTGAVHRHLMHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH
5917	1242	000	PTRLILQ*NQATADKNN*TTALLQPHQRL\VSPRMABA
1 251/ )	1343	827	AHQILTYLEP/ICLVVNYNKILTVFLTKSVLEI*KFIHTPQTYR

				· · · · · · · · · · · · · · · · · · ·
	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding to first	to first	L=Leucine, M-Methionine, N-Asparagine,
	Ì	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence		\=possible nucleotide insertion)
				3*NDFFGIKEVYVSRRLRKTSF/RLAVTFLEQAVVSKBCVPVDQ
	1			FMEHLLPSLLSLASDPVPNVRVLLAKALROMLLEKAYPRNAGNP
	5918	13	2045	HLEVIRETILALQSDRDQDVSFPAALEPKRRNIIDTAVLBKQN
	2310	13	1247	EGAQVARRRSRRQWRAGRCGRGRGGRRAERTGGRGPPGRPRPLP PGPARRGRRRMETPFYGDBALSGLGGGASGSGGTFASPGRLFPG
	Į.		İ	APPTAAAGSMMKKDALTISISEQVAAALKPAPAPASYPPA\ADG
			1	APSAAPPDGLLASPDLGLLKLASPKLKRLIIQSNGLVTTTPTSS
			i	QFLYPKVAASEEQEFAEGFVKALEDLHKONQLGAGRAAAAAAA
	_			AGGPSGTATGSAPPGELAPAAAAPEAPVYA\NLSSY\AGGCRGL
•				RGGAAT\VAFAABPVPFPPPPPPPGALGPRRP/RLALQGRRPQTV
		ł	Į.	PDVP\SFGESP\PLSPIET\DTPRRI\KAKRKRL\RNPQIRAPK
	1	1	l	PASRKLGAQSRALERESEDPS*SPEHGSLASTASLLREQVAQLK
	5919	1	4254	QKVLSHVNSGCQLLPQHQVPAY TSVQGDSQGTPTSSQGSINMRHWISQAIHGSTTSTTSSSTQSG
		_	1	GSGAAHRLADVMAQTHIENHSAPPDVTTYTSEHSIQVERPQGST
				GSRTAPKYGNABLMETGDGVPVSSRVSAKIQQLVNTLKRPKRPP
	ľ			LREFPVDDFEELLEVQQPDPNQPKPEGAQMLAMRGEQLGVVTNW
				PPSLEAALQRWGTISPKAPCLTTMDTNGKPLYILTYGKLWTRSM
	ł			KVAYSILHKIGTKQEPMVRPGDRVALVFPNNDPAAFMAAFYGCL
				LAKVVPVPIEVPLTRKDAGSQQIGFLLGSCGVTVALTSDACHRG
				LPKSPTGEIPQFKGWPKLLWFVTRSKHLSKPPRDWF\PHIKDAN NDTAYIEYKTCK\DGSVLGVTVTRTALLTHCOALTOACGYTRAE
	1			TIVNVLDPKKDVGLWHGILTSVMNMHVISIPYSLMKVNPLSWI
	Ì			QKVCQYKAKVACVKSRDMHWALVAHRDQRDINLSSLRMLIVADG
	İ		•	ANPWSISSCDAFLNVFQSKGLRQEVICPCASSPEALTVAIRRPT
	l '			DDSNQPPGRGVLSMHGLTYGVIRVDSEEKLSVLTVQDVGLVMPG
		-		AIMCSVKPDGVPQLCRTDEIGELCVCAVATGTSYYGLSGMTKNT
		* -		PEVFAMTSSGAPISEYPFIRTGLLGFVGPGGLVFVVGKMDGLMV VSGRRHNADDIVATALAVEPMKFVYRGRIAVFSVTVLHDERIVI
			,	VAEQRPDSTEEDSFQWMSRVLQAIDSIHQVGVYCLALVPANTLP
				KTPLGGIHLSETKQLFLEGSLHPCNVLMCPHTCVTNLPKPROKO
				PRIGPASVMVGNLVSGKRIAQASGRDLGQIBDNDQARKFLFLSE
				VLQWRAQTTPDHILYTLLNCRGAIANSLTCVQLHKRARKIAVML
				MERGHLQDGDHVALVYPPGIDLIAAFYGCLYAGCVPITVRPPHP QNIATTLPTVKMIVEVSRSACLMTTQLICKLLRSRBAAAAVDVR
				TWPLILDTDD*PKKRPAQICKPCNPDTLAYLDFSVSTTGMLACV
				KMSHAATSAPCRSIKLQCELYPSREVAICLDPYCGLGFVLWCLC
				SVYSGHQSILIPPSELETNPALWLLAVSQYKVRDTFCSYSVMEL
				CTKGLGSQTESLKARGLDLSRVRTCVVVAKERPRIALTQSFSKL
		I		FKDLGLHPRAVSTSFGCRVNLAICLQGTSGPDPTTVYVDMRALR
l		İ		HDRVRLVERGSPHSLPLMRSGKILPGVRIIIANPETKGPLGDSH
			-	IGEIWYHSAHNASGYFTIYGDESLQSDHFNSRLSFGDTQTIWAR TGYLGFLRRTELTDANGERHDALYVVGALDEAMELRGMRYHPID
		1		IETSVIRAHKSVTECAVPTWTNLLVVVVELDGSEQEALDLVPLV
		ł		TNVVLREHYLIVGVVVVVDIGVIPINSRGEKQRMHLRDGFLADQ
Į				LDPIYVAYNM
1	5920	1381	1499	QLGAVAHAGVSRIPP*LPPPLHPTFLSLWCLHHKLP/HPPGASM
1				VRPPVVPRRPPAHISSVRQASTQVPRTVPHTQRVANIGTQTTGP
, I				SGVGCCTPGRPLLPCKCSSAAHSTYRVQEPAVHIPGQEPLTASM LAAAPLHEQKQMIGERLYPLIHDVHTQLAGKITGMLLEIDNSRL
İ			Î	LIMLESPESLHAKIDEAVAVLQAHQAMEQPKAYMH
ŀ	5921	727	157	VCPGTGGK*GLWGQLGGLPKETPLKPMDAFTGSGLKRKFDDVDV
l			j	GSSVSNSDDBISSSDSADSCDSLNPPTTASFTPTSILKROKOLR
Į	1		ļ	RKNVRFDQVTVYYFARRQGFTSVPSQGGSSLGMAQRHNSVRSYT
i	ļ		.	LCEFAQEQEVNHREILREHLKEEKLHAKKMKLTKNGTVESVEAD
- 1	Ì		ļ	GLTLDDVSDEDIDVENVEVDDYFFLQPLPTKRRRALLRASGVHR
ł	ł			IDAEEKQELRAIRLSREECGCDCRLYCDPEACACSQAGIKCQVD
i				RMSFPCGCSRDGCGNMAGRIEFNPIRVRTHYLHTIMKLELESKR
İ	l			Q\GAAQQPQ\*GALPDCQLQPDRSTGL*DPSWIGSKGLSFTGKG AAATHLIILRVIENRGAEGKRK
ŀ	5922	2475	495	SYSNWGLPPSVFIQVPRSRTGNLKPIFDFYSYYE\CMETLKG\T
L.				

	1 000 32 26 23	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID			
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	sequence	<del> </del>	CLYNATOYKVCSPRNDRPDACYNPSRPAATTVFEIRTGLLLGDT
			SKIITRTBEKEIPKQITLRFDACAAINSKKLEIGCGSLN*ERS*
	{	•	RVENKYVCHESGVCKNCAYWPCVI*AT*KKNKNDSVYLQKGEAN
	Į.	1	PSCAAGHCNPLELIITNPLDPHWKKGERVTLGINRTGLKPQVVI
	i e		LIKGEVHKCSPKPVFQTFYEELNLPAPELLKKTKNLFLQLAENV
	•		IFLLNGTSCYVRGGTTIGDRWPWBA*ELVPTDPAPDIIPI*KAB
	1	1	ASNF+VLKTSIIRQYCIAREGKDFIIPVGKPNCIGQKLYNSTTK
	Ĭ	Į.	TIT++DLANHTEKNPFSKFSKLKTA+AHABSH+DWTVPSGLY+IC
			RHRAYFRLPNKWADSCVIGTIKPSFFLLPIKMGELLGPSVYASR
	ł	1	EKKGIVIGNWKDNEWPRERIIQYYGPATWAQDGSWGYR/TP/VY
	I		
			MLNWIIRLQAILEIISNETGRALTVLAWQETQMRNAIYQNRLAL
ĺ	1	1	DYLLVAEGGVCRKFNLTNCCLQINDQGQVVKNIVRDMTKLAHVP
l		1	IQVWHKFDPESLFGKWFPAIGGFKTLIVGVLLVIRTCLLLPCVL
1	l .	1	PĻLFQMIKGIVATLVHQKTSAHVNYMNHYRSISQRDSKSEDESE
ŀ			NSH
5923	137	638	OLCGRRGORFRISIKRMHPI*RTCPNTNL/IILLSQENTQIRDL
			OOENRELWISLEEHQUALELIMSKYRKQMLQLMVAKKAVDAEPV
l			LKAHQSHSABIESQIDRICEMGBVMRKAVQVDDDQFCKIQBKLA
<b>,</b>	ł		OLELENKELRELLSISSESLOARKENSMOTASQAIK
		2246	EKGKVKDAGAEOWISISLSCKGSWETOFSNHLINSLTPPTSVRRM
5924	274	2146	# · · · · · · · · · · · · · · · · · · ·
l	Į.		PLITTVTLLKMVARHHMKLLCSKAFSTQLQQKIFLHSQMGIHHQ
ŀ	1		SVCMKLKPNTSHIISILMGQPMALVQLETLAPLTIIIQKFQTQD
<u> </u>	ł.		HMKFWKNLPLHSHHLTPSVPQTVIPKKTGSPBIKLKITKTIQNG
i	1		RELFESSLCGDLLNRVQASE\Q*NQSIBSRKEKRKKSNKHDSSR
1	1		SEERKSHKIPKLEPEEQNRPNERVDTVSEKPREEPVLKEGSPSS
	1		ANTIFCSNNGSVHW\FKFQVGDLVWSKVGTYFWWPCMVSSDPQL
1	}	1	EVHTKINTRGARBYHVQFFSNQPBRAWVHBKRVREYKGHKQYEE
1	Į.	į ·	LLAEATKOASNHSEKOKIRKPRPORERAQWDIGIAHAEKALKMT
1	1		REERIEOYTFIYIDKOPEBALSQAKKSVASKTEVKKTRRPRSVL
1	1	i .	1 -
l	ł		NTOPEQTNAGEVASSLSSTBIRRHSQRRHTSAEEEEPPPVKIAW
1	1 .	}	KTAAARKSLPASITMHKGSLDLQKCNMSPVVKIBQVFALQNATG
Į	I.		DGKFIDQFVYSTKGIGNKTRISVRGQDRLIISTPNQRNEKPTQS
}	1 .		vsspeatsgstgsvekkoorrsirtrsesekstevvpkkkikke
l .	}		QVGFLHVES
5925	216	1911	MMTABSREATGLSPQAAQEKDGIVIVKVEREDERDHMNGQDSTL
	1		QDTPPPDPEIFRQRFRRFCYQNTFGPREALSRLKELCHQWLRPB
Į.	Į.		INTKEQILELLVLEQFLSILPKELQVWLQEYRPDSGEEAVTLLK
ŀ	I		DLELDLSGQQVPGQVHGPEMLARGMVPLDPVQESSSFDLHHEAT
1	ì		OSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDQAMASALFT
1	1	l	ADSOAMVKIEDMAVSLILEEWGCONLARRNLSRDNRQENYGSAF
	1		POGGENRNENERSTSKARTSEDSASRGETTGRSQKEFGEKRDQE
1	1	1	CKTCEROOKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK
l	1		
1	}	1	GLGRSPSLSSNFTTPEKVPTGTKSHRCDECGKCFTRSSSLIRHK
1	1	1	IIHTGEKPYECSECGKAP\SLNS\NLVLHQRI\HTGEKPHECNE
I	1		CGKAFSHSSNLILHQRIHSGEKPYBCNECGKAFSQSSD\LTKHQ
<u> </u>	1	l .	RIHTGEKPYECSECGKAPNRNSYLILHRRVHTREKPYKCTKCGK
i	i		\AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV
5926	2	233	DRCLMLKQGSQPGSPPAT/CKPPAPPVYQAPCQSCPBPPGAHEP
3320	1 *	233	SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS
	ļ	<del>  - ,,,,</del>	
5927	4146	1248	KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA
l	}		YKKYGDKKLHEKKPLQKHKQAHQTPBKRVNTGEERRKISEBAAR
1	1	1	KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG
1	1	1	wrnvlsaggsgevkapflgsggtiapssfssrgqyehyhaifdq
l	]	1	MQQQRAEDNEAKWKRBIYGRGLPERQKGQLAVERAKQVEEPLQR
1	Į.	Į.	KREAMONKARAEGHMGILONLAAMYGGRPSSSRGGKPRNKEEEV
l		I	YLARLRQIRLQNPNERQQIKAKLRGEKKEANHSEGQEGSEEADM
}	5	]	RRKK\ IESLKAHANARAAVLKEQLERKRKEAYEREKKVWBEHLV
1	1 .		
}	}	)	AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS
l	1	į.	SLIDTRETSEEMQKINNAISSKREILRRLNRNLKAQKDEKGKON
	1		LSDTFEINVHEDAKKHEKEKSVSSDRKKWEAGGQLVIPLDELTL
1	l .		DTSFSTTERHTVGEVIKLGPNGSPRRANGKSPTDSVLKILGEAE
		<del></del>	

		( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( )	Transport to the second second second second second second second second second second second second second se
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	1	P=Proline, Q=Glutamine, R=Arginine,
		amino acid	
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /-possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
<u> </u>	Doquezae	<b></b> -	LOLOTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHRINPS
	ì	İ	
1	ì		AIVDSPVETKSPEFSRASPQMSLKLEGNLEEPDDLETEILQEPS
ł	ł	ł.	GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG
l		<b>l</b> .	VSSTVDQLSDTHIRPGTNDSQHSKCDVDKSVQPRPFFHKVVHSB
1	<b>5</b>	1	HLNLVPOVOSVOCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG
ſ		Ĭ	LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLBIDEI
l .	i	i	EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYS
ł	1	1	
ì	ì	1	EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
ł	ļ	Į.	GBIASECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKAIHE
l	1	I	DEDENIEICSKIVÇNILGNEHQHLYAKILHLVMADGAYQEDNDE
5928	4146	1248	KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA
1 55.50	1	1	YKKYGDKKLHEKKPLQKHKQAHQTPBKRVNTGEERRKISEEAAR
<b>S</b>	1	1	
]	I	1	KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG
1	1	ì	WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ
l	1	1	MQQQRAEDNBAKWKRBIYGRGLPERQKGQLAVERAKQVEEFLQR
1	Ì	}	KREAMONKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEREV
l	Į.		YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
Į.	1	1	RRKK\ IESLKAHANARAAVLKEQLERKRKBAYEREKKVWEEHLV
ł	{	§	AKGVKSSDVSPPLGOHETGGSPSKQQMRSVISVTSALKBVGVDS
	i .		SLTDTRETSBEMOKINNAISSKREILRRINENLKAQEDBKGKON
i	1	1	
	l	1	LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL
1	l	1	DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGRAB
[	Į.		LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
ļ			ATVDSPVBTKSPEFSEASPOMSLKLEGNLEEPDDLETEILQEPS
Į.	ŧ.	*	GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG
		]	VSSTVDQLSDIHIBPGTNDSQHSKCDVDKSVQPEPFFHKVVHSE
<b>1</b> .	1	<b>1</b>	HLNLVPQVQSVQCSPEESFAPRSHSHLPPKNKNKNSLLIGLSTG
1	·		
ì	1	1	LYDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLBIDEI
Į	Į.	i	EDENTKEGPSDSEDIVFRETDTDLQELQASMEQLLREQPGEEYS
ĺ		1	REERSVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
Į.	•		GETASECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKTKATHE
1.		ľ	DEDENIEICSKIVONILGNEHOHLYAKILHLVMADGAYQEDNDE
F000	<del></del>	1660	LDFSMTTQLPAYVAILLFYVSRASCQDTFTAAVYEHAAILPNAT
5929	3	1558	
i	1		LTPVSREEALALMNRNLDILEGAITSAADQGAHIIVTPEDAIYG
			WNPNRDSLYPYLEDIPDPEVNWIPCNNRNRFGQTPVQERLSCL\
1		l	AKNNSIYVVANIGDKKPCDTSDPQCPPDGRYQYNTDVVF\DSQG
Į.			KLVARYHKONLFMGRNOFNVPKEPBIVTFNTTFGSFGIFTCFDI
ł		]	LFHDPAVTLVKDFHVDTIVFPTAWMNVLPHLSAVEFHSAWAMGM
1		1	RVNFLASNIHYPSKKMTGSGIYAPNSSRAFHYDMKTEBGKLLLS
1		1	QLDSHPSHSAVVNWTSYASSIRALSSGNKEFKGTVFFDEFTFVK
1	]	1	
l l	1		LTGVAGNYTVCQKOLCCHLSYKMSENIPNEVYALGAFDGLHTVE
J		1	GRYYLQICTLLKCKTTNLNTCGDSAETASTRFEMPSLSGTFGTQ
ł		1	YVFPEVLLSENQLAPGEFQVSTDGRLFSLKPTSGPVLTVTLFGR
1	1	1	LYEKDWASNASSGLTAQARIIMLIVIAPIVCSLSW
5930	113	6082	RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK
1 2230	***	3000	KLVWIPSERHGPEAASIKBERGDEVMVELAENGKKAMVNKDDIQ
1	}	1	
l	Į.	1	KMNPPKFSKVBDMARLTCLNEASVLHNLKDRYYSGLIYTYSGLP
I	•	Ī	CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM
Į.		]	LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN
I	1	1	IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV
i	}	}	TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL
I			KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG
ì	1	1	
1	I		PSHBEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL
1	1		CHILGMNVMEFTRAILTPRIKVGRDYVÇKAQTKEQADFAVEALA
Į.	Į.	Į	KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN
ſ			SPEOLCINYTNEKLOOLFNHTMPILEQEEYQREGIEWNFIDFGL
{	1	Į.	DLOPCIDLIERPANPPGVLALLDEBCWFPKATDKTFVEKLVQEQ
l	1	1	**** <b>=</b>
1	1	1	GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
l	[	I	NVATLLHQSSDRFVARLWKDVDRIVGLDQVTGMTBTAFGSAYKT
}	1	]	KKGMFRTVGQLYKESLTKLMATLKNTNPNFVRCIIPNHRKRAGK
i		l	LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP
1			

	T 50 - 37 - 5 - 5	Predicted end	Dates and amount amount and the
SEQ	Predicted	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	beginning nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
f	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
<b>\</b>	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ţ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	ľ	Bequence	\=possible nucleotide insertion)
	sequence		NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH
}	1	Ì	LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR
ŀ			NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK
i i			BKOTKVEGELEEMERKHQOLLEEKNILAEQLQAETELFAEAEEM
1	1		RARLAAKKQELEBILHDLESRVEEBEERNOILONEKKKMQAHIQ
Į.	Į.	ļ.	DLEBOLDREEGAROKLOLEKVTAEAKIKKMEEEILLLEDONSKF
ĺ			IKEKKLMEDRIAECSSQLAEEKEKAKNLAKIRNKQEVMISDLEE
	}		RLKKKEKTROELEKAKRKLOGETTDLODQIAELQAQIDELKIQL
l		ŀ	AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES
]		i	EKASRNKAEKOKROLSEELEALKTELEDTLOTTAAQQELRTKRE
1	1	1	
}	1	į.	CRVAELKKALEBETKNHBAQIQDMRQRHATALBELSBQLBQAKR FKANLBKNKQGLETDNKBLACBVKVLQQVKAESEHKRKKLDAQV
1	1	{	QELHAKVSEGDRLRVELABKASKLQNELDNVSTLLEEABKKGIK
1	}	1	FAKDAASLESQLODTOELLQEETRQKLNLSSRIRQLEEEKNSLQ
1	l		EQUERERRY KUTEKOATYTOOTIKKKADDDTGIIESPEEV
]	I		KKKLLKDAEALSQRLERKALAYDKLEXTKNRLQQELDDLTVDLD
1	)	ļ	HOROVASNLEKKO\KKFDQLLABEKSISARYAEERDRABARAR
ì		}	KETKALSLARALBEALEAKBEFERONKOLRADMEDLMSSKDDVG
	<b>,</b>		KNVHELEKSKRALEQQV\BEMRTQLEBLEDBLQATEDAKLRLEV
}	į.	}	NMOAMKAOPERDLOTRDEONBEKKRILLIKOVRELEAELEDERKO
1	1		RALAVASKKKMBIDLKDLBAQIBAANKARDEVIKQLRKLQAQMK
l	Į.	Į.	DYORELEEARASRDEIFAQSKESEKKLKSLEAEILQLQEELASS
1			ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLEE
ł		1	ELEEEQSNMELLNDRFRKTTLQVDTLNAELAAERSAAQKSDNAR
1	1		QOLERONKELKAKLOELEGAVKSKFKATISALEAKIGQLEEQLE
ı	J	1	QEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA
ſ	1	ļ	NARMKQLKRQLBBAEEEATRANASRRKLQRBLDDATEANEGLSR
	ł	Ī	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK
Į.		Ì	TSDVNRTQPPQSR
5931	113	6082	RGNCFWIVPFIMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK
1 2202	1 772	1	KLVWIPSERHGFRAASIKEERGDEVMVELAENGKKAMVNKDDIQ
}		j	KMNPPKPSKVRDMARLTCLNEASVLHNLKDRYYSGLIYTYSGLF
1			CVVINPYKNLPTYSENIIEMYRGKKRHEMPPHIYAISESAYRCM
1	<b>\</b>	<b>,</b>	LODREDOSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN
į.	1	1	IPGE\LERQLLQANPILESPGNARTVQNDNSSRFGKFIRINFDV
į	ł		TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL
[		Ī	KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNPRGDPGRAMHING
1	1	[	PSHBETLSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL
1	Ĭ	}	CHLLCMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA
1		ļ	KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN
}	1	1	SPEQUCINYTHEKLOQLENHTMFILEQBEYQREGIEWNFIDFGL
ŀ	[	1	DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ
ļ		1	GSHSKPQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
1	ł	1 .	NVATLLHQSSDRFVARLWKDVDRIVGLDQVTGMTETAFGSAYKT
!	1		KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK
}	]	1	LOPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP
ļ	[	1	NAIPKGFMDGKQACBRMIRALRLDPNLYRIGQSKIFFRAGVLAH
1	1	1	LBEEROLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR
1	1	1	NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEBLLKVK
Į.	[		EKQTKVEGBLEEMERKHQQLLREKNI LAEQLQAETELPAEAEEM
	I	1	RARLAAKKQELEBILHDLESRVBEEEERNQILQNEKKKMQAHIQ
!	ľ	Į.	DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF
ł	1	1	IKEKKLMEDRIAECSSQLAEBERKAKNLAKIRNKQEVMISDLER
		1	RLKKEEKTROBLEKAKRKLDGETTDLQDQIAGLQAQIDELKLQL
1	j		AKKEELQGALARGDDETLHKNNALKVVRELQAQIABLQEDFES
	i	i	RKASRNKAEKQKRDLSBELEALKTELEDTLDTTAAQQELRTKRE
1			
		<b>[</b>	QEVAKLKKALEEETKNHRAQIQDMRQRHATALEELSEQLEQAKR
			QEVAKLKKALEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLBKNKQGLETDNKBLACEVKVLQQVKAESEHKRKKLDAQV
			<del>-</del>
			PKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV
			PKANLEKNKQGLETDNKBLACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVBLABKASKLQNELDNVSTLLEEABKKGIK

<u></u>	11.7	•	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= '
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
INO:	1		H=Histidine, I=Isoleucine, K=Lysine,
}	location	corresponding	
	corresponding	to first	L-Leucine, M-Mcthionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l .	amino acid	sequence	Codon, /=possible nucleotide deletion,
]	sequence		\=possible nucleotide insertion)
			KKKLLKDAEALSQRLEBKALAYDKLEKTKNRLQQBLDDLTVDLD
1	1		HOROVASNIEKKO\KKFDOLLAEEKSISARYAEERDRAEAEARE
	i		KETKALSLARALERALEAKEEFERONKOLRADMEDLMSSKDDVG
i	ŀ		
l	į	ļ	KNVHELEKSKRALEQQV\EEMRTQLEELEDELQATEDAKLRLEV
1		Ì	NMQAMKAQFERDLQTRDEQNEEKKRLLIKQVRELEAELEDERKQ
l		ŀ	RALAVASKKKMBIDLKDLEAQIRAANKARDEVIKQLRKLQAQMK
l		l	DYORELEKARASRDEIFAQSKESEKKLKSLEABILQLQEELASS
1	1	1	ERARRHABOERDELADEITNSASGKSALLDEKRRLEARIAQLEE
ĺ	į.	•	
		<b>;</b>	BLEEEQSNMELLNDRFRKTTLQVDTLNAKLAAERSAAQKSDNAR
ì	1		QQLERQNKELKAKLQELEGAVESKFKATISALEAKIGQLEEQLE
I	ĺ	1	QEAKBRAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMBKA
	ĺ	1	NARMKOLKROLBEABERATRANASRRKLORELDDATRANEGLSR
1	l	1	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK
i .	ĺ	I	TSDVNETOPPOSE
H	<del> </del>	Fax	RHLEEICPLFLOKGRKLKLSGPRWEEGKPRGTGGLWVKAEANMG
5932	33	572	•
1	Ī		FGATLAVGLTIFVLSVVTIIICFTCSCCCLYKTCRRPRPV\APP
	[	1	PHPP/PVVHAPYPQPPSVPPSYPGPSYQGYHTMPPQPGMPAAPY
1		1	PMQYPPPYPAQPMGPPAYHETLAGGAAAPYPASQPPYNPAYMDA
		Ì	PKAAL
5933	1	3190	GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD
3,33		1 3250	SDMPSRTRPKSPRKHNYRNESARESLCDSPHONLSRPLLENKLK
ļ	ŀ	{	AFSIGKMSTAKRTLSKKEQEELKKKEDEKAAABIYEEFLAAFEG
j			
}	l	i	SDGNKVKTFVRGGVVNAAKEKHETDEKRGKIYKPSSRFADQKNP
1 .	ļ.	}	PNQSSNERPPSLLVIBTKKPPLKKGEKUKKKSNLELFKEELKQI
		<b>,</b>	QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL
1		1 .	DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQBFGRFGP
1	1	i	LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI
	1		MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP
1	l .	l	
1	1		RERLKNPNAPMLPPPKNKEDPBKTLSQAIVKVVIPTERNLLALI
l .	I		HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENOTPAHVYYRW
1		ł	KLYSILQGDSPTKWRTBDFRMFKNGSFWRPPPLNPYLHGMSEEQ
1			ETRAPVEBPSKKGALKBEQRDKLBEILRGLTPRKNDIGDAMVFC
	1	1	LNNAEAAKEIVDCITESLSILKTPLPKKIARLYLVBDVLYNSSA
	ı	1	KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM
		1	TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIKEKETEDVPDDLD
1	į.	1	
1		ì	GAPIBEBLOGAPLEDVDGIPIDATPIDOLDGVPIKSLDDDLDGV
1	İ		PLDATEDSKKNEPIFKVAPSKWEAVDESELRAQAVTTSKWELFD
I	1	1	QHEESEEENQNQEEESEDEKDTQSSKSEKHELYSNPIKBEMTE
	1	i	SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKPGQSF
1	1	1	<b>QEQUEHYRDKLLQREKEKELERERERDKKDKEKLESRSKDKKBK</b>
I		I	DECTPTRKERKRRESTSPSPSRSSSGRRVKSPSPKSERSERSER
1		<b>[</b>	•
l			SHKESSRSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRSRSRSP
1		1	KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKPFKKAVTYWKCDLF
1	i	ì	LCPERSVF
5934	1	3190	GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD
1		1	SOMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK
l			APSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEEFLAAFEG
1		I	SDGNKVKTFVRGGVVNAAKERHETDEKRGKIYKPSSRFADQKNP
1	1	Į.	
			PNOSSNERPPSLLVIETKKPPLKKGEKEKKKSNLKLFKEELKQI
1	1	Į.	QKERDBRHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL
1	Î	I	DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP
i	1		LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI
i		1	MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP
1		1	T **
I		1	RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNILALI
}	§	I	HRMIEFVVREGPMFBAMIMNREINNPMFRFLFBNQTPAHVYYRW
1		<b>!</b>	KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ
	1		BTEAFVEEPSKKGALKEFORDKLEBILRGLTPRKNDIGDAMVFC
1	į.	1	LNNARAAEBIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA
1	Į.		
1	i		KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM
1	1	]	TCFRAWEDWAIYPBPFLIKLONIFIGLVNIIEEKETEDVPDDLD
1	i	]	GAPIERRLDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV
	<del></del>	1	<u> </u>

	and the second of the second	<u>**</u>	
SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ΊD	beginning:	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l wo:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l			L=Leucine, M=Methionine, N=Asparagine,
ł	corresponding	to first	
[	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
l .	sequence	1	\=possible nucleotide insertion)
ļ	Bequence		PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD
	1	1	OHEESEKERNONGEESEDEEDTGSSKSEEHHLYSNPIKEEMTE
		1	
1	ľ	1	SKYSKYSEMSEEKRAKLRBIBLKVMKFQDELESGKRPKKPGQSF
1		1	QEQVEHYRDKLLQREKEKELBRERERDKKDKEKLESRSKDKKEK
		ì	DECTPTRKERKRRHSTSPSPSRSSSGRRVKSPSPKSERSERSER
1			SHKESSRSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRSRSRSP
	l	1	KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKFFKKAVTYWKCDLF
ł		1	LCPERSVP
5935	3	4493	SYNLSGWRLSRPPRQFWAGWRGIGRFGTMAPVHGDDCBIGASAL
	f	]	SDSGSFVSSRARREKKSKKGRQEALERLKKAKAGERYKYEVEDF
i		1	TGVYEBVDEEQYSKLVQARQDDDWIVDDDGIGYVEDGREIFDDD
l	1	1	LEDDALDADBKGKDGKARNKDKRNVKKLAVTKPNNIKSMFIACA
ŀ		1	GKKTADKAVDLSKDGLLGDILQDLNTETPQITPPPVMILKKKRS
1		I	IGASPNPFSVHTATAVPSGKIASPVSRKEPPLTPVPLKRAEFAG
	ĺ		DDVQVESTEEEQESGAMEFEDGDFDEPMEVEEVDLEPMAAKAWD
	1	[	KESEPABEVKQZADSGKGTVSYLGSFLPDVSCWDIDQEGDSSFS
I			VOEVOVDSSHLPLVKGADEEOVFHFYWLDAYEDQYNQPGVVFLF
1	l	i	
l	i	ſ	GKVWIESAETHVSCCVMVKNIERTLYFLPREMKIDLNTGKETGT
	1		FISMKDVYBEPDEKIATKYKIMKPKSKPVEKNYAFEIPDVPEKS
1	1		KYLEVKYSAEMPQLPQDLKGETFSHVFGTNTSSLELFLMNRKIK
			GPCWLEVKKSTALNQPVSWCKVRAMALKPDLVNVIKDVSPPPLV
l	ļ	1	VMAFSMKTMQNAKNHQNBI IAMAALVHHSFALDKAAPKPPFQSH
1	1		FCVVSKPKDCIFPYAPKEVIRKKNVKVEVAATERTLLGFFLAKV
{	·		HKIDPDIIVGHNIYGFELEVLLQRINVCKAPHWSKIGRLKRSNM
l	j	,	PKLGGRSGFGERNATCGRMICDVEISAKELIRCKSYHLSELVQQ
	1 .	1	ILKTERVVIPMENIQNMYSESSQLLYLLEHTWEDA\KFILQIMC
	i .		ELNVLPLALQITNIAGNIMSRTIMGGRSERNEFLLLHAFYENNY
	1 .		
1			IVPDKQIFRKPQQKLGDBDBBIDGDTNKYKKGRKKGAYAGGLVL
ļ ·			DPKVGFYDKFILLLDFNSLYPSIIQEFNICFTTVQRVASBAQKV
ł	1		TEDGEQEQIPELPDPSLEMGILPREIRKLVERRKQVKQLMKQQD
[	1	1	INPOLILOYDIROKALKLTANSMYGCLGFSYSRFYAKPLAALVT
ļ	1	1	YKGREILMHTKEMVOKMNLEVIXGDTDSIMINTNSTNLEEVFKL
1			GNKVKSBVNKLYKLLBIDIDGVFKSLLLLKKKKYAALVVBPTSD
		ł	CNYVTKQELKGLDIVRRDWCDLAKDTGNFVIGQILSDQSRDTIV
i	1	1	ENIOKRLIBIGENVLNGSVPVSQFEINKALTKDPQDYPDKKSLP
ł		1.	
	1	1	HVHVALWINSQGGRKVKAGDTVSYVICQDGSNLTASQRAYAPEQ
I	1		LQKQDNLTIDTQYYLAQQIHPVVARICEPIDGIDAVLIATGWEL
1	1	1	\DPTQFKVHHYHKDEENDALLGGPAQLTDEEKYRDCERFKCPCP
			TOGTENIYONVFDGSGTDMBPSLYRCSNIDCKASPLTFTVQLSN
	1		KLIMDIRRFIKKYYDGWLICEEPTCRNRTRHLPLQFSRTGPLCP
Į.		1	ACMKATLQPHYSDKSLYTQLCFYRYIFDAECALBKLTTDHBKDK
1			LKKOFFTPKVLQDYRKLKNTAEQFLSRSGYSEVNLSKLFAGCAV
1			KS
	1	130	RGEEQFDAEFRRFACLGFGERLQEFSRLLRAVHRSRAWTCYLAI
5936	1124	139	RUDEUT DAEFRRYACIATUS CONTRACTOR DES DE DE L'HOVERS DECCE S DE C
	1		RMLMATCCPSPTTTACTGPWQRAPPLRLLVQKRRADSSGLAFAS
ì	1	1	NSLQRRKKGLLLRPVAPLRTRPPLLISLPQDFRQVSSVIDVDLL
!		1	PETHRRVRLHKHGSDRPLGFYIRDGMSVRVAPQG\LERVPGIFI
1			SRLVRGGLAESTGLLAVSDEILEVNGIEVAGKTLNQVTDMMVAN
	1		SHN\LIVTVKPANQRNNVVRGASGRLTGPPSAGPGPAEPDSDDD
1	1	}	SSDLVIENROPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPSLDD
1	1		OEQASSGWGSRIRGDGSGFSL
	<u> </u>		PTSLLKSTVQLMCRLLQDKRYQCVYSLAEIFKVLASFYVILVIL
5937	31	1600	
	1		YGLTSSYSLWWMLRSSLKQYSFEALREKSNYSDIPDVKNDFAFI
1	1	1	LHLADQYDPLYSKRPSIFLSEVSENKLKQINLNNBWTVEKLKSK
1	1	1	LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS
i	1	1	AVSQLVNLKBLRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK
1	1	1	IPRWYFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL
	1	1	KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKS
I	1	1	LELISCOLERIPHSIFSINNIHELDLRENNLKTVEBIISFQHLQ
	1		DEDISCUBLISHED ASSESSMENT OF DEDICATION OF THE PROPERTY OF THE
	1		NLSCLKLWHNNIAYIPAQIGALSNLEQLSLDHNNIENLPLQLFL
}	L		CTKLHYLDLSYNHLTFIPERIQYL\SNLQYFAVTNNNIRMLPDG

Predicted   Pred		<del></del>	· · · · · · · · · · · · · · · · · · ·	
No: mucleotide location corresponding to first amino acid residue of samino acid residue of samino acid residue of samino acid sequence corresponding to first amino acid residue of samino acid sequence corresponding to first samino acid sequence corresponding to first samino acid sequence corresponding to first samino acid sequence corresponding to first corresponding to first samino acid sequence corresponding to	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding to first amino acid residue of anino acid residue of anino acid residue of anino acid sequence se				
to first anino acid anino acid anino acid anino acid sequence  Fernidue of anino acid sequence  Fernidue of anino acid sequence  Fernidue of anino acid sequence  Fernidue of anino acid sequence  Fernidue of anino acid sequence  Fernidue of anino acid sequence  Fernidue of anino acid sequence  Fernidue of  Fernidue o	NO:	nucleotide		
to first amino acid residue of amino acid sequence  sequence  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \possible nucleotide insertion)  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /-possible nucleotide deletion, \possible nucleotide insertion)  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /-possible nucleotide deletion, \possible nucleotide insertion)  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop PppEleSCQSLERENGIPERNLIPTELPYPTELCYCLOKC ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop PppEleSCQSLERENGIPERNLIPTELPYPTELCYCLOKC ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop PppEleSCQSLERENGIPERNLIPTELPYPTELCYCLOKC ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop PppEleSCQSLERENGIPERNLIPTERNL	ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence codon, /-possible nucleotide deletion (-possible nucleotide deletion) (-possible nucleotide) (-possible nucleotide) (-possible nucleotide) (-possible nucleotide) (-possible nucleotide deletion) (-possible nucleotide) (-possible nucleotide) (-possible nucleotide) (-possible nucleotide) (-possible nucleotide) (-possible nucleotide) (-possible nucleotide) (-possible nucleotide) (-possible nucleotide) (-possible nucleotide) (-possible nucleotide) (-possible nucleotide) (-possible nucleotide) (-possi	l	corresponding	to first	L=Leucine, M=Nethionine, N=Asparagine,
amino acid residue of amino acid sequence  Codon, /-possible nucleotide deletion,	1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
maino acid sequence  ### Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,		V	1	S=Serine, T=Threonine, V=Valine,
amino acid sequence				II
A-possible nucleotide insertion	l	1	1	
LPCCKNOCLLIGENSLANKS.PRVCELSKI.PRICEPIGNYLEFI  PPELSCOSLARNALLVEENLANTS.PUTTERLOCALDKC  VKESSPENGSRANGEEDEKKKARASSENIKSTGSSVESTPYPOSOK  TYVELLLIGSLIVETPSKGSDODYSTANSHTVATUTERVESDOV  TYVENLLIGSLIVETPSKGSDODYSTANSHTVATUTERVESDOV  TYVENLLIGSLIVETPSKGSDODYSTANSHTVATUTERVESDOV  TYVENLLIGSLIVETPSKGSDODYSTANSHTVATUTERVESDOV  TYVENLLIGSLIVETPSKGSDODYSTANSHTVATUTERVESDOV  TYVENLIGSLIVETPSKGSDODYSTANSHTVATUTERVESDOV  KRODANITTERMINER WADGRUISTELLITINATURISTELPPSRALLYQESP  MOMISCOPIES SYSTYPREELY TYRKERSVATISTICH TOPPRANTAME  WEIRNITTEVALTTSSOTVANSTYTICHTSTANSLERVUS  VERNATTEVALTTSSOTVANSTYTICHTSTANSLERVUS  TYVENDLIPVEVCET PYVESALVERY CHIEFYSWRREPSKOKKKK  KRPAPTIDIRFRSATIQHNANTHLQEDDEGVITELIGGROCASP  PCCPEDCRYGNARRISHIRITARADISTICHTYSVARREPSKOKKKK  KRPAPTIDIRFRSATIQHNANTHLQEDDEGVITELIGGROCASP  PCCPEDCRYGNARRISHIRITARADISTICHTYSVARREPSKOKKKK  KRPAPTIDIRFRSATIQHNANTHLQEDDEGVITELIGGROCASP  PCSPOGARRANNAMILLUSVASSAPALLALDEBISSITICHTYNIAVY  VSILLI  SEDLESLITETIBEARPILLYVANTOTORGEBVILTPREARMOGGS  LIGGIGVOVILIRLIPPERGKKILSLEPISSVASSAPANGOGGIALOVSIR  PCSPOGARRANNAMILLUSVASSAPALLALDEBISSITICHTRAGOFUNGTY  PTPPLUEPCVANGLITYSVENSSAPALLEGUNGAPTITERKOGFUNGTY  PTPPLUEPCVANGLITYSVENSSAPALLEGUNGAPTITERKOGFUNGTY  PTPPLUEPCVANGLITYSVENSSAPALLEGUNGAPTITERKOGFUNGTY  PTPPLUEPCVANGLITYSVENSSAPANGOGGANAPTITERKOGFUNGTY  PTPPLUEPCVANGLITYSVENSSAPANGOGGANITARAGOFUNGAPTITERKOFTE  VQLSSVAPPSILSPOTTICIDEGISTICISSTPP, PANSSVILSTGYV  PTPLUEPCVANGLITYSVENSSAPANGOGGANITERAGOFUNGAPTITERKOFTE  VQLSSVAPPSILSPOTTICISGISTICISSTPP, PANSSVILSTGYV  VDANASSESP  TTAKADAASSITVOVTPPTAKAPTTVEDRUGSTPVSKEVARAA  APLPLPSERLASPELVENSSAPANGOGGANAPTATATOTORGEBVILSTINSSAPDAAT  TTAKADAASSITVOVTPPTAKAPTTVEDRUGSTPVSKEVALDANDOMANGAPTATATATATATATATATATATATATATATATATATAT	ļ		bequence	1.
5938  395  1865  1865  1865  1865  1865  1865  1865  1865  1865  1865  1865  1865  1865  1865  1865  1865  1865  1865  1865  1874  1		sequence		
5938  395  1865  YKKEESPERUKRANGSERIKKYKENSENIKSTISSVYSTPYPPOK MYTVILLILLISLIKYPTSKREDDIVSKYSNENIKVYLTEKYPEDIV TVILINILLISLIKYPTSKREDDIVSKYSNENIKVYLTEKYPEDIV TVILINILLISLIKYPTSKREDIVSKYSNENIKVYLTEKYPEDIV TVILINILLISLIKYPTSKREDIVSKYSNENIKVYLTEKYPEDIV TVILINILLISLIKYPTSKRENIKYSKITIKYLIKITILDISCOLOLIBIPPY MEDISCHARSSKYSTYPREKTYPKINEKSTRUKYSKENIKYPTSKITLITTILDISCOLOLIBIPPY MEDISCHARSSKYSTYPREKTYPKINEKSTRUKYSKYTTOTYTIPTILI WYLSWISPWIRKOMPARPTSLCITTVILNYTILSTIARKSLEKYS VYTAMOLEWSVETTYPTSATIQENIKATILQEROBISTOTELDIGKOCASH ROPATTOIRTPRISATIQENIKATILQEROBISTOTELDIGKOCASH ROPATTOIRTPRISATIQENIKATILQEROBISTOTELDIGKOCASH ROPATTOIRTPRISATIQENIKATILQEROBISTOTELDIGKOCASH ROPATTOIRTPRISATIQENIKATILQEROBISTOTELDIGKOCASH PCSPROKANIKANEKUKUKIYSSKIPALLAGENISTYITIQHINIVA WSILIL  5939  66  1404  1ROPICHERVORUSKIPENIKATYVANTOTINCIBVILITENISAMOGISSI LIGGIGGOVALIRLIFERPEGKIKISLERISTOTESHINGOCCILLIVSIIR PCSPROKANIKANIKATISTSPREGKIKISLERISTOTESHINGOCCILLIVSIIR PCSPROKANIKANIKATISTSPREGKIKISLERISTOTENIKOOPTUKINGOTELIVORUSKISTITYVITTOIRCIBVILITENISAMOGISSI LIGGIGGOVALIRLIFERPEGKIKISLERISTOTENIKOOPTUKINGOTELIVORUSKISTITYVITTOIRCIBVILITENISAMOGISSI LIGGIGGOVALIRLIPERPEGKIKISLERISTOTENISAPPINICALI PTPPLURPINIPTSTSPRENTERPEGKIKISLERISTOPTINISAPPINICALI PTPPLURPINIPTSTSPRENTENISTORUSKISSIPPOTANICIBVILITENISAMOGISSI VALANASSEP PTPPLURPINIPTSTSPRENTENISSISSARSELLISLISIPPSTSKANSODADOV VALANASSEP  5940  145  717  REGARRABABRITUDUTPPTIKADPTTVEDRUCDISTISTYDIM CGIFRENNISKIMOELIKAQOBILIGIDOCSKYSPRANSONODOV KANINASSEP SILCKANGASSPASSERVOPPADICLIPICSSKAPPENINDOODOV KANINASSEP SILCKANGASSPASSERVOPPADICLIPICSSTRANSONODOV KANINASSEP SILCKANGASSPASSERVOPPADICLIPICSTSTANSONODOV KANINASSEP SILCKANGASSPASSERVOPPADICLIPICSTSTANSONODOV KANINASSEP SILCKANSWATAARORERIKANSPERVICALANANGERISKONOPPONIKANI VALVARENINGATANICANSPERVICALANANGERISKONOPPONIKANI VALVARENINGATANICANSPERVICALANANGERISKONOPPONIKANI VALVARENINGATANICANSPERVICANANGERISKONOPPONIKANI VALVARENINGATANICANSPERVICANANGERISKONOPPONIKANI VALVARENINGATANICANANGERIKANGANICANANGERIANGANICANANGERISKONOPPONIKAN	}	1		· - ·
MYWHILLIGINTOR POIGNETH THROWS THE PVAINTER  YTLINIEGYDNILGEN THROTON TO THE WAS THE PART THROWS THE PVAINTER  YTLINIEGYDNILGEN THROUGH VISUALITIAN COLUMNS  SKANAMHITTENBRUNG THROUGH VISUALITIAN COLUMNS  WIGHRITE VIGUALITA THROUGH VISUALITIAN COLUMNS  WIGHRITE VIGUALITA THROUGH VISUALITIAN COLUMNS  WIGHRITE VIGUALITA THROUGH VISUALITIAN COLUMNS  WIGHRITE VIGUALITA THROUGH VISUALITA THROU	ļ	1		PPELEGCQSLKRNCLIVEENLLNTLPLPVTERLQTCLDKC
TVILINILIBOTINILIBOTINILIBOTINILIBOTININISIBONINI THE PTOPEN SKRADAHHITTENBRILIBOTINILIBASININGKINI POTFENE SKRADAHHITTENBRILIBOTINILIBASININGKINI POTFENE SKRADAHHITTENBRILIBOTINILIBASININGKINI POTFENE MORRICOPERS SEVERY PERITYON MUSSUS VERUITENSKILLORPP MORRICOPERS SEVERY PERITYON MUSSUS VERUITENSKILLORPP WORRICOPERS SEVERY PERITYON MUSSUS VERUITENSKILLORPP WORRICOPERS SEVERY PERITYON MUSSUS VERUITENSKILLORPP VOLKEN PROPERTIO INFERSATION MUSSUS VERUITENSKILLOR COLOR VERUITENSKILLOR	5938	395	1865	YKGEGFFCNQEARGERRKKKKAMSSPNIWSTGSSVYSTPVFSQK
STIDLEPROTWORRLEFESTIXVIALISSINWOKINI PIDTERS SKARDAHITTERWINTSIGNTUTARCIQUIGHEP MORHSCPLER'SSYDYPRESIVYOWKISSEVEKOPTESWRILYOSP VGLORPTTERVATTSCOVYMSSYDYDESSRWAYTIQTY PCTLI VVLSWUSSHUNDAUPARTSIGLITTUINTHTISTIARKSLEVUS YVTAMDLEVSYCPIPYPSALVEYGYLHIYPVSHRRPSKOKOKK KIPAPTIDIEPISATIQMINATHIQERDETIOTECLIGKOCASE PCCPSDCRTGAMRISHIHITIAMNATHIQERDETIOTECLIGKOCASE PCCPSDCRTGAMRISHIHITIAMNATHIQERDETIOTECLIGKOCASE PCCPSDCRTGAMRISHIHITIAMNATHIQERDETIOTECLIGKOCASE PCCPSDCRTGAMRISHIHITIAMNATHIQERDETIOTECLIGKOCASE PCCPSDCRTGAMRISHIHITIAMNATHIQERDETIOTECLIGKOCASE PCCPSDCRTGAMRISHIHITIAMNATHIQERDETIOTECLIGKOCASE PCCPSDCRTGAMRISHIHITIAMNATHIQERDETIOTECLIGKOCASE PCCPSDCRTGAMRISHIHITIAMNATHIQERSISTICHATOWN SELLET PSPGANIRAVHILEVSKYLLEVYNTDHOCREVITTERSANGOGGI LIGGIGVOYJUBLIPTRPPEGOKLISJSTYP PANSANGSTOTE PTOPLILIPOVAGGITTSVPPHESSYTHILGELISTSTYP PANSANGSTOTE PTOPLILIPOVAGGITTSVPPHESSYTHILGELISTSTYP PANSANGSTOTE PTOPLILIPOVAGGITTSVPPHESSYTHILGELISTSTYP PANSANGSTOTE PTOPLILIPOVAGGITTSVPHESSYTHILGELISTSTYP PANSANGSTOTE PTOPLILIPOVAGGITTSVPHESSYTHILGELISTSTYP PANSANGSTOTE PTOPLILIPOVAGGITTSVPHESSYTHILGELISTSTYP PANSANGSTOTE PTOPLILIPOVAGGITTSVPHESSYTHILGELISTSTYP PANSANGSTOTE PTOPLILIPOVAGGITTSVPHESSYTHILGENSTYPPHESPRINDOVA VDANASESP  5940  145  717  RESAGRRSASPEGGACTAVTTOTRAGGTCLAAAHRIMBERGAGGS LEKLEVPHIGUVITSVOORPSPEDIASLAVVOILAALVYDIA CHICHAAVKUS PENGRADIVARAQDECQLARQKOKRPTDLOVOT LAVILOMWULILI  PCCGRRGASSPESDEPOGOPADELIPYCCGSSILAVVOILAALVYDIA CHICHAAVKUS PENGRADIVARAQDECQLARQKOKRPTDLOVOT LAVILOMWULILI  5941  13  6147  MCCGRRGASSPESDEPOGOPADELIPYCCGSSILAVVOILAALVYDIAALVA MCCGRRGASSPESDEPOGOPADELIPYCCGSSILAVVOILATURORE PROTATRAGGITTSVANDAMATUROTRAGGITTSVANDAMATUROTROPS ITTINODETISTRRESTINGSVVTTECNRCSGGRAVELINGSPSTY PTOPLICARROTRAGGITTSCOMPANNITIVICATIONSPSTY VIDAGRTGARGANGCTYCGOP VIDAGRTGASSPSTVCIAGMSSILANGSVPOROMATUROTROPPOT CRETECTOR PORTAGRAGGITTSVANDAMATUROTPOTORSGGGRAV VIDAGRGASASTCVIAGMSSILANGSVPOROMATUROSGGRAV PELVORPSTYCTSDOVICUSSPSTACTORMISSINGSVPOROMATUROTROPPOT CRETECTICALVYSCORPSTANGSPSTATCORPOTATION PPONEGRITALVSTORMSPSTANGSV	·		Ī	MIVWILLLSLYPGPTSQKSDDDYRDYASNKTWVLTPKVPEGDV
STIDLEPROTWORRLEFESTIXVIALISSINWOKINI PIDTERS SKARDAHITTERWINTSIGNTUTARCIQUIGHEP MORHSCPLER'SSYDYPRESIVYOWKISSEVEKOPTESWRILYOSP VGLORPTTERVATTSCOVYMSSYDYDESSRWAYTIQTY PCTLI VVLSWUSSHUNDAUPARTSIGLITTUINTHTISTIARKSLEVUS YVTAMDLEVSYCPIPYPSALVEYGYLHIYPVSHRRPSKOKOKK KIPAPTIDIEPISATIQMINATHIQERDETIOTECLIGKOCASE PCCPSDCRTGAMRISHIHITIAMNATHIQERDETIOTECLIGKOCASE PCCPSDCRTGAMRISHIHITIAMNATHIQERDETIOTECLIGKOCASE PCCPSDCRTGAMRISHIHITIAMNATHIQERDETIOTECLIGKOCASE PCCPSDCRTGAMRISHIHITIAMNATHIQERDETIOTECLIGKOCASE PCCPSDCRTGAMRISHIHITIAMNATHIQERDETIOTECLIGKOCASE PCCPSDCRTGAMRISHIHITIAMNATHIQERDETIOTECLIGKOCASE PCCPSDCRTGAMRISHIHITIAMNATHIQERDETIOTECLIGKOCASE PCCPSDCRTGAMRISHIHITIAMNATHIQERSISTICHATOWN SELLET PSPGANIRAVHILEVSKYLLEVYNTDHOCREVITTERSANGOGGI LIGGIGVOYJUBLIPTRPPEGOKLISJSTYP PANSANGSTOTE PTOPLILIPOVAGGITTSVPPHESSYTHILGELISTSTYP PANSANGSTOTE PTOPLILIPOVAGGITTSVPPHESSYTHILGELISTSTYP PANSANGSTOTE PTOPLILIPOVAGGITTSVPPHESSYTHILGELISTSTYP PANSANGSTOTE PTOPLILIPOVAGGITTSVPHESSYTHILGELISTSTYP PANSANGSTOTE PTOPLILIPOVAGGITTSVPHESSYTHILGELISTSTYP PANSANGSTOTE PTOPLILIPOVAGGITTSVPHESSYTHILGELISTSTYP PANSANGSTOTE PTOPLILIPOVAGGITTSVPHESSYTHILGELISTSTYP PANSANGSTOTE PTOPLILIPOVAGGITTSVPHESSYTHILGENSTYPPHESPRINDOVA VDANASESP  5940  145  717  RESAGRRSASPEGGACTAVTTOTRAGGTCLAAAHRIMBERGAGGS LEKLEVPHIGUVITSVOORPSPEDIASLAVVOILAALVYDIA CHICHAAVKUS PENGRADIVARAQDECQLARQKOKRPTDLOVOT LAVILOMWULILI  PCCGRRGASSPESDEPOGOPADELIPYCCGSSILAVVOILAALVYDIA CHICHAAVKUS PENGRADIVARAQDECQLARQKOKRPTDLOVOT LAVILOMWULILI  5941  13  6147  MCCGRRGASSPESDEPOGOPADELIPYCCGSSILAVVOILAALVYDIAALVA MCCGRRGASSPESDEPOGOPADELIPYCCGSSILAVVOILATURORE PROTATRAGGITTSVANDAMATUROTRAGGITTSVANDAMATUROTROPS ITTINODETISTRRESTINGSVVTTECNRCSGGRAVELINGSPSTY PTOPLICARROTRAGGITTSCOMPANNITIVICATIONSPSTY VIDAGRTGARGANGCTYCGOP VIDAGRTGASSPSTVCIAGMSSILANGSVPOROMATUROTROPPOT CRETECTOR PORTAGRAGGITTSVANDAMATUROTPOTORSGGGRAV VIDAGRGASASTCVIAGMSSILANGSVPOROMATUROSGGRAV PELVORPSTYCTSDOVICUSSPSTACTORMISSINGSVPOROMATUROTROPPOT CRETECTICALVYSCORPSTANGSPSTATCORPOTATION PPONEGRITALVSTORMSPSTANGSV		ì	]	TVILNNLLEGYDNKLRPDIGVKPTITHTDMYVNSIGPVNAINME
SKRADAHHITTENBURGEVIJSERGUISERGUISER WERDER HERDER PRESSERGUISER LEQUES WERDERITESVYETTSCOPYUMSSVEPULSERWIZUSER UVGENTTSVVETTSCOPYUMSSVEPULSERWIZUSERIZUSER VGENTERGE VVGUNSVEPULSERWIZUSERIZUSER VGENTERGER VGEN	l	1	1	i ·
MORRIS CPLRESSYLYPRESILVYOWKISSEWSYLTYTYPT PCTLI VGLENTTERVATTEGOTVOWSVUPPLOSERSWYTTGYTPCTLI VVI.SWUSEWINKONVPROTITYVISTANKSLEPVS VGLENTTERVATTGOTVOWSVUPPLOSERSWYTTGYTPCTLI VVI.SWUSEWINKONVPROTITYVISTANKSLEPVS VYTANDLFVSVCPIFVPSALVEYGYLHYPVSNRKPSKOKOKK KRPAPTIDIRPISATIGMRNATHLGERDENTOFELLGGKOCASE PCCPSDCRTGARMRIGHIRTAKMOSYRAT FPYTAPCLENINYW VSTLIL  IRRGYLKKYQENSGHERAGLEPFPDFIVSINGSKLINKONDTIKD LLKARVIKEVPKMILYSSKYLBLERTSVYPSNIMAGGGLLGVSIF FCSPDGANRAWHULBVSBNSPAALAGREPSDYLIGADTVANN SRDLESLIETBERRHELKLVVANTDHORRSVITIANSMOGGSI LGGGIGVGYLIBLIPTREFEGKKISLPGOMAGTPITTELKOGETE VOLSSWAPPSLSPOPTOTIGSCILIGALSTSTY PANSSVISTGY PTYP\LLPQVANGLITSVPPHESSYLHLGHAPTTRGGLENLPQ PTYPLLEPQVANGLITSVPPHESSYLHLGHAPTTRGGLENLPQ PTYPLLEPQVANGLITSVPPHESSYLHLGHAPTTRGGLENLPQ PTYPLLEPQVANGLITSVPPHESSYLHLGHAPTTRGGLENLPQ PTYPLLEPQVANGLITSVPPHESSYLHLGHAPTTRGGLENLPQ PTYPLLEPQVANGLITSVPTSKGGLIGALSSTYPPANSSVLSTGY VOLNASSESP TAKADAASSILVVUTTPTAKAPTTVEDRUGSTFVSEKEVVSAN VOLNASSESP VOLNASSESP TAKADAASSILVVUTTPTAKAPTTVEDRUGSTFVSEKEVVSAN VOLNASSESP GGIFFRENNSRLMDELLKQQQSILGLDCSKYSPEPANSNIKDDOV LICHLAAVKULSPENGRADIVENGRADVETGOLDCCLVARGKORFFVIGURDT LAVVILVOMVILLI  SEGREGSSPENGRADVENGRADVETGOLDCCLVARGKORFFVIGURDT LAVVILVOMVILLI SEGREGSSPENGRADVENGRADVETGOLDCCLVARGKORFFVIGURDS IKVSCTRCSVRLIGGSSANCTI ISGDYV HUMBREPLOGRIPPE TITNIDPLISTINKENFPYGSVVYTYKCNPGSGGREVFELVGSPI VELTARETQGENNINFSPGGREVYFELDGESTICTSDPQOMM SPAAPTCEWSCDDPMOGLINGKVLFPVNLIGGARKOPPCDOBP VILHARETQGENNINFSPGGREVYFELDGESTICTSDPQOMM SPAAPTCEWSCDDPMOGLINGKVLFPVNLIGGARKOPPCMORM VMSSSASYCVLAGMESLAMISSVVYTRCDDEGGGREV PELYGRESTTCLONLWSSPROVCKRISCKTPDPVNANNIL VELTAPTTRONPHYGSVVYTRCDDPMOGRISMCTPQDIM VMSSSASYCVLAGMESLAMISSVVYTRCDDGGGGREV PELYGRESTICTSDPQOMW SPAAPTCGWRSCDDPMOGLINGKVLFPVNLIGGARGER CREYYGRPSITCLONLWSSPROVCKRISCKTPDPVNANNIL VSONSILFSLABVVERCQDPFVIRGHRITCDDPMOGRISMCTPQDIM VSSSASYCVLAGMESLAMISSVVYTRCDDFROGREPVIRGHRITC CREYYGRPSITCLONLWSSPROVCKRISCKTPDPVNANNIL VSONSILFSLABVVERCQDFVIRGHRITCDDPMOGRISSACCILISCN TAMMSTUPPICGRIF TORGONPRARCEGORVYTCA PPOPUNGMINISTERPTGORPSTANGSVPTCORPIVAGGREV CRESPPOR		ì	ſ	
WGLRNTTEVVICTSCOPYUMSUYPOLSREMYFILOTY IPCLI  VVISWSEMINKONDAPRISCITUTUTIMITETSTÄRKILPKUS  YVTANDLEVSUCPI FUPSALVEYG\TLITYVSINKERSHIKDKIK  KMPAPTIDIRPRSATIOMNINTHLQREDBEYGYECLOGOCASP  PCCYEDCETCAMRIKKITHIRTAKMOSYARIPPTAPCLENILVYW  VSILIL  5939  66  1404  IRRGYLKRYQENSFGHRAGLEPPYDFIVSINGSRLMKONDTLKD  LLKANVKRYVKHLIYSSKYLLALRETSVYPENILMGQGGLLGVYBIR  FCSPDGANRKWHILVENSENS PALALBLRENSEYI TENSARGOGGS  LLGGIGYGYLIBLIFTERSKRULLVYNTOTINGRENI TENSARGOGGS  LLGGIGYGYLIBLIFTERSKRULLVYNTOTINGRENI TENSARGOGGS  LLGGIGYGYLIBLIFTERPFERGKIK SLEPOPMATT ITTEKOGFIS  VQLSSUMPPSLSPPOTTGI EQSLIGLSI SSTYP PRAVSSVLSTING  PTYPLLPRY PTISMRCUGLI OF FURFOLLPRISSM PPRALICO\  PTYPLLPRY PTISMRCUGLI OF FURFOLLPRISSM PPRALICO\  PTYPLLPRY PTISMRCUGLI OF FURFOLLPRISSM PPRALICO\  PTYPLLPRY PTISMRCUGLI OF FURFOLLPRISSM PPRALICO\  PTYPLLPRY PTISMRCUGLI OF FURFOLLPRISSM PPRALICO\  PTYPLLPRY PTISMRCUGLI OF FURFOLLPRISSM PPRALICO\  PTYPLLPRY PTISMRCUGLI OF FURFOLLPRISSM PPRALICO\  PTYPLEVESHLEN PTISMRCUGLI OF FURFOLLPRISSM PPRALICO\  PTYPLLPRY PTISMRCUGLI OF FURFOLLPRISSM PPRALICO\  PTYPLLPRY PTISMRCUGLI OF FURFOLL STANDARD  TAKADAASSILPYDUT PPTAKAPTTVEDRUGST PVSEKVYSAA  VANANGSESP  PTYPLER PTISMRCUGLI OF FURFOLL STANDARD  TAKADAASSILPYDUT PTISKRAPTTVEDRUGST PVSEKVYSAA  VANANGSESP  TAKADASSILPYDHING PRAVITOR PURFOLL STANDARD  GGI FKRNNSRLMDBILKQQGILLGLOCKYSPEPANSNDKDDQU  LACILLANIVALS PEDGRADI TVRARQDF COLVARKOKRYP TOLLDUT  LAVILOWWILLI  FULFOLADAR ALPAPTMILDERSPE LOTLINYEGCROYSGRP  SILCLMSINWITCARDRENS CHIPPERCESSILLAVVULLALPVA  MCCICADEN ALPAPTMILDERSPE LOTLINYEGCROYSGRP  SILCLMSINWITCARDRENS CHIPPERCESSILLAVVULLALPVA  MCCICADEN ALPAPTMILDERSPE LOTLINYEGCROYSGRP  SILCLMSINWITCARDRENS CHIPPERCESSILLAVVULLALPVA  MCCICADEN ALPAPTMILDERSPE LOTLINYEGCROYSGRP  ILKSCCTKONLLIGSSANCILLS CHIPPERCESSILLAVVILLALPVA  MCCICADEN ALPAPTMILTERSPE LOTLINYEGCROYSGRP  ILKSCCTKONLIGSSANCILLS CHIPPERCESSILLAVVILLALPVA  MCCICADEN ALPAPTMILTERSPE LOTLINYEGCROYSGRP  ILKSCCTKONLIGSSANCILLS CHIPPERCESSILLAVVILLALPVA  MCCICADEN ALPAPTMILTERSPE PROVILLANILISM CHIPPERCESSILLAV  MCC				, <del>-</del>
VVI.SHVSFWINKONVPARTSLGITTVI.TMTT.STIGHKSLEPVS YVYTADILEVSEVGY,THYPSALVEVGY,THYPSALVEVGY,THYPSALVEVGY,THYPSALVEVGY,THYPSALVEVGY,THYPSALVENDKOKOKK KNPAPTID IRPRSATIQMINATHLQERDBEYGYECLDGKDCASF PCCFBDCKTGAMHERILIRIAKHDSTARIFFPTACCLUMIVW VSILIL  1RPGYLKRVQBSPGHERGLEFPYDFIVSINSGKINKDNDTLKD LLEANVRRPVMILVSSKTLEERFISVTPSINMGGGGLLGVSIR FCSPDGANRAVHRULEVENSPALAGLEPPTSTIPSINMGGGGLLGVSIR FCSPDGANRAVHRULEVENSPALAGLEPPTSTIPSINMGGGGLLGVSIR SERLESLETBERAPELKIVYVNTDTDKCREVJITPNSANGGGGS LGGGIGVYLHRIPTRPFEGKKISLFOGMAGTFITPLKDGFTE VQLSSWPPBJLEPOTYTGIRGSLGTGLISSTY LTPNSANGGGGS LGGGIGVYLHRIPTRPFEGKKISLFOGMAGTFITPLKDGFTE VQLSSWPPBJLEPOTYTGIRGPTVEVGCHEPPTSMOSSDBAT TTAKADANSGLP PTYPLLEPQYNOSLTSYPPMGSSTLHIGIMPFTRGGIPLEQ PSTFRIPP, PTTEMSWCGULOGPTVEVGCUPLPSISMPPRILOC), APPLPESFYLEPSPTJUPSSSSAASSGELLSSLPFTSNASSBBAT TTAKADANSGLP VARNASSED VAR	i		<b>!</b>	<u> </u>
S939   66	ł	i		=
SPAPTIOIRPRINTIQMINATHIQEEDEYOYECLDGEDCASE   PCCPBDCRTGAMRHGRIHIRLAKMDSYARIPPPTAPCLYBILVYW   VSYLYL   IRRGYLKRVQENSPGHRAGLEPPYDFIVSINGSRLNKDNDTLKD   LEKANVRKPVMLIVSKYLEERETSVTPSMIMGGGGLGVSIR   FCSPDGANRAVMBULEVENSPARLAGLEPPYDFIVSINGSRLNKDNDTVMR   SERLEKANVRKPVMLIVSKYLEERETSVTPSMIMGGGGLGVSIR   FCSPDGANRAVMBULEVENSPARLAGLEPPYDTITORGROUT ITPRISANGGGG   LGGGIGVYLHRIPTRPEGKKISLFGOMAGTFITPLKOFTE   VQUSSWPPBGLSPOTTGIGLSSTPIPANASOGGG   LGGGIGVYLHRIPTRPEGKKISLFGOMAGTFITPLKOFTE   VQUSSWPPBGLSPOTTGIGLSSTPIPANASOGGGG   FFFRLER   FTTESWCGULOGEFVEROULPFISSMPPRIHCQIT   APIPPESELPSFTUVESSSAASGELLISSIPPINABSDPAT   TAKADANASILTVDVTPPTKARPTVEDRUGDSTPUSERPVSA   VANASESP   TATAKADANASILTVDVTPPTAKAPTTVEDRUGDSTPUSERPVSA   VANASESP   LEELPVINGSIVTTEVEGREPSFEDIOSILVANGGRSTPUSERPVSA   VANASESP   LEELPVINGSSGRTVESTIVATE   LEELPVINGSIVTTEVEGREPSFEDIOSILVANGGRSP   LEELPVINGSTPUSERP   LEELPVINGSVATURE   LEELPVINGSTPUSERP   LEELPVINGSVATURE   LEELPVINGSTPUSERP   LEELPVING	<b>[</b>			VVLSWVSPWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVS
FCCPEDCRTGAMRHGRIHIRIAKMDSYARIFFPTAFCLPMLVYW VSYLYL  5939  66  1404  1RRGYLKBVQRNSFGHRAGLEPFPDFIVSINGSRLINKDNDTLKD LLKANVRKPVKMLIYSSKTLBLRETSVTESHLMGCGGLIGGIR FCSPFDGANRBWHULEVESHS PAALAGLERBISDVIGADTVMNE SBDLSSLIETHBARELKIVYVRTDTDKCRVIITPRSMGCGGLIGGIGVGYLIMEPTRYPEPEGKKISLFGOMAGTFITPLKDGFTE VQLSSWMPPBLSFPGTTGIRGSLTGLSISSTT\PANSSVLSTGV PTVP\LLPPQVMQSLTSVPPBMSSSTLHLGHAMPFTRGGIPALPQ PTYP\LLPPQVMQSLTSVPPBMSSSTLHLGHAMPFTRGGIPALPQ PTTPLLPR\PTBSMGGGLVGEFVLPPGLSSMPPRHLQNI APPLPSSRIPESFTJVRSSSSAASSGLLISSLPPISNADSDPAT TTAKADAAGSILTVDVTPPTAKAPTTVEDRUGDSTPVSEKPVSAA VDANASSBP  5940  145  717  REBASRRSSPRGSAGTAVTTGTRÄGGTCLAAAHHRMRWRADGRS LEKLEVIMGIVITEVEGBEPFBDIASLVWCMAVGISYLSVDRI QGIFKRNNSKLAMPBLLQQQCBLGLGCCSKSYSPEPANSNDKDQV LICHLAVVUJSPBDKADIVTRAQDFCQLVAQKKRPTDLDVDT LAVVIJOMVULLIL  5941  13  6147  WCGGRRGSSPBSPEFBPOPPADELPFCGGSLLAVVVILLAPVA WCGCRASSBPSPEFBPOPPADELPFCGGSLLAVVVILLAPVA WCGGRRGSSPBSPEFBPOPPADELPFCGGSLLAVVVILLAPVA WCGCRASSBATCIISGDTVIMONETPICCRIPTCSLPP TITNGDFISTRARRSHNGGSVVTYRCNGSGGRRVFLEVSERSIIV CTSNDDQVGIMSGPARPCIIPMCPPPNVENSILVSDNSLFFL NEVVERRCQFGVMGFRRWKCVQLANKWRERBISGSRVCQPPPD VLHARRTQRDKNNFSPGGBFYSGERGYDLGRASASRCTPGDVMGWH VLHARRTQRDKNNFSPGGBFYSGERGYDLGRASASRCTPGDVMGWH VLHARRTQRDKNNFSPGGBFTSPDLIGBSTGCTTRGTGDPQOMG VMSSPAPTCGVISCDDFMQGLIMGRVLFFVNLGARASSRCTPGDVMGWH VERLEYPPGKANNYTCOREDBGTSPDLIGBSTGCTTRGTGDPQOMG VMSSPAPTCGVISCDDFMQGLIMGRVLFFVNLGARASSRCTPGDVMGWH VTDTQVGSRINYSCTTGRILGISSABCLISGRAAHMSTRPEIC CREVYGRPSTTCLDBLWSSPROVCRRSCKTPEDFVMGWH VTDTQVGSRINYSCTTGRILGISSABCLISGRAAHMSTRPEIC CREVTGRPSTTCLMBLWSSPGROPQCIFMCKTPDLAGGRRV FELVGBFSINSFSTLGGBFSPLIGGSRAV SRCTQCDMSPAAPTGVKSCDDFMQGLIMGRPULPPVHLQLGA SRCTQCDMSPAAPTGVKSCDDFMQGLIMGRPURCPQLIPCSPP PVIPMGRITGRYLBRVFRGQGFVMGGRRVKCQALMKMPSPLPS CSRCCPQDMSPAAPTGVKSCDDFMQGLIMGRPLPPVHLQLGA SRCTGCDGMSPAAPTGVKSCDDFMQGLIMGRPLPPVHLQLGA FPLTGSLKYKCPGBFVGRFSTCLIGGNSTFDLIGGSSTTCLIGGNSTFDLIGGSTT CHINGSPFILGSSRCUTGRACHTPSHTGGVVTTRS PPDPVMCMVHVTTDCQUSSRINYSCTTGRIBLIGGSSACUTGSCWT PPDPVMCMVHVTTDCQUSSRINYSCTTGRIBLIGGSSACUTGSCWT CHILGSGGRVPFILVGBFSTYCTGSHDQWGTMSGPAPQCII PING TPRISKLYF	1	i	]	YVTAMDLFVSVCF1FVFSALVBYG\TLHYFVSNRKPSKDKDKKK
FCCPEDCRTGAMRHGRIHIRIAKMDSYARIFFPTAFCLPMLVYW VSYLYL  5939  66  1404  1RRGYLKBVQRNSFGHRAGLEPFPDFIVSINGSRLINKDNDTLKD LLKANVRKPVKMLIYSSKTLBLRETSVTESHLMGCGGLIGGIR FCSPFDGANRBWHULEVESHS PAALAGLERBISDVIGADTVMNE SBDLSSLIETHBARELKIVYVRTDTDKCRVIITPRSMGCGGLIGGIGVGYLIMEPTRYPEPEGKKISLFGOMAGTFITPLKDGFTE VQLSSWMPPBLSFPGTTGIRGSLTGLSISSTT\PANSSVLSTGV PTVP\LLPPQVMQSLTSVPPBMSSSTLHLGHAMPFTRGGIPALPQ PTYP\LLPPQVMQSLTSVPPBMSSSTLHLGHAMPFTRGGIPALPQ PTTPLLPR\PTBSMGGGLVGEFVLPPGLSSMPPRHLQNI APPLPSSRIPESFTJVRSSSSAASSGLLISSLPPISNADSDPAT TTAKADAAGSILTVDVTPPTAKAPTTVEDRUGDSTPVSEKPVSAA VDANASSBP  5940  145  717  REBASRRSSPRGSAGTAVTTGTRÄGGTCLAAAHHRMRWRADGRS LEKLEVIMGIVITEVEGBEPFBDIASLVWCMAVGISYLSVDRI QGIFKRNNSKLAMPBLLQQQCBLGLGCCSKSYSPEPANSNDKDQV LICHLAVVUJSPBDKADIVTRAQDFCQLVAQKKRPTDLDVDT LAVVIJOMVULLIL  5941  13  6147  WCGGRRGSSPBSPEFBPOPPADELPFCGGSLLAVVVILLAPVA WCGCRASSBPSPEFBPOPPADELPFCGGSLLAVVVILLAPVA WCGGRRGSSPBSPEFBPOPPADELPFCGGSLLAVVVILLAPVA WCGCRASSBATCIISGDTVIMONETPICCRIPTCSLPP TITNGDFISTRARRSHNGGSVVTYRCNGSGGRRVFLEVSERSIIV CTSNDDQVGIMSGPARPCIIPMCPPPNVENSILVSDNSLFFL NEVVERRCQFGVMGFRRWKCVQLANKWRERBISGSRVCQPPPD VLHARRTQRDKNNFSPGGBFYSGERGYDLGRASASRCTPGDVMGWH VLHARRTQRDKNNFSPGGBFYSGERGYDLGRASASRCTPGDVMGWH VLHARRTQRDKNNFSPGGBFTSPDLIGBSTGCTTRGTGDPQOMG VMSSPAPTCGVISCDDFMQGLIMGRVLFFVNLGARASSRCTPGDVMGWH VERLEYPPGKANNYTCOREDBGTSPDLIGBSTGCTTRGTGDPQOMG VMSSPAPTCGVISCDDFMQGLIMGRVLFFVNLGARASSRCTPGDVMGWH VTDTQVGSRINYSCTTGRILGISSABCLISGRAAHMSTRPEIC CREVYGRPSTTCLDBLWSSPROVCRRSCKTPEDFVMGWH VTDTQVGSRINYSCTTGRILGISSABCLISGRAAHMSTRPEIC CREVTGRPSTTCLMBLWSSPGROPQCIFMCKTPDLAGGRRV FELVGBFSINSFSTLGGBFSPLIGGSRAV SRCTQCDMSPAAPTGVKSCDDFMQGLIMGRPULPPVHLQLGA SRCTQCDMSPAAPTGVKSCDDFMQGLIMGRPURCPQLIPCSPP PVIPMGRITGRYLBRVFRGQGFVMGGRRVKCQALMKMPSPLPS CSRCCPQDMSPAAPTGVKSCDDFMQGLIMGRPLPPVHLQLGA SRCTGCDGMSPAAPTGVKSCDDFMQGLIMGRPLPPVHLQLGA FPLTGSLKYKCPGBFVGRFSTCLIGGNSTFDLIGGSSTTCLIGGNSTFDLIGGSTT CHINGSPFILGSSRCUTGRACHTPSHTGGVVTTRS PPDPVMCMVHVTTDCQUSSRINYSCTTGRIBLIGGSSACUTGSCWT PPDPVMCMVHVTTDCQUSSRINYSCTTGRIBLIGGSSACUTGSCWT CHILGSGGRVPFILVGBFSTYCTGSHDQWGTMSGPAPQCII PING TPRISKLYF	1	ļ	}	KNPAPTIDIRPRSATIOMNNATHLOERDBEYGYECLDGKDCASF
VSTLYL  IRPGYLKEVQENSPGHEAGLEPPEDFIVSINGSRLAKONDYLKD  LIKANVERPVOMI.1YSSKTLERIESTSVTFENLAGGGGLIGVSIR  FCSPOGANERVONIVLEVESNSPAALAGLERPISDYLIGHTYMEE  SEBLESLIETHEARCHLIKLYVANTOTIONGERPISDYLIGHTYMEE  SEBLESLIETHEARCHLIKLYVANTOTIONGERPISDYLIGHTYMEG  LIGGIGVGYLHRIPTEPPEBGKKISJPGGGAGTPITPLKDGFTE  VQLSSWNPPSLSPOTTGIEGSJUTGISISTPJANSSVSLTGV  PTPY_LLPPQUNGSLTSVPPBESSYLHILGEMPTETGGJPFLEPQ  PTTPY_LLPP_PTHSMPCVGLYDEPVKSSYLHILGEMPTETGGJPFLEPQ  PTTPYLLPP_PTHSMPCVGLYDEPVKSSYLHILGEMPTETGGJPFLEPQ  PTTYLLPP_PTHSMPCVGLYDEPVKSSYLHILGEMPTTGGJPFLEPQ  PTTYLALPP_PTHSMPCVGLYDEPVKSSSAASSGELLSSLPPTSNAPSDDAT  TTAKADAASELTTUDVTPPTAGAPTTVEDRVGGSTFVSKRVSAA  APLPLPSEFLPSPPTLVPESSSAASSGELLSSLPPTSNAPSDDAT  TTAKADAASELTTUDVTPPTAGAPTTVEDRVGGSTFVSKRVSAA  VANANSESS  LEKLPY-MEGLYTTEVGGRPSSPDIASLVVCMAVGISYISVYDH  QGIFKRNSRIMDBILKQQQELIGJDCSKYSPBPANSINDXDOV  LICHGLAVAVISPBGGRADTVARAQDFCQLVARKORRPTDLDVDT  LA\VYLVQMVVLLIL  5941  13  6147  MCLGRBGRSSBESBESPUPPADAGTCCGGSLLAVVULIALPVA  MCGCRAPBK, LPPARPTHLIDBERFPIGTYLINVECRECPGSGRP  SILCLKNSVMTGAKORCREKSCRNPPDPVNCMVULVLALPVA  MCGCRAPBK, LPPARPTHLIDBERFPIGTYLINVECRECPGSRPP  TTINGDFTSTMRRNPPIGSVVTTCNPGSGGRKVFTGLUGFGSGR  IKVSCTRCYRLIGGSSATCI ISGDYT UNDNFFFICOR IPCGLPP  TTINGDFTSTMRRNPPIGSVVTTCNPGSGGRKVFTGLUGFGSGRP  TONDDGVGTMSGPAPCCI IBNCTPPNVRGVLFGGGRSWESTCDGLPPD  VILHBERTGRDKNPSPQGBVPYSCEPGYDLIGGASMRCTPQGDN  SPAAPTCSVKSCDDFMGQLIMGRULPPVNLQLGAKVDFVCDGEF  QLKGSSASYCVLAGMESLMNSSVVCEQIFCDSFPVI INGRHTO  KPLEVPPFRGRAVNYTCDHDPGTSSTDLIGESTITCTSDPQGNN  VMSSPAPRCGSTLAHCQAPDHFLFAKLKYQTMASDP INGRHTMSHPTKPJ  CORIPCGLPFTIANGFTSTRINSPRVGSVVTYCNPGGGRKV  FELVGEPSITCLBLVMSSPROUGHTSCSCTTPPDVNMVM  VITDIQVGSRINYSCTTCHRLIGESSACCILGSTAHMSTKPPLES  CRRVQQPPPDVLARRTGRONDMSSPGOVYTSCBGGTKV  FELVGEPSITCLBLVMSSPROUGHTSCSCTTPPDVRMGHL  VSNNSSLESILNEVVERCQDFFVMSPRRVKCQALMNSSPRVCGBGRKV  FELVGEPSITLEVERCRBPTYGRNDFFGCGCTRKSCCTTPPDVRMGHL  VSNNSSLESILNEVVERCQDFFVMSPRRVKCQALMNSSPRVCGGRKSCCTT  PDPDVMGWVRITTD;QVGSRRNYSCTCHRIGHTGNACC  TAMSTEPPI-TAMOGTSTTANSNPSPVCGGTRKSCCTT  PDPDVMGWVRITGDRNSSPROUGHTRKSCCLITPRICCOL  THENSTEPPI-TIANGESTSTANSVVTCDPHD	i	l	İ	
1404  1RPGYLKBYDENSEGHENGLEPPPDFIVSINGSELDKUNDTYLKN LLKANVERPVKMLIYSSKTLELRETSYTPSMLOGQGILJOVSIR FCSFDGARBRYMBIVLEVESNS PAALJAGLEPBISDY IIGADTYMME SEBLESLIETHERACHLKLYVYNTDTDNCERVIITYBRAGGEGS LGGGIGVGYLHRI PTEPFERBEKKISLPGCHAGTFITPLKOGFTE VQLSSWNPPSLISPGYTGIEGSLIGLSISSTP\PAVSSYLSTGY PTPY\LLEPGYMOSLITSYP PHERSYLHLIPMPTRGGLPATLPQ PSTFWLPR\PTHSWPGVGLYQEFVKPGVLPPLSSMPPRALPGAI ARLPUSSFLESTPLVPBSSSAASSGELLSSLEPTSMAPSDPAT TTAKADAASSESP REASREASPRQSAGTAVITGTRAGGTCLAAAHHRMWRADGRS LEKLEVENGLVITSVORPSSPSDLASLVVMCMAVGIYSTYSVDR GGIFKRNNSRLMBELLKQOGELIGLDCSKYSPBRANSNDKODQ LIKCHLAVKVLSPEDGKADIVRAAQDFCQLVAQKKRPTDLDVDT LA\VYLVMWVLLIL GUIFKRNSRLMBELLKQOGELIGLDCSKYSPBRANSNDKODQ LIKCHLAVKVLSPEDGKADIVRAAQDFCQLVAQKKRPTDLDVDT LA\VYLVMWVLLIL GUIFKRNSRLMBELLKQOGELIGLDCSKYSPBRANSNDKODQ LIKSGCTKGYRLIGSSSATCI ISGDTVINDMFTELGREGGERF SIICLKNSWWTGAKDCRSKSCSNPPDPUWGUVIKGRGGGSGRV FILTNSDPISTMRENFHYGSVVTYRCNPGSGGRKVFELVGRESI UKYSCFKGYRLIGSSSATCI ISGDTVINDMFTELGRECHPGGINF CRESSASSCVLAAMBESLMNSSVPVCGGLTDLGGASMRCTPQDDW VIHABETTGNKDMFSHGGGWYTYSCBCDTLLGGASMRCTPQDW SPRAPTCSVKSCDDPWGQLLMGRUFPVNLQLGAASMCTPQDW VMSSPAPTCSVKSCDDPWGQLLMGRUFPVNLQLGAASMCTPQDW WSSPAPTCSVKSCDDPWGQLLMGRUFPVNLQLGAASMCTPDGWO WSSPAPTCSVCVLAAMBESLMSSVPVCGGLTPGTSLATE CREYYGRPFSITCLDNLWSSPKDVCKRKSCCTPPDPVNMWH VITDIQVGSKINYSCTVCHRILIGBSABCILISGNAHMSTKPPI CGRIPGGPFTIANGDFISTMRNPHYGSVATCRCGGGRKV PELVGBPSIVCTSNDDQVGINSGFAPQCI IPNKCTPPDVRMGHT VSDNRSLFSINEVPFRCQPGFVMKGCTHPDFNGTSFPLIGGSTI RCTSDPQOMSPAPTCSVKSCDDPWGQLLMGRUFPVNLQLGA KVDPVCDEGFQLLWSSASSYCVLAAMBESLMNSSVPVCGGI FCFSF PVLPRGRITCKPLEVPPFGKANYTCDPHDRGTSFPDLIGGSTI RCTSDPQOMSPAPTCSVKSCDDPWGQLLMGRVFTCRPGGGRKV PELVGBPSIVCTSNDDQVGINSGFAPQCI IPNKCTPPDVLNGGA KVDPVCDEGFCLLGGGSGACCTPOLIGGSTI RCTSDPQOMSPAPTCSVKSCDDPHROGLINGSVLPPNLIGGSTI RCTSDPQOMSPAPTCSVKSCDDPHROGLINGSVLPPNLIGGSTI RCTSDPQOMSSAPPRCGI LLGGCADPHRYRKQA LIKWEPBLPSCSRVCQPPPSILTGGBNTSSSPVVCGGI FCFSF PVLPNENGILTGNNSSSPDVCGTRKSCCATARSLAKTOTAASG PPIGTSLKYRCRPBTYGRPSITTCTDHQGVGINGGCPAQCI IPNK CPLGGRGRKVFELVGGBSITCTCTDHQGVGINGGCPAQCI IPNK CPLGGRGRKVFELVGGBSTTCTCTDHQGVGINGGCPAQCI IPNK CPLG	1	ļ	[	
LIKANURRPVMMILYESKTIRLERTSUTPSNIHMEGGLIGUSTIR PCSPCAMBENNIHULEVSENS PARLAGICAPHSDYTIGADTUMNE SEDLFSLIETHERAPLKLYVYNTDTDNCREVITTPNSAMGGEGS LIGGIGNGYLHRIPTRPPEBGIKKISJPGOMAGTPITTPKOGFTE VQLSSUNPPSLISPOTTGITEDSLITGGISTSTYPRAVSSVLSTGV PTDY\LLPPQVNQSLTSVPPMESSYLHILGIMPTRGLIPRILOY PSTFNLEPP\PTESMCVGLYGPVKGGVLPPLSSMPPRNLEG\X ADLPPSEKPLSPPTUPESSSAASSGELISSLPPTSNABSDPAT TTAKADANSSITTDVTPPTAKAPTTVEDRVGDSTPVSEKPVSAA VDANASESP  5940  145  717  RREASERSPPQSGAGTAVTGTRAGGTCLAAAHHRMWRADGRS LEKLEVENGLUTTEVEQSPSSDIASLVVMCMAVGISYISYUDH QGIFKRNNSRLMDBILKQQQELIGIDCSKTSPEPANSHOKDQDV LKCHLAVAVISPBDGRADIVARAQDPCQLVAQKOKRPTDLDVDT LA\VILVOMVULLI  6147  MCCHREMGSSSPSSPSDEVGDPAPCLPPCGGSLLAVVVLLALPVA MCQCHAPEN\LPPARPTMLTDEFEPPIGTYLNVECRPGYSGRPP SIICLKNSVMTGAKORGREKSCRNPPDFVNGWHVIVGLOGPSG IKVSCTKOSYHLIGSSSATCI ISGDVI UNDMSFPICORI PCGLPP TTINGDPISTMRENPFRYGSVUTTKCPGSGGRKVFELVSEFSIY CTSNDDQVGIMSOPAPCLI IPNKCTPPNVENGILVSDNRSLFSI NEVVERKCDGFFWMSPRIVKCOALNKWEPBLBSSCRVQDPPD VHIABETORUKNPSHGGBVYSCBECTULGGSTIRCTSDPQOM SPAAPTCEVKSCDDPMGLLINGRVLFPVNLQLGAKWDZVCDEGF QLKGSSASYCVLAGMESLMNSSVPVCBQI PCESFEVI INGRITTO KLEVPPGKAVNYTCDHPDRGTSFDL IGESTITACTSDPQOM VMSSPAPRCGILGHCQAPDHFLPAKLKTQTNASDPF ITSIKKTE CPRFYYGRPFSITCDLNIVMSSPKDVCKRSCKCTPPDFVNGWH VTDJQVGSRINYSCTYCTRILIGESTARCTSDPQOM VMSSPAPRCSILLSHVVERFRQDGFFWMSPRRVKQALNKWEPBLES CSRVQOPPPDVLARRTGDRAWSPRODENSSPRVEGGGRKVEPPLIGIGKT PELVGRPSIICTDLNIVMSSPKDVCKRSCKCTPPDFVNGWH VTDJQVGSRINYSCTYGRNDFFSGGGRVYTCDHDGGGGRKV FELVGRPSIICTDLNIVMSSPKDVCKRSCKCTTPPDFVNGWH VTDJQVGSRINYSCTYGRNDFFSGGGRVYFCCBGFTDLAGAA KVDFVCDEGFQLKGSSASYCVLAGMESLMNSSVPVCEQIFCPSF PVLPMGRITGKPLRVPPPGRANDSPRFTSTRSNFHYGSVVTYR CRIGSGGRKVPELVGRPSITCTENDDQUGINGSVLPPNLIGESTI RCTSDPQGMGVWSSPAPRCGILGHCQADDHFFPAKLKTQTNASD FPIGTSLKYRCERBYYGRPSTTODDQUGINGSVLPPNLIGGSTI TARBSTRP FTCGQIR FOGGPFT IANGBTT STRSNFHYGSVVTYR CRIGSGGRKVPELVGRPSTYCTENDDQUGINGSVLPPNLYGCA LEKWEPBLPSCSRVCQPPPBILLGGBSTRYCTGCDHGRVCAD LEKWEPBLPSCSRVCQPPPBILLGGBRSTANSSPRVCGARSCLISHENG LEKWEPBLPSCSRVCQPPPBILLGGBRSTANSSPRVCGARSCLISH LEKWEPBLPSCSRVCQPPPBILLGGBRSTANSSPRVCGARSCLISHENG	5030		1404	
### SEGLPSLIETHEAKPLKLYVYNTOTDNCREVITTPNSAMGGGS LGGGIGVSTLERTPTRPEBGKKISLPGANGTPITTPNSAMGGGS LGGGIGVSTLERTPTRPEBGKKISLPGANGTPITTPNSAMGGGS LGGGIGVSTLERTPTRPEBGKKISLPGANGTPITTPNSAMGGGS PTVP\LLPGVONGSLTSVPPMESSYTHLEGHPTTGGERFLCQ PTTP\LLPGVONGSLTSVPPMESSYTHLEGHPTTGGERFLCQ PTTP\LLPGVONGSLTSVPPMESSYTHLEGHPTTGGERFLCQ PSTFALLPG\PTHSWFGVGLYGEVURGVLPPLSSWPPRALCQ PSTFALLPG\PTHSWFGVGLYGEVURGVLPPLSSWPPRALCQ APPLPSEFFLPSPFULPSSSAAGSGGLEDPTNADSDPAT TTAKADAASGLTUDVTPPTAKAPTTVEDRVGDSTPVSEKPVSAA VDANASGSP SERSASRSPPGGSGTAVTTCTRÄGGTCLAAAHHRMWRADGRS LEKLEVHGUVTTBVGQRPSFBIDLSLVVNCMAVGISTISVYDR GGFFKRNSKIMDBLIKQGGELIGLGCSKASPSPRANSINKDDQV LNCHLAVKULSPEDGKADIVRAAQDFCQLVAQKGKRPTDLDVDT LA\V1VQMVVLILI  ### MCGCRADEN\LPPARPTMLTDERFFPIGTTINVEGFGSCRPV SICLKNSVWTKCANGGRSKSCSRPPDPVORCWEVIKGIGFGSS IKYSCTKGVHLIGSSSATCIISGDTVINNTSTPICLDFCGLPP TTUNGDFISTMRNPHYGGKVTTKCANGGGRKVPELVGSBPS IKYSCTKGVHLIGSSSATCIISGDTVINNTSTPICLDFCGLPP TTUNGDFISTMRNPHYGGSVTVTKCANGGGRKVPELVGSBPSIY CTSINDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NKVVERCQGGFWMSGRRVCXCALRGASMRCTPQDDN SPAAPTCGVKSCDDFWGGLAMGKWFPULGGASKMRCTPQDDN SPAAPTCGVKCANGSRRVKVCALRGASSMRCTPQDDN SPAAPTCGVKSCDDFWGGLAMGKWFPULGGASKMRCTPQDN SPAAPTCGVKSCDDFWGGLAMGKWFPVALGGASKMRCTPQDN WWSSPAPRCGILGHCQAPDHFLPAKLKTYTNASDPFIGTSLKYE CREYYGRPSITCLDNIVMSSPROVCKRKSCTEPDPVNMVH VITDLQVGSRINYSCTTGHELIGHSSARCIISGARMKTPPPI CGRIPGGFPTIANGDFISTMRNPHYGSVCALRKWESTPPLIGGAA KVDFVCDEGFGLKGSSASYCTAMGSBARGVFCDGGGRK FELVGRPSITCTSNDDQVGIMSGAPQCIIPNKCTPPVRMGHIL VSDNSLFSLEBBVFFRCODFFVWGGLAMGSVPPUGGGRK FELVGRPSITCCHMINTSPROPGSGRKV FELVGRPSITCTSNDDQVGIMSGAPQCIIPNKCTPPVRMGHIL VSDNSLFSLEBBVFFRCODFFVWGGARMSSVPVCGGTFCFS PVIPMGRHTGKFLBVFFFGGDFVANGFFRKYGGAVTXCHGGGRK FPLYGRPSITCTSNDDQVGIMSGAPAPCCIIPNKCTPPULGGAA KVDFVCDEGFGLKGSSASYCVLAMMESLMNSSVFVCGGTFCFS PVIPMGRHTGKFLBVFFFGGBFVTANGDGVGIMSGVPPAGCIIFNKC TPPNVENGILTGNNSSPFDTIANGDFISTNSNFFYGGVVTTA CRIGSGGRKVFELVGGBSTVCTSNDDQVGIMSGPAPQCIIFNKC TPPNVENGILTGNNSSPFDTIANGDFISTNSNFFYGGVVTTA CRIGSGGRKVFELVGGBSTVCTSNDDQVGIMSGPAPQCIIFNKC TPPNVENGILTGNNSSDFSIGNEVVFFCCPGDFWGGFFRXGCALGCDHERU LHKWEPBLPSCSRVQPPPSILGG	ودرد	1 00	1303	<u> </u>
SERLIFSLIETHERAPLELIVUMYDTDNORGRUTITDNSAMGGISGS LGCGIGYGYLIRIPTRPFEEGKKISLPGQAGTPITPLKDGFTE VQLSWNPPSLSPRGTTGIEQSLTGLSISSTY\PAVSSVLSTGV PTVP\LLPPQVNQSLTSVPPMESSYLHLEGLMPFTRQGLWALPQ PSTFMLPR\PTHSMEQGIJOSFVVPHESSSYLHLEGLMPFTRQGLWALPQ PSTFMLPR\PTHSMEQGIJOSFVVPHESSSMPPSLDG\I ADLPLESEFLBSPFLVPBSSSPASGELLSSLPPSNAPSDPAT TTAKADAASSLTVDVTPFTAKAPTTVEDRUGDSTPVSEKPVSAA VDANASESP SHARDLAVTTTGTRAGGTCLAAAHRMRMRADGBS LERLPYHMGLVITTVEQBPSFBOILSLVVNCNAVGISTISVTDH QGIFKRNNSRIMBELLKQQGELIGLDCSKTSPFFANSNDKDDQV LNCHLAVKVLSPBDGKADIVRAAQDFCQLVAKKKPPTDLDVDT LA\VILDYDMVVLILI  5941  13 6147 MCLGERGASSPESSEVGPPAPGLPFCGGSLLAVVULLALPVA MCGCNAPSKA\PPAPFHNIDDSFBPTGTTIANFCRPGYSGRP SILCLKNSVWTGAADKCREKSCRNPPDPVWSWHIVIKGIQFGSQ IKYSCTKSYRLIGSSSATCLISGDTVTGTTANBEFICCRIPTCGLPP TITNODPISTMRNFHYGSVVTYRCNNGSGGRKVFELVGGPSTY CTSNDDQVGINSGPAPCLIINGKCTPPNVSNGILNDSNRSLFSL NEVVERFCQPGFVMKGRRVKCQAINKBPELDSCRVCOPPD VHARRTORDKOMPSPGGRVFYSCBPGYDLRGAASMCTTPQGDW SPAAPTCZEVRSCDDPMGJLLAGRLFPGTLGAASMCTTPQGDW SPAAPTCZEVRSCDDPMGJLLAGRLFPGTLGAASMCTTPQGDW SPAAPTCZEVRSCDDPMGJLLAGRLFTGTBLTGSDQGNG VMSSPAPRGGILGHCQADPHTPFARLITQTNNSDPFIOTSIKTE CRPEYYGRPFSITCLDNLWSSPROVCKRKSCTTPDPVNSMGIL VSDNRSLFSLESUSVETCRGRLGGISGAGTLGSNAARMSTRPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGERPSITCLDNLWSSPROVCKRKSCTTPDPVNSMGIL VSDNRSLFSLESUSVETCRQPGFVMKGFRKYCQAINKREPELPS CSRVCQPPPDVLIAABRTQRDKDNPSPGQBVFYSCBPGTDLAGAA SWRCTPQGDWSPAAPTCEVKSCDDFMGLIAGRVLPPVNLQAIA KVDFVCDBGFQLKGSSASYCVLAGMSELMNSVPVCBQIFCPSP PVIPMGRITTGCPLEVPFFGKAVNTTCDPHDERSTFDLLGGST RCTSDQGGWSSPAAPTCEVKSCDDFMGLIMGRVLPPVNLQAG KVDFVCDBGFQLKGSSASYCVLAGMSELMNSVPVCBQIFCPSP PVIPMGRITTGCPLEVPFFGKAVNTTCDPHDERSTFDLLIGGST RCTSDQGGWSSPAAPTCSVSCDDFMGLIMGRVLPPVNLQAG KVDFVCDBGFQLKGSSASYCVLAGMSELMNSVPVCBQIFCPSP PVIPMGRITTGCPLFEVPFFGKAVNTTCDPHDERSTFDLLIGGST RCTSDGGGWSSPAAPTGCFGVSCCDDFMGLMRSPFLCSVCT PPDVPMGRITTGCPLFEVPFFGKAVNTTCDPHDERSTFDLLIGGST RCTSDGGGWSSPAAPTGCTGKSCCDTFLGGSVTTA	l	1		
LGGGIGYGYLIRL PIRPPEGRKISLPGQMAGTPTTPLKDGFTE VQLSSVNPPSLSPPOTTGIEQSITGLSISTYP PAVSSVLSTGV PTVP\LLPPQVNQSLTSVPPMSSSIALICHEMPTRGSLFNLPQ PTTFNLPR\PTHSWGGGLYGSFVRPGGLPGLSSPPRNLPG\I APLPLPSSEPLSPFULPPSSSAASSELLSSLPPTNNAPSDPAT TTAKADAASGLTVDVTPTAKAPTTVEDRUGDSTPVSEKPVSAA VDANASGSP SPAU  145  717  REGARSASPRQSAGTAVTTGTRAGGTCLAAAHHRMRWRADGRS LBKLPVHGGLVITTVEGPEPSBIASLVVNCHAVGISTISVYND QGIFKNNSRIMDBILLAQQBILGGLOSKYSPPANSDKODQV LNCHLAVKVLSPBGBGRADIVTAQQDFLGLGCKYSPPANSDKODQV LNCHLAVKVLSPBGBGRADIVRAQDFCQLVAQKOKRPTDLDVDT LA\VTLVQMVVLILI  5941  13  6147  MCIGRRGASSPRSSEPVGPPAPGLPFCCGSSLLAVVVLLALPVA WGCNAPSR\LPPARPTNLTDERBEPIGTTLNYECRPGYSGRPP SIICLKNSVWTGAKDRCRKSCRNPPDPVNAWNVIVIKGIQFOSQ IKYSCTKSYRLIGSSSRTCIISGDIVLWONSTPICDRLPGGSEP TTTNODPISTMRKNFHYGSVVTYTRCNGSGGRKVFLVGSFSIY CTSNDQVGINSGPAPGCIIPNKCTPPNVSNGILVSDNRSLFSL NEVURPKCOPGFVMKGFRVKCOALNEMBERLSSRNCCUPPDD VLHARETQRINDNSPPGGBVFYSCERGYDLGGASMRCTPQDDW SPAAPTCSVKSCDDFMQLLMGRVLFPVNLQLGAKVDFVCDGGF QLKGSSASYCVLAGMESLMNSSVPVCRQIFCEPSPVIFNGHTGS KPLEVVP FERVANNTTCDPHDPRGTSFPVIFNCHSTPVIFNGHTG KPLEVP FERVANNTTCDPHDPRGTSFPVIFNCHSTPVIFNGHTG KPLEVGPSITYCTSNDDVGINGSPAPGCIIPKCTPPDFVGRMUH VTDTQVGRSINTSCTTGRILLGISSACCILSCANARWSTVFPI CGRIPGGPPTIANGDFISTNRENPHYGSVVTYRCNGGGGRKV PELVGRSTSTYCTSNDDVGINGSPAPGCIIPKCTPPDFVRSNGIL VSDNRSLFSLNSVVFRCQDFFVMKGPRVKCQALNKWEPELPS CSRVCQPPPDVLARBTQRDKDNFSPGGBVFYSCGFCFDLRGAA SKRCTTPQGOMSPAPAPCEVKSCDDFMGQLINGRVLFPVNLQLGA KVDFVCDGGFQLKGSSASYCVLAGMESLMNSSVPVCRQIFCESP PVIPNGRHTGKFLEVFFFKAVNYTCDPHDPRGTSFDLIGESTI RCTSDPQGNGWSSPAPRGGILGGCADDFFLFALKTQTNASD PPIGTSLKYECRPSYGRPSTTCLDNIVWSSPKOVCKRKSCKT PPDPVNGNGTHYTTD, OVGSR TNYSCTFRALGHSSSSTLIGST TAHMSTKPPICQRIPCGRFTYGRDPSTTRNSHFYGSVVTYR CALGSGRKVFELVGSSSTSTCTSKDDQVGWGRFRAPCCIIFNKC TPPNVNGILFLUNDNSSLEJSLANVVERGCDFFLGGSTILGGN TAHMSTKPPICQRIPCGBSPTYCTSKDDDVGWGRFRAPGCIIFNKC EFFONLOGGSRKVFELVGSSSVSCVARGDDFLFGCDFVYNGG LAWWEBBLPSCSRVCQDPPEILHGGHTPSGODNTSSPGGEVTYSC ERGOLDGASALHCTPQGDMSPEAPGCAURGCDFILGOLPHGRV	ĺ			
VQLSSWNPSILSPOTTGIEQSLTGLSISSTV_PAVSSVISTGY PTVP\LLPPQVNQSLTSVPPMESSYLHELGNPTTRQGLPNLPQ PSTFALPP\LPPQVNQSLTSVPPMESSYLHELGNPTTRQGLPNLPQ PSTFALPP\LPPGSSSAPSGELLSSLPPSNAPSDPAT TTAKADAASSITUTUTEPTAKAPTTVEDRUSTPVSEKPVSAA VDANASESP  5940  145  717  REASERSAPRQSACTAVTTGTRAGGTCLAAAHHRMRARADGRS LEELPVSMSIVITTSVEQEPSPSDLASLVVNCNAVGISISVYDH QGIFKRNNSRLMDELLKQQQELIGLDCSKYSPFANSDRDDDV LAVVIVVDNVVLLILI  6147  MCLGRMGASSPESPEPUPPAPGLPFCCGCSILAVVVLLALPVA MCQCAADEM\LPPARPTNITDERSPPIGTTLANYECREPGYSGRP SILCLKNSVWTGAADRCREKSCRNPPDPVMGWVHIVKGIQFGSQ KYKSCKYSTRLIGGSSATCIISGDVYLUDMETPICDRITPGCSPP TTTNGDPJSTMRRMFHYGSVVTYRCNPGSGGRVVELVGSFSIY CTSNDDQVGIWSGPAPCLIPNKCTPPIVVERGILVSDNRSLFSL NRVEFRCQPGFVMKGPRVKCQALNKWEBELPSSRVCQPPPD VIHABRTQRDKDMFSPGQBVFYSCBFCYDLRGAARMCTPQODN SPAAPTCSEVSCODFMGLIAGRULFPVNLQLGARVDPVCDBGF QLKGSSASYCULAGMESLMNSSVDVCBQIFCDSPPVIFNLHGARVDPVCDBGF QLKGSSASYCULAGMESLMNSSVDVCBQIFCDSPPVIFNLHGARVDPVCDBGF QLKGSSASYCULAGMESLMNSSVDVCRGIFCSTDVIFNSMTFPPI VPDQVGRSTNYSTCTGRRLIGHSSAFLGTSNAMMSTFPPI CQRIPCGLPPTIANGDFISTNENFHYGSVVTYRCNPGSGGRKV FELWGEPSIVCTSTDDQVCIMBGPAPCIIFSTNETSDPVGMSMM VMSSAPRCGILGHCQAPDHFLFAALKTQTNNSDPFIGTSLKTE CRPEYYGRPFSITCLDNLWSSPRWVCKRECTTPDPVMSMMM VTDTQVGSRINYSCTFGRRLIGHSSAFLSSANAMMSTFPPI CQRIPCGLPPTIANGDFISTNENFHYGSVVTYRCNPGSGGRKV FELWGEPSIVCTSTDDQVGIMSGPAPQCIIFMKCPPNVSMGIL VSDNRSLIFSLINEVEFRCQPGFVMKGQARVKCQALNKWEPELPS CSRVCQPPPDVLHABRTQGDKDNPSPGQBVFYSCGPGTDLRGAA SKRCTQGGDMSPAAPTCEVKSCDDPMGQLIMGRUP.PPVNLQLGA KVDEVCDEGFQLKGSSASYCVLAGMESLMNSSVPVCBQIPCPSP PVIPNGRRITGKPIEVFPFGKAVNTTCDPHDBRGTSFDLIGGSTI RCTSDQGGMWSSAPAPGGILGHGADPBFLFFALKTVTNASD PPIGTSLKYECRPSYGGPPSTCTGNDDQVGIMGGPAPQCIIPNKC TPPNVENGTLVSDNSLIFSLANVVBRGCFVMKGCGTFVNLAGA  FRACTEQGGWSSAPAPGGILGHGADPSFFDLIGGSTI RCTSDQGGWSSAPAPGGILGHGADPSFFALKGSVYTR CRIGSRGRKVPELWGSPSTYCTSNDDQVGIMGGPAPQCIIPNKC TPPNVENGTLIVSDNSLIFSLANVVBRGCFVMKGCGRPWKCQA LINKWPBLPSCSRVCQPPSILHGBHFSSNODHSGCGEVYSC EPGYDLRGAASLICTTQGDMSPBAPRCAVKSCCDDFLCOLPRRV LEPLMLQLGARVSFVCDBGFFLKGSSVSHCVLVGMRSLMNNSVP	1		1	
PTTP\LLPPCWQSLTSYPPMESSYLHEGLMPTTRGSLPNLPQ\ PSTFNLPR\PTHSWPGVGLYQEPVLPPLSSMPPRNLPG\I ATLPLESEFLESFLVPESSSASSGELLSSLPPTSMAPSDPAT TTAKADAASSITVDVTPPTAKAPTTVEDRUGDSTPVSEKPVSAA VDANASESP  5940  145  717  RESASRSASPRQSAGTAVTTGTRAGGTCLAAAHHRMRWRADGRS LEKLPV:MSILVITEVEGEPSFSDLASLVWGCMAVGISYISVTPH QGIFKRMSRLMDEILKQQGELIGLGCSKYSPEPRAMSNDKDDQV LNCHLAVKVLSPEDGKADIVRAAQDFCQLVAQKQKRPTDLDVDT LAVYLVLYOWVLILLI  5941  13  6147  MCLGRMGSSPESPEPVGPPAPGLPFCCGSLLAVVVLLALPVA WGCMAPEN\LDPARPTNLTDEFFFIGTYLNYEGRPGYSGRPP SICLKINSWMTGAKDKCREKSCRPPDPVNGWLWIVKIGLQGGG IKYSCTKGYRLIGSSATCIISGDTVINDMFPICDRIPGGLPP TITNGDPISTNRENPHYGSVVTYRCNPGSGRKVPELVGEPSIY CTSNDDQVGINSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSI NEWVERRCQPGGVMKGPRRVKCQALMKWEPELPSCSRVCQPPPD VHAREKTQDKOMPSPGGBVYVEQVFPCDEFFVLTNGRHTG KPLEVFPFGKAVNTTCDPHDPDGTSFDLIGBSTIRCTSDPQOMG VMSSPAPTCEVKSCDDFMOQLLMGRVLFPVNLQLGAKVDFVCDEF QLKGSSASYCVLACMESLMNSSVPVCEQIFCPSPPVI NICRHTG KPLEVFPFGKAVNTTCDPHDPDGTSFDLIGBSTIRCTSDPQOMG VMSSPAPTCSVKSCDDFMOQLLMGRVLFPVNLQLGAKVDFVCDEF CORIPCGLPFTIANGDFISTNRENPHYGSVVTYRCNPGSGRRV VTTDLQVGSRINYSCTTGRRLIGHSSARCILSGRAAHMSTKPPI CORIPCGLPFTIANGDFISTNRENPHYGSVVTYRCNPGSGRRV FELUGRBFSITCLDNLVWSSPRDVCKRSCKTPPDPVNSMGIL VSDNRSLFSLNBVVEFRCQPGFVMKGPRVKCQALNKWEPELPS CSRVCQPPPDUHABERTQRKDNFPSGGRVYCGQIFCPSP PVIPNGRHTGKPLEVFSCDDFMOQLLMGRVLFPVNLQLGA KVDPVCDEGFQLKGSSASYCVLAGMESLMNSSVPVCRQIFCPSP PVIPNGRHTGKPLEVFSCDDFMOQLLMGRVLFPVNLQLGA KVDPVCDEGFQLKGSSASYCVLAGMESLMNSSVPVCRQIFCPSP PVIPNGRHTGKPLEVFSCDDFMOQLLMGRVLFPVNLQLGA KVDPVCDEGFQLKGSSASYCVLAGMESLMSSVPVCRQIFCPSP PVIPNGRHTGKPLEVFSCDDFMOQLLMGRVLFPVNLQLGA KVDPVCDEGFQLKGSSASYCVLAGMESLMSSVPVCRQIFCPSP PPIPNGRHTGKPLEVFFCDFMFCTFGRLIGHGSABCILGSRT AHMSTRPPICQRIPCGUSSRINYSCTTGRRLIGHGSABCILGSRT THNWSTRPPICQRSINYSCTTGRRLIGHGSABCILGSRT THENSTKPPICQRSPLFSFFILHGRISSSRDVCKRRSCKT PPDPVMGILVSDNRSLFFSILHGVBRGAPQCIIPRKC ALMWEBBLPSCSRVCQPPFILHGRHTPSHQDNFSPGQEVTYSC EPGYULRGAASLHCTPQGDWSPEAPCZVSCDDPLOQDPHRSC	l	(	ł	
PSTFMLPR\PTISMECUSLYQUEVURGULFULSSMPPENILQQLI APIPLPSEFILPSFPILVPESSAASGELLSSLPPTSNAPSDPAT TTAKADAASSITVUVTPPTAKAPTTVEDRUGDSTPUSEKEVENAA VUDANASESP  145 717 RESASRASPRQSAGTAVTTGTRAGGTCLAAAHHRMENRADGRS LEKLEVUNGLVITEVEQEPSFSDIASLVVMCMAVGISYISVYDH QGIFKRNNSRLMDEILMQQQELLGLDCSKYSSPRAMSNDKDDQV LAVULAVVLSPEDGEKADIVRAAQDPCQLVAQKQKRPTDLDVDT LA\VYLVOMVULLI  13 6147 MCCGREGSSPSFEPVGPPAPGLPFCCGGSLLAVVULLALPVA MCGCMAPEN\LPPARPTNLTDEMEPFIGTYLNYEGRPGYSGRPP SIICLKNSWYGAKORCREKSCRNPPDPVMCMVIVIKSIQPGSQ IKYSCTKGYRLIGSSATCIISGDTVIWDHETPICDRIPCGLPP TTINGDPISTMREMPHGSVVTTKCMPGSGGRKVPELVGERSIY CTSNDDQVGINSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVURBRCQPGFVMKGPRRVKCQALMKMERELPSKCVQDPPD VLHAERTQRDKDNFSPQGBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLMGRULFVNLIQLGAKVDFVCDGEP QLKGSSASVCVLAGMERIMNSSVPVCBQIFCRSPPVI*NGRHTO KPLEVPPFGKAVNTTCDHENDRGTSFDLIGESTIRCTSDPQGMG VMSSPAPRCGIIGHCQAPDHFLPAKLKTQTNASDPPIGTSLKYE CREYYGRPFSITCLDMLWWSSPKDVCKRKSCKTPPDPVMGMVH VTTDIQVGSRINYSCTTGHRLIGISSAECILSGMAAHNSTKPPI CQRIPCGLPPTIANGDFISTNRENPHYGSVVTYRCNPGSGGRKV FELVCEPSIYGRPFSITCLDMLWSSSFWCQALMXMEPBLES CSRVCQPPPDULHARTQRDKDMFSPGQEVFYSCEPGFDLGGST SHCTPQGDMSPAAPTCEVKSCDDFMGGLLMGRULPPVNLQLGA KVDFVCDGSFGLKGSSASYCVLAGMESLMNSSVEVCGQIFCRSP PVIPNGRITGKGLBVFPFGKAVWTYCTFGRILGGESAECILSGN TAHMSTKPPICORIPCGUSSRINYSCTTGRILGGSAECILSGN TAHMSTKPPICORIPCGUSSRINYSCTTGRILGGSAECILSGN TAHMSTKPPICORIPCGUSSRINYSCTTGRILGGSAECILSGN TAHMSTKPPICORIPCGUSSRINYSCTTGRILGGSAECILSGN TAHMSTKPPICORIPCGUSSRINYSCTTGRILGGSAECILSGN TAHMSTKPPICORIPCGUSSRINYSCTTGRILGGSAECILSGN TAHMSTKPPICORIPCGUSSRINYSCTTGRILGGSAECILSGN TAHMSTKPPICORIPCGSFTLKGGSVSYSCCUCHMSGPRRVKCQA LAKWEPBLPSCSRVCQPPEILIGGHTFSHODMRSPGQEVTYSC EPGYDLRGAASLHCTPQGGBWSPAPPCGVKSCDDFLOQLPHKC LYPLMLQLAGAKUSVVCDEGFRLKGSSVSHCVLNGWRINGSVMKVCP LEPLMLQLAGAKUSVVCDEGFRLKGGSSVSHCVLNGWRINGSLMNNSVP LEPLMLQLAGAKUSVCDEGFRLKGGSSVSHCVLNGWRINGSLMNNSVP	l		1	VQLSSVNPPSLSPPGTTGIEQSLTGLSISSTP\PAVSSVLSTGV
APIPLPSEFILPSPPLVPBSSSAASSGELLSSLPPTSNAPSDPAT TTAKADAASESP  5940  145  717  RESARRAPBROSAGTAVTTOTRAGGTCLAAAHHRMKRADGRS LEKLPVHMSLVITTSVEQEPSPSDLASLVVWCANOUSYSLVYDH QCIFKRNNSRLMDEILKQQGELIGLDCSKYSPBPANNDKDDQV LEKLLAVKVLSPEDGKADIVRAAQDFCQLVAQKQKRFTDLDVDT LAVTLVQMVVLILI  13  6147  MCGCRASEN\PEPPPVDPPAPGLPFCGCSSLAVVVLLALDVA MCGCNAPEN\LDPPAPPTNLTDEFFPIGTTYLNYECRPGYSGRPP SILLKNSVWTGAKORCRESCRNPPDPVNCWUVLIKGIQFGSQ IKYSCTKGYRLIGSSSATCIISGDTVINDNEPPLCDRIPCGLPP TTTNGDPJTSTRREBFPHYGSVVTTRAGGSGCRKVPELVGEBFIY NEWVERCQPGFVMKGPRRVKCQALMKWBFELDSCRVCQPPD VILHBRETRQBKUNPPSPGGBVFYSCERVDLGASANRCTPQGDW SPAAPTCSVKSCDPFMGULMGRVLFPVHLQLGAKVDPVCDEGF QLKGSSASYCVLAGMESLMSSVPVCQBIPPDFWGTSTLTTE KELEVPPFGKAVNTTCDPHDDRGTSFDLIGBSTIRCTSDPQORG VMSSPAPRGGIIGHCQAPDHFLFAKLKTQTNASDFPIGTSLKTE CRPTYGRPFBITCLIBLWSWSFDVKRKSKCTPPDFWSKGHI VITDLQVGSRINYSCTTGHRLIGHSSAECILSGNAHWSFKPPI CORIFCGLPPTIANGDFISTNRENHYGSVVYTKOMPGSGRKV FBLVGGBPSIYCTSDDQVGIMSGPAQCIIPNKCTPPNVSKGII. VSDNRSLFSLHSVWFFQCDFFWKGPRRVKQALNKWBEBLBS CSRVCQPPPDVLHABRTQDKDMPSGCGVFYSCBPGYDLGRSA KVDFVCDEGFQLKGSSASYCVLAGMESLMSVPVCRQIFCPSP PVIPNGRHTGKPLBVFFGCAVTYTCRDFSGSRKV FPIVGRBFGTLKFCCRPSYVGRPFSITCLDNIJWSSPDUCKRSCCT PPDFWNKGHTGKPLBVFFGCAVTYTCTTGHPROTSGRT RCTSDPQGNGWMSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD FPIGTSLKYFCRPSYVGRPPSITCLDNIJWSSPRDUCKRSCCT PPDFWNKWHVTTD.GVGSRINYSCTTGHRLIGHSSABCILSGN TAHMSTKPPICQRIPCGLBFTIANGDPISTNRENFHYGSVVTYR CALGSRGKVVELWGBSITCTSHDDQVGIKGPRQVCCKRSCCT PPPPWNGILLYSDRASHFFSHQUNGSPRQCLIPRKC TPPNVENGILLYSDRSJFFSINGVBRCGPGPVKCGA LAKWFBBLPSCSRVCQPPFBILGGRHTPSHQDNFSPGQEVTYSC EPFGYDLRGAASLHCTPQGDWSPRAPCCVDPFVKMGPRRVKCQA LAKWFBBLPSCSRVCQPPPBILGGRHTPSHQDPRSGFQEVTYSC EPFGYDLRGAASLHCTPQGDWSPRAPCCVDFUNGSRINNSVPVCB			i	PTVP\LLPPQVNQSLTSVPPMESSYLHLPGLMPFTRQGLPNLPQ
TTAKADAAS GLTVDVTPPTAKAPTTVEDRUGDSTPVSEKPVSAA VDANAS ESP  S940  145  717  REGAGREAS PROSACTAVITGTRAGGICLAAAHERMEWRADGES LEKLPVEMGLVITEVEQEPS PEDLASLVVMCMAVGLSY IS VYDH QGIFKRNNSRLMDEILKQQQELLGLOCKYSPEPANSNDKDQV LNCHLAVKVLS PEDGKADIVRAQDPCQLVAQKOKRPTDLDVDT LAVVLVMVVLLLI  S941  13  6147  MCLGREGASSPES PEPEVOPPADGLEFCCGGLLAVVVLLALPVA WGQCNAPEW\LPPARPTMLIDEFEPPIGTYLNYECRPGYSGRPP SIICLENSWWTCAKORCREKS CERPPPPVNCHWIVLKGIQFGSQ IXYSCKTGYRLIGSS SATCIL SEGTV I MONETIC LORL PCGLEP TITINGDPISTNRENPHYGS VYTYRCNPGSGGRKVPELVGEPS I Y CTSINDQVGINSGPAPQCI I PINKCT PPRIVENGIL VSDINRSLYS L NEVVERPCOPG PWMGERRIV COQALIRMEPELLES CRIVCOPPED VLHARETORIKNINPS PGGBV PYS CEPCYDLAGAAS MRCTPQGDW SPAAPTCEVKS CDDFMGQLLNGRVLFPVNLQLGAKVDFVCDBGF QLKGSSAS YCVLAGMESLMINS SVEVCEQ I PCPSPPVI PINGRING KPLEVYP PFGKAVNYTCDPHPDRGTSPDLIGEST TECTS PQGMG VMSS PARGGILGHCQAPDHPLFAKLTYQTNAS DPFIGTSLKYE CREYYGRPS I TCLDNIVWS SPKOVCKRESCTPPDPVNGWVH VTIDIQVGSR INYSCTTGHRLIGHSSABCILSGNAAHMSTKPPI CORL PGGLPPTIANGPT STATKHYGSVEVTCENGEGGRKV YSDINSLFSLANGVVERRQOPFVMGGPRIVCQALAKWEPELLES CSRVCQPPPDVLIARBTORDKDNPSGCGBVFYSCERCYDLAGGA KVDFVCDBGFQLKGSSAS YCVLAGMESLMINSVFVCEQE I PCESP PVIPNGHTIGK LEKPYPPGKAVNTTCDPHPDRGTSFDLIGGSTI RCTSDPQGRGWISS PAPRCG LIGHCQAPDHPLFAKLKTYNNAS D FPIGTSLKYECRPBYYGRPPS I TCLDILIVWSS PKDVCKRKSCKT PDPPVNGMYHVTTD QVGSR INYSCTTGHRLIGHSSABCILGGN TAHMSTKPP LOQUS I PCGLPPTIANGPI STMRSNFHYGSVYTYR CRIGGSGRKVFELVGEPS I YCTSNDDVGSPGAVGSVFSCVCLAG TAHMSTKPP LOQUS I PCGLPPTIANGPI STMRSNFHYGSVYTYR CRIGGSGRKVFELVGEPS I YCTSNDDVGSPGAVGCI PPNKC TPNVENGI LVSDNESLESLINGVSPRCOQDEFWKGPRVKCQA LIKWEPBLPSCSRVCOPPPI LHGEHTPSIODMFSGGBVFYSC EPGYDLRGAASHACTPCOBSPERLHGSSVENCUNGGRSLANNSVP LIPKUNGL	í	i	ĺ	PSTFNLPR\PTHSWPGVGLYQEFVKPGVLPPLSSMPPRNLPG\I
VDANASESP  145  717  RESASEASPROSAGTAVITGTRAGGTCLAAAHHRMERADGES LEKLPY-MIGLVITEVEQEPS-FADIASLVVMCMAVGISYISVYDH QGIFKRNNSRLMDEILKQQQELLGLDCSKYSPEPANSNDKDDQV LACHLAAVKULS PEDGKADIVRAAGDFCQLVAQKQKRPTDLDVDT LAVVILVOMVVLILI  5941  13  6147  MCLGREGASSPESPEPVOGPAPGLDFCCGGSLLAVVULLALPVA MCGCNASEN LPPARPTNLIDEFBEPTGTYLNYECRPGYSGRPF SILCLKNSWTGAKRORCRKSCRNPPDPVNCMVEVLKGIQFGSQ IKYSCTKGFRLIGSSATCII-GUTVINDHSTPICDRIPGGLPP TITNGDPISTNRENPHYGSVVTYRCNPGSGGRKVFELVEGPSY KYSCTKGFRLIGSSATCII-GUTVINDHSTPICDRIPGGLPP TITNGDPISTNRENPHYGSVVTYRCNPGSGRKVFELVEGPSY NRVVBPRCQPGFVMKSPRVKCQALNKWBPELPSCSRVCQPPPD VLHAERTQRIKNNSGVPVCBQIFCPGSPVI-PNGRHTG SPAAPTCEVKSCDDFMGQLAKGRVLFPVNLQLGAKVDFVCDBG- QLKGSSASVVLAGMESLWNSSVPVCBQIFCPGSPVI-PNGRHTG KPLEVPFPGKAVNYTCDPHDPGGTSFDLIGESTIRCTSDPQOMG VMSSPAPRGGILGHCQADHFLFAKLTQTNASDFFIGTSLKYE CRPEYYGRPFSITCLDNLWSSPKOVCKRKSCKTPPDPVMGWH VITDLQVGSRINYSCTTGHRLIGHSSAECILSGNAAHMSTKPPI CCRIPCGLPFTIANDDFISTNRKMFHYGSVVTYRCRFGSGGRKV FELVGBPSITCTSNDDQVGINSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVBFRCQPGFVMKGPRVKCQALMKWEDELPS CSRVCQPPPDVLHARRTQRDKDNPSPQGBVYTSCBGTVLKGAA SKRCTTQGDMSPAAPTCEVKSCDDFMGGLINGRULPPVNLQLGA KVDFVCDGGFQLKGSSASYCVLAGMESLWNSSVPUCBQIFCPSP PIPMGRHTGKPLBVPPFSKAVNTTCDPHDPGTSFDLIGESTI RCTSDPQGRGWSSASASYCVLAGMESLWNSSVPUCBQIFCPSP PIPMGRHTGKPLBVPFSTAVNTTCDPHDPGTSFDLIGESTI RCTSDPQGRGWSSSASPCGILGHCQAPDHFLFAKLKTQTNASD FPIGTSLKYECRPSYTGRPPSITCTSNDDQVGTWSSPKDUCKRKSCKT TAHMSTKPPICQRIPGGPFTTANDDFISTNENFHYGSVVTYR CNLGSGRKVPELVGBPSITCTSNDDQVGTWSSPKDUCKRKSCKT TAHMSTKPPICQRIPGGBPTTANDDDYSTNRSNFHYGSVVTYR CNLGSGRKVPELVGBPSITCTSNDDQVGTWSSPKDVCKRKSCKT TPHNVENGILMSDNSLFSLMSVVPRCQRGFVMKGPRVKCQA LMKWEPBLFSCSRVCQPPPTLHGEHTPSRQDMFSGQRVTYSC EPGYDLRGAASHCTPQGDSPBRAPCCAVKSCDDFIGQLPHGV	ļ	1		APLPLPSEFLPSFPLVPESSSAASSGELLSSLPPTSNAPSDPAT
VDANASESP  145  717  RESASEASPROSAGTAVITGTRAGGTCLAAAHHRMERADGES LEKLPY-MIGLVITEVEQEPS-FADIASLVVMCMAVGISYISVYDH QGIFKRNNSRLMDEILKQQQELLGLDCSKYSPEPANSNDKDDQV LACHLAAVKULS PEDGKADIVRAAGDFCQLVAQKQKRPTDLDVDT LAVVILVOMVVLILI  5941  13  6147  MCLGREGASSPESPEPVOGPAPGLDFCCGGSLLAVVULLALPVA MCGCNASEN LPPARPTNLIDEFBEPTGTYLNYECRPGYSGRPF SILCLKNSWTGAKRORCRKSCRNPPDPVNCMVEVLKGIQFGSQ IKYSCTKGFRLIGSSATCII-GUTVINDHSTPICDRIPGGLPP TITNGDPISTNRENPHYGSVVTYRCNPGSGGRKVFELVEGPSY KYSCTKGFRLIGSSATCII-GUTVINDHSTPICDRIPGGLPP TITNGDPISTNRENPHYGSVVTYRCNPGSGRKVFELVEGPSY NRVVBPRCQPGFVMKSPRVKCQALNKWBPELPSCSRVCQPPPD VLHAERTQRIKNNSGVPVCBQIFCPGSPVI-PNGRHTG SPAAPTCEVKSCDDFMGQLAKGRVLFPVNLQLGAKVDFVCDBG- QLKGSSASVVLAGMESLWNSSVPVCBQIFCPGSPVI-PNGRHTG KPLEVPFPGKAVNYTCDPHDPGGTSFDLIGESTIRCTSDPQOMG VMSSPAPRGGILGHCQADHFLFAKLTQTNASDFFIGTSLKYE CRPEYYGRPFSITCLDNLWSSPKOVCKRKSCKTPPDPVMGWH VITDLQVGSRINYSCTTGHRLIGHSSAECILSGNAAHMSTKPPI CCRIPCGLPFTIANDDFISTNRKMFHYGSVVTYRCRFGSGGRKV FELVGBPSITCTSNDDQVGINSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVBFRCQPGFVMKGPRVKCQALMKWEDELPS CSRVCQPPPDVLHARRTQRDKDNPSPQGBVYTSCBGTVLKGAA SKRCTTQGDMSPAAPTCEVKSCDDFMGGLINGRULPPVNLQLGA KVDFVCDGGFQLKGSSASYCVLAGMESLWNSSVPUCBQIFCPSP PIPMGRHTGKPLBVPPFSKAVNTTCDPHDPGTSFDLIGESTI RCTSDPQGRGWSSASASYCVLAGMESLWNSSVPUCBQIFCPSP PIPMGRHTGKPLBVPFSTAVNTTCDPHDPGTSFDLIGESTI RCTSDPQGRGWSSSASPCGILGHCQAPDHFLFAKLKTQTNASD FPIGTSLKYECRPSYTGRPPSITCTSNDDQVGTWSSPKDUCKRKSCKT TAHMSTKPPICQRIPGGPFTTANDDFISTNENFHYGSVVTYR CNLGSGRKVPELVGBPSITCTSNDDQVGTWSSPKDUCKRKSCKT TAHMSTKPPICQRIPGGBPTTANDDDYSTNRSNFHYGSVVTYR CNLGSGRKVPELVGBPSITCTSNDDQVGTWSSPKDVCKRKSCKT TPHNVENGILMSDNSLFSLMSVVPRCQRGFVMKGPRVKCQA LMKWEPBLFSCSRVCQPPPTLHGEHTPSRQDMFSGQRVTYSC EPGYDLRGAASHCTPQGDSPBRAPCCAVKSCDDFIGQLPHGV		Ī	[	TTAKADAASSLTVDVTPPTAKAPTTVEDRVGDSTPVSEKPVSAA
145 717 RRSASRSASPRQSAGTAVITGTRAGGTCLAAAHHRMRWRADGRS LEKLPVHWGLVITEVEQEPSBILASLVWCWAVGISYISVYH QGIFKRNNSRLMBEILKQQQELIGLDCSKYSPFANSNNDDDQV LNCHLAVVLSPEDGKADIVRAAQDFCQLVAQKQKRPTDLDVDT LA\VYLVOWVVLIII  5941 13 6147 MCIGRWGASSPESPEVGPPAPEDFYCGGSLLAVVVLLALPVA MCGCNAJEW\LPPARPTNLTDEWEFPPIGTLINYECRPGYSGRPP SIICLKNSVWTGAKDRCRRKSCRPPDPVMCMVHVIKGIQFGSQ IKYSCTKSYRLIGSSSATCIISGDYVIMDBEPFICRRIPGSQ TTTNGDPISTNRRNFHYGSVVTYKCMPSGGGRVFFLVGEPSIY CTSNDDQVGIWSGPAPQCIIPNKCTPPNVERGLVSDNRSLFSL NEWVEFRCQPGFVMKGFRRVKCQALMKWEPEHDSCSRVCQDPPD VIHABETQRDKDNFSPGGBVFYSCEPSTVLGGASSMRCTPQGDW SPAAPTCEVKSCDFMSGLIMGRVLFPVNLQLGAKVDFVCDBGP QLKGSSASYCVLAGMESLMNSSVPVCBQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHDDRGTSFDLIGESTIRCTSDPQGMG VMSSPAPRGGIIGHCQADPHFLFAKLKTYTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGWH VTTDLQVGSRINYSCTTGERLIGHSSACCILSGNAAHWSTKPPI CQRIPGLPFTIANGFISTNRNFHYGSVVTYCROPGSGGRVV FELVGRPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPRNVENGIL VSDNNSLFSLNBVVEFRCQPGFVWKGFRRVKCQALNKWEPELDS CGRVCQPPPDVLHABETQRKDNFSEQGEVFYSCBGFVLGGAA SHRCTPQGDWSPAAPTCEVKSCDPMGGLINGRVLFPVNLQLGA SKRCTPQGDWSPAAPTCEVKSCDPMGGLINGRVLFPVNLQLGA SKRCTPQGDWSPAAPTCEVKSCDPMGGLINGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLMNSVFVCBQIFCPSP PVIPNGRHTGKFLBVPPFGKAVMYTCDPHPDRGTSFDLLGESTI RCTSDPGGRGVWSSPAPRGSILGHCQADPHFLFAKLKTQTNASD FPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PDDPVNGMHVLTDLQUSRIMYSCTTGERLIGHSSABCILGSM TAHMSTKPPLCRIPGGIPFTANGDFISTNENFHYGGVVTYR CNLGSRGRKVFELVGRBFIYCTSDDQVGIWSGPAPQCIIPNKC TPPNVENGILLVSDNNSLFSILNEVVBRCQGFVMGGPRVKCQA LINKWPBLPSCSRVCQPPPEILHGBHTTSHQDNFSEGGEVFYSC EPGYDLRGAASLHCTPQGDWSPAPRCAVKSCDDFLGQLPPHKC LANKWPBLPSCSRVCQDFPCMGGPRVKGGALKNNNSVP	ì			
LEKLPV:IMGLVITEVEQEPSFBDIASLVVWCMAVGISYISVYDH QGIFKRNNSRLMDEILKQQQELLGLDCSKYSPERANSNDXDDQV LNCHLAVKULS PBGGKADIVGQCLVAQKQKRPTDLDVDT LA\VYLVQMVVLILI  13 6147 MCIGRRGASSPESPEPVGPPAPCLPYCCGSLLAVVVLLALPVA MGCANAPM\LPPARPTNLTDEBERPIGTYLNYECRPGYSGRPP SIICLKNSVWTGAKDRCRRKSCRNPPDPVNCMVIVIKGIQFGSQ IKYSCTKSYRLIGSSSATCIISGDYVIMDNETPICDRIPCGLPP TITNGPFISTNRRNFHYGSVVTYRCNPGSGGRVFFLVGEPSIY CTSNDDQVGIWSGPAPQCIIPNRCTPPNVENGILVSDNRSLPSL NRVVBFRCQPFVMKGPRVVKCQALMKBEBLBSCSRVCQDPPD ULHBETQRUKDNFSPGGRVYSCREGYDLRGASSNRCTPGOW SPAAPTCEVKSCDDFM3QLLNGRVLFPVNLQLGAKVDFVCDEGP QLKGSSASYCVLAGMESLMNSSVPVCEQIFCESPVINGRITG KPLBVPFFGKAVNYTCDBHDDRGTSFDLIGESTIRCTSDPQONG VMSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDPPIGTSLKYE CRPYYGRFFSITCLDNLWWSSRBVVKKRSCKTEPDFVNGWH VTTDIQVGSR INYSCTTGRILIGHSSAECILESANAHMSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPBNVENGIL VSDNRSLFSLNEVVFRCQDFWKGPRRVKCQALMKWEPBLPS CSRVCQPPPDVLHABRTQRDKDNFSPGQEVFYSCBPGYDLRGAA SKRCTPQGDWSPAAPTCBVKSCDDFWGQLLNGRVLFPVNLQLGA KVDFVCDGGFQLKGSSASYCVLAGMESLMNSSVPVCEQIFCSP PVIPNGRHTGKPLBVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGRGVWSSPAPRGGILGHCQADPHFLFAKLKTQTNASD PPIGTSLKYECRPRYYGRPSITCLDNLWSSPFDLVCRKSCKT PPDPVNGMVHVITDLQVGSR INYSCTTGRILIGHSSAECILSGN TAHMSTKPPICQRIPGGLPFTIANGDFISTNENFHYGSVVTYR CNLGSGRRXVFELVGRSSTYCTDDQDVGIUSGPAPQCIIPNKC TPPNVENGILLVSDNRSLFSLNEVVBRCQDFFFRGFRVKCQA LMKWFBBLPSCSRVCQPPEILHGBSTTSGDDNFGSFGRVVTYC EPGYDLRGAASLHCTPQGDWSPBAPRCAVKSCDDFLGQLPHKC LPPKLAUGHBRAVSFVCDBGFRRKGSCNTSCO EPGYDLRGAASLHCTPQGDWSPBAPRCAVKSCDDFLGQLPHKC	5940	145	717	
QGIFKRNNSRLMDBILKQQQBLIGLDCSKYSPEPANSNDKDDQV LACHLAVVIJSPBGBGADIVRAAQDFCQLVAQKQKRPTDLDVDT LAVVIJVOMVVLILI  5941  13  6147  MCLGRMGASSPESPEPUGPPAPGLPFCCGSLLAVVVLLALPVA WGQCNAJEWA\DPARPTNITDBFBFBIGTLHAYECREYSGRPF SIICLKNSWTGARRCRRKSCRNPPDPVMGWUHVLKGIQFGSQ IKYSCTKGYRLIGSSSATCIISGDTVIMDNBTPICDRIPPGLPP TTTNGDPISTNRRNFHYGSVVTTRCNPGSGGRRVFFLVGEPSIY CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLPSL NBVVBFRCQPGFVMKGPRRVKCQALMKWBBELBSCSRVCQPPPD VLHABETQRDKDNPSPGQBVPYSCBPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLMGRVLFPVNLQLGAKVDFVCDBGF QLKGSSASVCVLAGMSSLMNSSVPVCBQIFCBSPPVIPMGRITG KPLEVPPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLWMSSPKDVCKRRGCKTPPDPVNGWH VITDIQVGSRINYSCTTGHRLIGHSSABCILSGNAAHWSTKPPI CQRIPGGLPFTIANGDFISTNRENPHYGSVVYYRCNPGSGGRKV FELVGRPSIYCTSNDDQVGIRGPPAQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALMKWEPELPS CSRVCQPPPDVLHABRTQRDKDNFSPGQSVFYSCBGYDLRGAA SHRCTPQGDMSPAAPTCEVKSCDDFMGQLLMGRVLPPVNLQLGA KVDPVCDBGFQLKGSSASYCVLAGMSSLMNSSVPVCBQIFCBSP PVIPNGRHTGKPLBVPPFGKAVMYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGWSSPAPRCGILGDDHFFLARLKTQTNASD FPIGTSLKYECRPBYYGRPFSITCLDNLWSSPKDVCRKSCKT PPDPVNGMVHVTTDLQGSRINYSCTTGHRLIGHSSABCILGGN TAHWSTKPPICQRIPGGEPFILAGBSTISTNRENPHYGSVVTYR CXLGSRGRKVFELVGRPSITCTSDDQVGIWGGPRAVCQA LMKWEBELPSCSRVCQPPPEILHGBHTPSHQDNFSFGQRVTYSC EPGYDLRGAASLHCTPQGDWSPBAPRCAVKSCDDFLGQLPHGRV LEPLANLQGGAKVSFVCDBGFRLKGSSVSHCVLVGMRSLMNNSVP	3940	1 143	l '±'	
INCHLAVKULS PEDGKADT VRAAQDFCQLVAQKQKRPTDLDVDT LA\VILVOMVULLI.  5941  13  6147  MCIGRMEASSPESPEPVOPPAPGLPFCCGCSLLAVVULLALPVA MGQCNAPEW\LPPARPTNLTDEFEPP IGTYLNYECRPGYSGRPF SIICLKNSWATGAKDRCRRKS CRRPPDPVNCHWINTKGIQFOSQ IKYSCTKGYRLIGGSSATCIIGDTVINNETPPICDRIPGILPP TITNGDPISTNRENPHYGSVVTYRCNPGSGGRKVFELVGEPSIY CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NRWVERRCOPFYMKGPRRVKCQALNKWSPLDSGSTWCQPPPD VLHAERTORDKDNFSPQBVFYSCEPGYDLRGASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLMGRVI,FVNLQLGAKVDFVCDBGF QLKGSSASYCVLAGMESLWNSSVVVCBQIFCPSPPVI PMGRITFO KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VMSSPAPRCSILGHCQAPDHFLFARLKTQTMASDPFIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRCKCTPPDPVNGMVH VTTD1QVGSRINTSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CQRIPCGLPFTIANGDFISTNRENHYGSVVTYRCNPGSGGRKV VSDNRSLFSLNBVVEREQDGFVMKGPRRVKCQALNKWEPBLPS CSRVCQPPPDVLHARRTQRDKDNFSPGGVFYSCEPGTDLGAGA SHRCTPGGDWSPAAPTCEVKSDDFMGQLLNGRVLPPVNLQLGA KVDFVCDEGFQLKGSSASYCVIAGMESLMNSSVFVCBQIFCPSP PVIPNGRHTGKPLKVERPPSYGRAVNTTCDPHPDRGTSFDLLGESTI RCTSDPGGMSVWSSPAPRCGILGHCQAPDHFLFARLKTQTNASD FPIGTSLKYECRPSYYGRPFSITCLDNLVWSSPKDVCRKSCKT PPDPVNGMVHVITD1QVGSRINYSCTTGHRLIGHSSAECILSGN TAHMSTKPPICQRIPCGLPFTIANGDFISTNRSWFHYGSVVTYR CXLGSRGRKVWFELVGBESTYCTGNDDQVGIMSGPAPQCIIPMKC CXLGSRGRKVWFELVGBESTYCTGNDDQVGIMSGPAPQCIIPMKC CXLGSRGRKVWFELVGBESTYCTGNDDQVGIMSGPAPQCIIPMKC CXLGSRGRKVPELVGBESTYCTGNDDQVGIMSGPAPQCIIPMKC CXLGSRGRKVPELVGBESTYCTGNDDQVGIMSGPAPQCIIPMKC CXLGSRGRKVPELVGBESTYCTGNDDQVGIMSGPAPQCIIPMKC CXLGSRGRKVPELVGBESTYCTGNDDQVGIMSGPAPQCIIPMKC CXLGSRGRKVPELVGBESTYCTGNDDQVGIMSGPAPCCIIPMC CXLGSRGRKVPELVGBESTYCTGNDDQVGIMSGPAPCCIIPMC CXLGSRGRKVPELVGBESTYCTGNDDQVGIMSGPAPCCIIPMC CXLGSRGRKVPELVGBESTYCTGNDDQVGIMSGPAPCCIIPMC CXLGSRGRKVPELVGBESTYCTGNDDQVGIMSGPAPCCIVCQA LMWBPBLPSCSRVCQPPPEILHGRTTSHQDMFSPGGEV7YSC EPGYDLRGAASLHCTPQGDMSPEAPCCAVGCDDFIGQLPUCDLPHCH LMFLANGLPGAASLHCTPQGDMSPEAPCCAVGCDDFIGCDPTCHCOLDPHICH				<u>-</u>
LA\VYLVOMVVLILI  MCLGRMGASSPESEPUGPPAPGLPFCCGSLLAVVVLLALFVA MCGCNAPEN, L.PPARPTULTDEFBEPIGTYLNYECRPGYSGRPP SIICLKNSVWTGAKDRCRRKSCRNPPDPVNGWHVIKGIQFGSQ IKYSCTKGYRLIGGSSATCIISGDYVINDNETPICDRIPPGLPP TITINGDPISTNRENPHYGSVVTYRCNPGSGGRKVPELVGEPSIY CTSNDDQVGIWSGPAPCLIIPNKCTPPNVENGILVSDNRSLFSL NEVUBFRCQBGFVMKGPRRVKCQALNKWEPBLPSGSRVCQPPPD VLHAERTQRDKDNFSPGGBVFYSCEPGYDLRGASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGARVDFVCDBGF (KELSVPFFGKAVNYTCDPHDPRGTSPDLIGBSTIRCTSDPQONG WMSSPAPRCSILGHCQADPHPLFARLKTQTNASDPPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGWH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGRPSIYCTSNDDQVGINSGRAPQCIINKKCPPRVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRVKCQALNKWEPBLPS CSRVCQPPPDVLHARTQRDVBFSQGLINGRVLFPVNLQLGA SKRCTTQGDWSPAAPTCEVKSCDDEMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLMNSVPVCEQIFCPSP PVIPNCHTGKPLEVFPFGKAVNTTCDPHPDRGTSFDLLGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFARLKTQTNASD FPIGTSLKYECRPSYYGRPPSITCLIGHCQAPDHFLFARLKTQTNASD FPIGTSLKYECRPSYTGRPPSITCTIGNLWSSPKDVCRKSCKT PPDPVMGMVHVITDIQVGSRINYSCTTGHRLIGHSABCILSGN TAHMSTKPPICQRIPCGLIPPTIANGDFISTRRNFHYGSVVTYR CRIGGGRGRKVFELWGBSPLYCTSNDDQVGINSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVBPRCQPGFVMKGPRRVKCQA LANKWERELPSCSRVCQPPPEILHGENTPSHQDNRSPGGEV7YSC EPGYDLGGAASLHCTPQGDNSPBAPRCAVSCDDFIGGLPHTRN LHYLNIGLGAKVSFVCDBGFRLKGSSUSHCVLVGMRSLNNSVP	1	ł	ł	
13 6147  MCIGRMGASSPESPEVGPPAPGLPFCCGGSLLAVVVLLALPVA MCGCMAPEW\LPPARPTMITDEBFFFIGTTIMYECRECYSGRPF SIICLKMSVWTGAKDRCRKSCRNPPDPVMGMUFVIKGIQPGSQ IKYSCTKGYRLIGSSSATCIISGDTVIMDMETFICDRIPCGLPP TITMGDPISTMREMSPHYGSVYTYKCMPGSGGRKVFELVGEPSIY CTSNDDQVGIWSGPAPQCIINKCTPPNVENGILVSDNRSLFSL NKWVBFRCQPGFVMKGPRRVKCQALMKWBPBLPSCSRVCOPPPD VLHAERTQRDKDNFSPGQBVFYSCBPGYDLRGASMRCTPQGDW SPAAPTCEVKSCDDFMGQILMGRVLFPVNLQIGAKVDFVCDBGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPMGHTG KPLEVFPFGKAVNTTCDPHPDRGTSFDLIGESTIRCTSDPQOMG VMSSPAPRCGILGHCQAPDHFLFAKLKTQTMASDPPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRESCKTPPDFVNGMVH VITDIQUGGSRINYSCTTGHRLIGHSSAECILSGMAAIMSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGRPSIYCTSMDQQGIWSGPAPQCIIPMKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQDFFVMKGPRRVKCQALMKWEPBLPS CSRVCQPPPDVLHAERTQRDKDNFSPQQEVFYSCBPGTDLRGAA SHRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLPPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLMMSSVPVCBGIFCPSP PVIPNGRHTGKPLEVFPPGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFRAKLKTQTMASD FPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDDFVMGMVHVITDLQVGSRINYSCTTGHRLIGHSSABCILSGM TAHMSTKPPICQRIPCGPSTYTANGDFISTNRENFHYGSVVTYR CXLGSRGRKVFELVGBPSITCTSNDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVBPRCQBFFVMKGPRRVKCQA LAKWEPBLPSCSRVCQPPPEILMGRHTSPGDVFNSCQSPTYSC BPGYDLRGAASLHCTPQGDWSPBAPRCAVKSCDDFLGGLPHSRV LPFLMIQLGAKVSFVCDEGFFLKGSSVSHCVLVGMRSLWNNSVP	}	1		
WGQCNAPEW\LPPARPTNLTDEBEPPIGTYLNYECRPGYSGRPP SIICLKRSWTGAKDRCRRKSCRNPEDPWAGWHUTIKGIPGSQ IKYSCTKGYRLIGGSSATCIISGDTVIWDMETPICDRIPGGLPP TITNGDPISTNRENFHYGSVVTYRCNPGSGGRKVPELVGEPSIY CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDDRSLFSL NEVVEPRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VHERETQRDKDNFSPEGBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCODFMGQLLNGRULFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLACMESLWNSSVPVCEQIPCPSPPVIPNERHTG KPLBVVPFGKAVNTYCDPHPDRGTSFDLIGESTIRCTSDPQONG VMSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDPPIGTSLKYE CRPEYYGRPFSITCLDNLWWSSPKDVCKRKSCKTPPDFVNGWH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNGGSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNBUVVFRCQPGFVMKCPRRVKCQALNKWEPBLPS CSRVCQPPPDVLHABTTQRDKDNFSPQEVFYSCEPGYDLRGAA SHRCTTQGDWSPAAPTCEVKSCDDPMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSVFVCBGIFCPSP PVIPNGRHTGKPLBVFPPGKAVTTCDPHPDRGTSFDLIGESTI RCTSDPGGNGVWSSFAPRCGILGHCQAPDHFLFRAKLTQTNASD FPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQVGSRINYSCTTGHBLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR CKLGSRGRKVFELVGEPSIYCTSNDDQVGTWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVBPRCQBGFVMKGPRRVKCQA LAKWEPBLPSCSRVCQPPPEILHGRHTPSGDNFSFCQEVTYSC BPGYDLRGAASLHCTPQGDWSPBAPRCAVKSCDDFIGGLFYHSKV LFPLMIQLGAKVSFVCDEGFFLKGSSVSHCVLVGMRSLWNNSVP				
SIICLKNSWTCAKDRCRRKSCRNPPDPVNCMVHVIKGIQFGSQ IXYSCTKGYRLIGSSSATCIISGDTVIWDBTPICDKIPCGLPP TITNGDPISTNRRNPHYGSVVTYRCNPGSGGRKVFBLVGEPSIY CTSNDDQVGINSGPAPQCIIPNKCTPPWVENGILVSDNRSLFSL NEVVBPRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHARRTORDKDNFSPGGBVYYSCEPGYDLAGAASNRCTPQODW SPAPPTCEVKSCDDFMSQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLMNSSVFVCEQIFCPSPPVIPNGRHTG KPLEVPPFGKAVNYTCDPHPDRGTSPDLIGESTIRCTSDPQONG VMSSPAPRCGILGHCQAPDHFJFAKLKTQTNASDPPIGTSLKYE CRPEYYGRPFSITCLDNLWSSPKDVCKRKSCKTPPDPVNGWH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAHWSTKPPI CORIPCGLPPTIANGDFISTNRENHYGSVYTYRCHPGSGGRKV PELVGBPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLMEVVBFRCQDGFVMKGPRVKCQALMKWEPBLPS CSRVCQPPPDVLHABRTORDKDNPSPGQEVFYSCBPGYDLRGAA SHRCTPQGDMSPAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLMNSVFVCBQFCPSP PVIPNGRHTGKPLKBVPPFGKAVNTYCDPHDRGTSFDLLGBSTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD PPIGTSLKYECRPBYYGRPPSITCLDNLWSSSPKDVCKRKSCKT PPDDPVNCMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHMSTKPPICQRIPGDEPTIANGDFISTNSNFHYGSVVTYR CRLGSRGRKVPELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVRNGILVSDNRSLFSLNBVVBPRCQPGFVMKGPRVKCQA LIKWEPBLPSCSRVCQPBSIYCTSNDDNSSPGQEVFYSC EPSYDLRGAASLHCTPQGBWSPBAPRCAVKSCDDFLGOLPHSRV LIFLBILQLGAKVSFVCDBGFRLKGSSVSHCVLVGMRSLWNNSVP	5941	13	6147	
IKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPP TITINGDFISTNRENFHYGSVYTTRCNEGSGGRKVFELVGEPSIY CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NRVVBFRCQPGFVMKGPRRVKCQALNRWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPQGBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDBGF QLKGSSASYCVLAGMESLWNSSVPVCBQIFCPSPPVIPNGRHTO KPLEVFPFGKAVNYTCDPHPDRGTSFPDLIGBSTIRCTSDPQGNG VMSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDPPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDLQVGSRINYSCTTGHRLIGHSSABCILSGAAHWSTKPPI CORIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGRPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHARRTQDRKDNFSPGQEVFYSCEPGYDLRGAA SHRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCBQIFCPSP PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGWSSPAPRCGILGHCQAPDHFLFAALKTQTNASD FPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGMVHVITDLQUGSRINYSCTTGHRLIGHSSABCILSGN TAHWSTKPPICQRIPCGLPPTIANGPFISTNRSNFHYGSVVTYR CNLGSRGRKVFELVGBPSIYCTSNDDQUGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVBFRCQPGFVMKGPRRVKCQA LMKWEPBLPSCSRVCQPPPEILHGBHTPSHQDNFSPGQEVFYSC BFGYDLRGAASLHCTPQGDWSPBAPRCAVKSCDDFIGQLPHGRV LKWEPBLPSCSRVCQPPPEILHGBHTPSHQDNFSPGQEVFYSC	1	1	İ	WGQCNAPEW\LPPARPTNLTDEFEFPIGTYLNYECRPGYSGRPF
TITNGDPISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIY CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEPRCQPGFVMKGPRIVKCQALNKWEPELPSCSRVCQPPPD VIHAERTQRDKUNFSPQGBVFYSCEBGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLMYSVPVCEQIFCPSPPVIPNGHHTG KPLEVFPGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VMSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSIKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQUGSRINYSCTTGHRLIGHSABCILSGNAAHWSTKPPI CORIPCGLPPTIANGDTITNRENFHYGSVVTYRCNPGSGGRKV FELVGBPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBRGYDLRGAA SHRCTFQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSVPVCBQIFCPSP PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD FPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRSCKT PPDPVNGMVHVITDIQUGSRINYSCTTGHRLIGHSSAECILSGN TAHMSTKPPICQRIPCGLEPPTIANGPFISTRENFHYGSVVTYR CNLGSRGRKVPELVGBPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVBFRCQPGFVMKGPRRVKCQA LENKWEPBLPSCSRVCQPPPELLGHSTFSHQDNFSPGQEVFYSC BEGYDLRGAASLHCTPQGDWSPBAPRCAVKSCDDFLGQLPHGRV LENKWEPBLPSCSRVCQPPPELLGHSTFSHQDNFSPGQEVFYSC BEGYDLRGAASLHCTPQGDWSPBAPRCAVKSCDDFLGQLPHGRV		<b>{</b>		SIICLKNSVWTGAKDRCRRKSCRNPPDPVNGMVHVIKGIQFGSQ
CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVBFRCQPGFVMKGPRRVKCQALNKWBPELPSCSRVCQPPPD VILHAERTQRDKDNFSPGQBVFYSCBGYDLRGAASMCTTPQDW SPAAPTCBVKSCDDFMGQLLNGRVLFPVNLQLGARVDFVCDBGF QLKGSSASYCVLAGMESLWNSSVFVCBQIFCPSPPVIPNGHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGBSTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFARLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSR INYSCTTGRRLIGHSABCCILSGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGBPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVBFRCQPGFVWKGPRRVKCQALNKWBEPELPS CSRVCQPPPDVLHABRTQRDKDNFSPGQBEVFYSCBPGYDLRGAA SKRCTPQGDWSPAAPTCBVKSCDDFMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCBQIFCPSP PVIPNGRHTGKPLBVFFPGKAVNTTCDPHPDRGTSFDLIGESTI RCTSDPGGNGVWSSFAPRCGILGHCQAPDHFLFRKLKTQTNASD PPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNCMVHVTTDLQVGSRINYSCTTGHRLIGHSSAECILGGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR CNLGSRGRKVFELVGBPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVBRCQPGFVWKGPRRVKCQA LMKWEPBLPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC BFGYDLRGAASLHCTPQGDWSPBAPRCAVKSCDDFLGOLPHGRV LFPLNLQLGAKVSFVCDBGFRLKGSSVSHCVLVGMRSLNNNSVP		·	ł	IKYSCTKGYRLIGSSSATCIISGDTVIWDNBTPICDRIPCGLPP
NEVVEPTCOPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDMFSPGGBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGGLLMGRVLFVNLQLGAKVDFVCDBGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNERHTO KPLEVFPFGKAVMYTCDPHPDRGTSPDLIGESTTRCTSDPQGNG VMSSPAPRCGILGHCQAPDHPLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECTLSGMAAHNSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGEPSIYCTSNDDQVGINSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNPSPGQEVFYSCBPGYDLRGAA SHRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLMNSSVEVCBQIFCPSP PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHPLFAKLKTQTNASD FPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRSWFHYGSVVTYR CRLGSRGRKVFELVGBPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLPSLNBVVVBRCQPGFVMKGPRRVKCQA LINKWEPBLPSCSRVCQPPPEILHGRHTPSHQDMFSPGQEVTYSC EFGYDLRGAASLHCTPQGDWSPRAPRCAVKSCDDFLGOLPHGRV LFPLNLQLGAKVSFVCDEGFFLKGSSVSHCVLVGMRSLWNNSVP	ŀ	}	,	TITNGDPISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIY
NEVVEPTCOPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDMFSPGGBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGGLLMGRVLFVNLQLGAKVDFVCDBGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNERHTO KPLEVFPFGKAVMYTCDPHPDRGTSPDLIGESTTRCTSDPQGNG VMSSPAPRCGILGHCQAPDHPLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECTLSGMAAHNSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGEPSIYCTSNDDQVGINSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNPSPGQEVFYSCBPGYDLRGAA SHRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLMNSSVEVCBQIFCPSP PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHPLFAKLKTQTNASD FPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRSWFHYGSVVTYR CRLGSRGRKVFELVGBPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLPSLNBVVVBRCQPGFVMKGPRRVKCQA LINKWEPBLPSCSRVCQPPPEILHGRHTPSHQDMFSPGQEVTYSC EFGYDLRGAASLHCTPQGDWSPRAPRCAVKSCDDFLGOLPHGRV LFPLNLQLGAKVSFVCDEGFFLKGSSVSHCVLVGMRSLWNNSVP		ł	1	CTSNDDOVGIWSGPAPCCIIPNKCTPPNVENGILVSDNRSLFSL
VIHAERTORDKDNFSPGGBVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCBVKSCDDFMGQLLMGRVLFPVNLQLGAKVDFVCDBGF QLKGSSASYCVLAGMBSLWNSSVPVCEQIFCESPPVI PMCRHTG KPLEVFPFGKAVNYTCDPHPDRGTSPDLIGESTIRCTSDPQGNG VMSSPAPRCGILIGHCQAPDHFLFAKLTTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHMSTKPPI CQRIPCGLPPTIANGDFISTMRENFHYGSVVTYRCNPGSGGRKV FELVGKPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPBLPS CSRVCQPPPDVLHAERTORDKDNFSPQGEVFYSCBPGYDLRGAA SHRCTPQGDMSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCBQIFCPSP PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPPRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD PPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQUGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRSNFHYGSVVTYR CNLGSRGRKVFELVGEPSITCTSNDDQUGIWSGPAPQCIIPNKC TPPNVENGILLVSDNSLFSLNEVVBPRCQPGFVMKGPRRVKCQA LLKWEPBLPSCSRVCQPPPEILHGRHTPSHQDNFSPGQEVFYSC ERGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGOLPHGRV LFPLNIQLGAKVSPVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP			İ	·
SPAAPTCEVKSCDDFMGQLLMGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLACHESLMNSSVPVCEQIFCP6PPVI PMGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VMSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDPPIGTSLKYE CRPEYYGRPFSITCLDNLVMSSPKDVCKRKSCKTPPDPVNGWVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CORIPCGLPPTIANGDFISTMRENFHYGSVVTYRCNPGSGGRKV FELVGKPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVKNGIL VSDNRSLFSLNEVVKFRCQPGFVMKGPRRVKCQALNKWEPBLPS CSRVCQPPPDVLHABRTQRKDNFSPGQBVFYSCBPGYDLRGAA SHRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCBQIFCPSP PVIPNGRHTGKPLBVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHPLFAKLKTQTNASD FPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PDDFVNGWVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRSNFHYGSVVTYR CNLGSGRKVFELVGEPSITCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVBPRCQPGFVMKGPRRVKCQA LLKWEPBLPSCSRVCQPPPEILHGRHTFSHQDNFSPGQEV*YSC EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGOLPHGRV LFPLNIQLGAKVSPVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP		l	1	
QLKGSSASYCVLAGMESLWNSSVPVCBQIFCPSPPVIPNCRHTG KPLEVFPEKKAVNYTCDPHPDRGTSPDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHPLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKKSCKTPPDFVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHMSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSCGRKV FELVGRPSIYCTSNDDQVGINSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNBVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHABRTQRDKDNFSPQGEVFYSCBPGYDLRGAA SKRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVMLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCBQIFCPSP PVIPNGRHTGKPLBVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHPLFAKLKTQTNASD FPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGNVHVITDIQUGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR CNLGSRGRKVFELWGEPSIYCTSNDDQWGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVBFRCQPGFVMKGPRRVKCQA LIKWEPBLPSCSRVCQPPPEILHGRHTFSHQDNFSPGQEVFYSC EFGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGOLPHGRV LFPLNIQLGAKVSFVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP	}	[		
KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VMSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CRPYYGRPFSITCLDNLVMSSPKDVCKRKSCKTPPDFVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHMSTKPPI CQRIPPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGKPSIYCTSNDDQVGIMSGPAPQCIIPMKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA SHRCTPQGDWSPAAPTCEVKSCDDFMGQILINGRVLFPVMLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCBQIFCPSP PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSFAPRCGILGHCQAPDHFLFAKLKTQTNASD FPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRSNFHYGSVVTYR CNLGSRGRKVFELVGEPSIYCTSNDDQVGIMSGPAPQCIIPNKC CNLGSRGKVFELVGEPSIYCTSNDDQVGIMSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVBPRCQPGFVMKGPRRVKCQA LIKWEPBLPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGMWSPEAPRCAVKSCDDFLGQLPHGRV LFPLNLQLGAKVSPVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP			ł	
VMSSPAPRCGILGHCQAPDHPLFAKLKTQTNASDPPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSABCILSGNAAHMSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV PELVGRPSIVCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNBVVEFRCQPGFVMKGPRRVKCQALNKWEPBLPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA SHRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA KVDFVCDBGFQLKGSSASYCVLAGMESLWNSSVFVCBGIFCPSP PVIPNGRHTGKPLBVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD FPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRSNFHYGSVVTYR CNLGSRGRKVFELVGEPSITCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDDRSLFSLNEVVBPRCQPGFVMKGPRRVKCQA LAKWEPBLPSCSRVCQPPPEILHGBHTPSHQDNFSPGQEV*YSC BPGYDLRGAASLHCTPQGWSPRAPRCAVKSCDDFLGOLPHGRV LFPLNIQLGAKVSFVCDBGFRLKGSSVSHCVLVGMRSLWNNSVP		l		- · · · · · · · · · · · · · · · · · · ·
CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSABCILSGNAAHMSTKPPI CQRIPCGLPPTIANGDFISTMRENFHYGSVYTYRCNPGSGGRKV PELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVBFRCQPGFVMKGPRRVKCQALNKWEPBLPS CSRVCQPPPDVLHABRTQRDKDNFSPGQEVFYSCBPGYDLRGAA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLPPVNLQLGA KVDFVCDBGFQLKGSSASYCVLAGMSELWNSSVFVCBQIFCPSP PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLPAKLKTQTNASD PPIGTSLKYECRPBYYGRPFSITCLDNI.VWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSABCILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRSNFHYGSVVTYR CNLGSRGRKVFELVGEPSITCTSNDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDDRSLFSLNEVVBPRCQPGFVMKGPRRVKCQA LAKWEPBLPSCSRVCQPPPELLHGRHTPSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGOWSPEAPRCAVKSCDDFLGOLPHGRV LFPLNIQLGAKVSFVCDBGFRLKGSSVSHCVLVGMRSLWNNSVP		Ī		<u> </u>
VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CORIPCGLPPTIANGDFISTMRENPHYGSVOTYRCNPGSGSRKV FELVGKPSIYCTSNDDQVGIWSGPAPQCIIPKCTPPNVENGIL VSDNRSLFSLNEVVERRCQPGFVMKGPRRVKCQALNKWEPBLPS CSRVCQPPPDVLHABRTORNKDNFSPGQBVFYSCBPGYDLRGAA SURCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLPPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCBQIFCPSP PVIPNGRHTGKPLBVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHPLFAKLKTQTNASD FPIGTSLKYECRPBYYGRPFSITCLDNI.VWSSPKDVCRRKSCKT PDDFVNGWVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRSNFHYGSVVTYR CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVBPRCQPGFVMKGPRRVKCQA LIKKWEPBLPSCSRVCQPPPEILHGRHTFSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGOLPHGRV LFPLNIQLGAKVSPVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP		[		
CQRIPCGLPPTIANGDFISTNRENFHYGSVTYRCNPGSCGRKV FELVGKPSIYCTSNDDQVGINSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNBVVERCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHABRTQRDKDNFSPGQEVFYSCBPGYDLRGAA SURCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCBQIFCPSP PVIPNGRHTGKPLBVFPFGKAVNYTCTDPHDRGTSFDLLGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD PPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGNVHVITDIQUGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR CNLGSRGRVFELUGEPSIYCTSNDDQVGIWGGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVBFRCQPGFVMKGPRRVKCQA LIKWEPBLPSCSRVCQPPPEILHGRHTFSHQDNFSPGQEVFYSC EFGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGOLPHGRV LFPLNIQLGAKVSFVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP		l		CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH
PELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRVKCQALNKWEPBLPS CSRVCQPPPDVLHABRTQRDKDNFSPGQEVFYECBPGYDLRGAA SURCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLPPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCBQIFCPSP PVIPNGRHTGKPLBVFPFGKAVNYTCDPHPDRGTSFDLLGESTI RCTSDPQGMGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD PPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGWHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTRPPICQRIPCGLPPTIANGDFISTNRSNFHYGSVVTYR CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNSVVBPKCQPGFVMKGPRVKCQA LINKWEPBLPSCSRVCQPPPEILHGBHTPSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRV LFPLNIQLGAKVSFVCDBGFRLKGSSVSHCVLVGMRSLWNNSVP				
VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA SHRCTPQGDWSPAAPTCEVKSCDDFMGQLLMGRVLFPVMLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWMSSVPVCBQIFCPSP PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGMGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD FPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDPISTNESNFHYGSVVTYR CNLGSRGKVFELVGEPSIYCTSNDQVGINSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVBPKCQPGFVMKGPRRVKCQA LINKWEPBLPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGWSPEAPRCAVKSCDDFLGQLPHGRV LFPLNIQLGAKVSPVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP				CORIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV
VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA SHRCTPQGDWSPAAPTCEVKSCDDFMGQLLMGRVLFPVMLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWMSSVPVCBQIFCPSP PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGMGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD FPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDPISTNESNFHYGSVVTYR CNLGSRGKVFELVGEPSIYCTSNDQVGINSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVBPKCQPGFVMKGPRRVKCQA LINKWEPBLPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGWSPEAPRCAVKSCDDFLGQLPHGRV LFPLNIQLGAKVSPVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP	· '	1		FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL
CSRVCQPPPDVIHABRTQRDKDNFSPGQBVFYSCBPGYDLRGAA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLPPVNLQLGA KVDFVCDBGFQLKGSSASYCVI.AGMESLWNSSVFVCBQIFCPSP PVIPNGRHTGKPLBVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLPAKLKTQTNASD PPIGTSLKYECRPBYYGRPFSITCLDNI.VWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSABCILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRSNFHYGSVVTYR CNLGSRGRKVFELVGEPSITCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDDRSLFSLNEVVBPRCQPGFVMKGPRRVKCQA LIMKWEPBLPSCSRVCQPPPEILHGRHTPSHQDNFSPGQEVFYSC BPGYDLRGAASLHCTPQGWSPEAPRCAVKSCDDFLGOLPHGRV LFFLNIQLGAKVSFVCDBGFRLKGSSVSHCVLVGMRSLWNNSVP		ł		
SHRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLPPVNLQLGA  KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVFVCBQIFCPSP  PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI  RCTSDPQGNGVWSSPAPRCGILGHCQAPDHPLFAKLKTQTNASD  FPIGTSLKYECRPBYYGRPFSITCLDNI.VWSSPKDVCKRKSCKT  PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN  TAHWSTKPPICQRIPCGLPPTIANGDFISTNRSNFHYGSVVTYR  CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC  TPPNVENGILVSDNRSLFSLNEVVBPRCQPGFVMKGPRRVKCQA  LIMKWEPBLPSCSRVCQPPPEILHGRHTPSHQDNFSPGQEVFYSC  EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGOLPHGRV  LFPLNIQLGAKVSFVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP		Į.	ļ	
KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCBQIFCPSP PVIPNGRHTGKPLBVPPFGKAVNYTCDPHDRGTSFDLLGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD PPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGKVHVITDIQVGSRINYSCTTGHRLIGHSSABCILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRSNFHYGSVVTYR CNLGSRGRKVFELVGBPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVBFRCQPGFVMKGPRRVKCQA LIKWEPBLPSCSRVCQPPPEILHGRHTPSHQDNFSPGQEVFYSC EFGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGOLPHGRV LFPLNIQLGAKVSPVCDBGFRLKGSSVSHCVLVGMRSLWNNSVP		j	]	1
PVIPNGRHTGKPLBVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD FPIGTSLKYECRPBYYGRPFSITCLDNI.VWSSPKDVCKRKSCKT PPDPVNCKWHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTRPPICQRPTIANGDPISTNRSNFHYGSVVTYR CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNBVVBPRCQPGFVMKGPRRVKCQA LIKWEPBLPSCSRVCQPPPEILHGKHTPSHODNFSPGGEVFYSC EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRV LFPLNIQLGAKVSFVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP		1		
RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD PPIGTSLKYECRPBYYGRPFSITCLDNI.VWSSPKDVCKRKSCKT PPDPVNCMVHVITDIQVGSRINYSCTTGHRLIGHSSABCILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNBVVBPKCQPGFVMKGPRRVKCQA LINKWEPBLPSCSRVCQPPPEILHGBHTPSHODNFSPGGEVFYSC EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRV LFPLNIQLGAKVSFVCDBGFRLKGSSVSHCVLVGMRSLWNNSVP				
FPIGTSLKYECRPBYYGRPPSITCLDNIJVWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGPPISTNRSNFHYGSVVTYR CNLGSRGKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNBVVBPRCQPGFVMKGPRRVKCQA LINKWEPBLPSCSRVCQPPPEILHGBHTPSHODNFSPGQBVFYSC EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRV LFPLNIQLGAKVSPVCDBGFRLKGSSVSHCVLVGMRSLWNNSVP				1
PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSABCILSGN TAHWSTKPPICQRIPCGLPPTIANGDPISTNRSNFHYGSVVTYR CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDDRSLFSLNEVVBPRCQPGFVMKGPRRVKCQA LINKWEPBLPSCSRVCQPPPEILHGRHTPSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGBWSPEAPRCAVKSCDDFLGOLPHGRV LFPLNIQLGAKVSPVCDBGPRLKGSSVSHCVLVGMRSLWNNSVP		l		<del>-</del>
TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCTIPNKC TPPNVERGILVSDNESLFSLNEVVBFRCQPGFVMKGPRRVKCQA LINKWEPBLPSCSRVCQPPPEILHGKHTPSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGOLPHGRV LFPLNIQLGAKVSPVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP		)		
CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVBPRCQPGFVMKGPRRVKCQA LMKWEPBLPSCSRVCQPPPBILHGKHTPSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGDWSPBAPRCAVKSCDDFLGQLPHGRV LFPLNIQLGAKVSFVCDBGPRLKGSSVSHCVLVGMRSLWNNSVP		l		PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN
CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVBPRCQPGFVMKGPRRVKCQA LMKWEPBLPSCSRVCQPPPBILHGKHTPSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGDWSPBAPRCAVKSCDDFLGQLPHGRV LFPLNIQLGAKVSFVCDBGPRLKGSSVSHCVLVGMRSLWNNSVP		İ	}	1 -7
TPPNVENGILVEDNRSLFSLNEVVBPRCQPGFVMKGPRRVKCQA LMKWEPBLPSCSRVCQPPPBILHGRHTPSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGDWSPBAPRCAVKSCDDFLGQLPHGRV LFPLNIQLGAKVSFVCDBGPRLKGSSVSHCVLVGMRSLWNNSVP				
Linkwepblpscsrvcopppbellhgbhtpshodnfspgqevfysc Bpgydlrgaaslhctpqgdwspbaprcavkscddflgqlphgrv Lfplniqlgakvsfvcdbgfrlkgssvshcvivgmrslwnnsvp				1
EPGYDLRGAASLHCTPQGDWSPBAPRCAVKSCDDFLGQLPHGRV LFPLNLQLGAKVSFVCDBGFRLKGSSVSHCVLVGMRSLWNNSVP		i		
LFPLNIQIGAKVSFVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP		{		
	1	[		
VCEHIFCPNPPAILNGRHTGTPSGDIPYGKEISYTCDPHPDRGM	ĺ	ł		
	i	i	i	VCKHIFCPNPPAILNGRHTGTPSGDIPYGKKISYTCDPHPDRGM

- 1	erin og den erin og den		
SEQ ID NO:	Predicted beginning nucleotide	Predicted end nucleotide location	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, B= Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	Warryptophan, Yarrosine, XaUnknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
}	1		TFNLIGESTIRCTSDPHGNGVWSSPAPRCELSVRAGHCKTPEQF PFASPTIPINDFEFPVGTSLNYECRPGYFGKMFSISCLENLVWS
l	,		SVEDNCRRKSCGPPPEPFNGMVHINTDTQFGSTVNYSCNEGFRL
1	•	ĺ	IGSPSTTCLVSGNNVTWDKKAPICEIISCEPPPTISNGDFYSNN
)	ļ.	Ì	RTSPHNGTVVTYQCHTGPDGBQLFELVGERSIYCTSKDDQVGVW
1			SSPPPRCISTNKCTAPBVENAIRVPGNRSFPSLTEIIRPRCQPG FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPBILHGEHTLSHQ
		İ	DNFSPGQEVFYSCBPSYDLRGAASLHCTPQGDWSPRAPRCTVKS
1			CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRSASHCV
Ì			LAGMKALWISSVPVCEQIFCPNPPAILIGRHTGTPLGDIPYGKE
	ļ		VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPAPRCEL PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDFGYLLVGK
}	]	ĺ	GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKBLEMKKVYHY
	ł		GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRTHDALI
ļ			VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAIHLHSQ GGSSVHPRTLQTNEENSRVLP
5942	4509	688	YLYVRMRANPLAYGISHKAYQIDPPL\RKHREQ\LVIE\VGRKL
1	1		DK\AQMIRPBERTGYFSSTDLGRTASHYYIKYNTIBTFNELFDA
{	[		HKTEGDIFAIVSKAEEFDQIKVREEEIBELDTLLSNFCELSTPG
	1		GVENSYGKINILLQTYINRGEMDSFSLISDSAYVAQNAARIVRA LFBIALRKRWPTMTYRLLNLSKAIDKRLWGWASPLRQFSILPPH
İ	ĺ		MLTRLEBKKLTVDKLKDMRKDBIGHILHHVNIGLKVKQCVHQIP
ļ	İ		SVMMRAFIQPITRTVLRVTLSIYADFTWNDQVHGTVGEPWWIWV
}			EDPTNDHIYHSEYFLALKKQVISKRAQLLVFTIPIFEPLPSQYY
1			IRAVSDRWLGARAVCIINFQHLILPERHPPHTELLDLQPLPITA LGCKAYEALYNFSHFNPVQTQIPHTLYHTDCNVLLGAPTGSGKT
	[		VAAELAIFRVFNKYPTSKAVYIAPLKALVRERMDDWKVRIEEKL
	•		GKKVIELTGDVTPDMKSIAKADLIVTTPEKWDGVSRSWQNRNYV
ł			QQVTILIIDEIHLIGEERGPVLEVIVSRTNFISSHTEKPVRIVG LSTALANARDLADWLNIKQMGLFNFRPSVRPVPLEVHIQGFPGQ
			HYCPRMASMNKPAFQAIRSHSPAKPVLIFVSSRRQTRLTALELI
			AFLATEEDPKOWLNMDERBMENIIATVRDSNLKLTLAFGIGMHH
i .		•	AGLHERDRKTVEBLFVNCKVQVLIATSTLAWGVNFPAHLVIIKG TEYYDGKTRRYVDFPITDVLOMMGRAGRPOFDDOGKAVILVHDI
			KKDFYKKFLYEPFPVESSLLGVLSDHLNAEIAGGTITSKQDALD
			YITWTYFFRRLIMNPSYYNLGDVSHDSVNKFLSHLIEKSLIELE
	i		LSYCIBIGEONRSIEPLTYGRIASYYYLKHQTVKMFKDRLKPEC STERLLSILSDAEEYTDLPVRHNEDHMNSELAKCLPIESNPHSF
]			DSPHTKAHLLLQAHLSRAMLPCPDYDTDTKTVLDQALRVCQAML
			DVAANQGWLVTVLNITNLIQMVIQGRWLKDSSLLTLPNIENHHL
			HLFKKWKPIMKGPHARGRTSIECLPELIHACGGKDHVFSSMVES  BLHAAKTKOAWNFLSHLPEINVGISVKGSWDDLVEGHNELSVST
			LTADKRDDNKWIKLHADQBYVLQVSLQRVHFGFHKGKPESCAVT
			PRFPKSKDEGWFLILGEVDKRELIALKRVGYIRNHHVASLSFYT
		,	PEIPGRYIYTLYFMSDCYLGLDQQYD/NLSQRYTSESFCTGQHQ
5943		2274	GL DKPTRHKTYLSSSWAKMAAAEGPVGDGELWOTWLPNHVVFLRLR
5,25	•	46/3	EGLKNQSPTRAEKPASSSLPSSPPPPQLLTRNVVPGLGGRLFLWD
	'		GEDSSFLVVRLRGPSGGG\EEPALSQYQRLLCINPPLFEIYQVL
]			LSPTOHHVALIGIKGLMVLELPKRWGKNSEFEGGKSTVNCSTTP
			VABREFFTSSTSLTLKHAAWYPSEILDPHVVLLTSDNVIRIYSLR EPQTPTNVIILSBABEBSLVLNKGRAYTASLGETAVAFDFGPLA
		•	AVPKTLFGQNGKDEVVAYPLYILYENGETFLTYISLLHSPGN/I
			WKAVGSIAHAS\AABDNYGYDACAVLCLPCVPNILVIATESGML
	]		YHCVVLEGREEDDHTSEKSWDSRIDLIPSLYVFECVBLELALKL
			ASGEDDPFDSDPSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI HKLHKFLGSDEEDKDSLOELSTEOKCFVEHILCTKPLPCRQPAP
			IRGPWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPILCTR
	]		EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD
			TAPPPEBCLQLLSRATQVFREQYTLKQDLAKEETQRRVKLLCDQ
L	L		KKKQLEDLSYCREERKSLREMAERI.ADKYERAKEKQEDIMNRMK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŧ	corresponding	to first	L=Leucine, M=Methionine, N-Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
<b></b>	<del></del>		KLLHSPHSBLPVLSDSBRDMKKELQLTPDQLRHLGNAIKQVTMK
			KDYOOOKMEKVLSLPKPTIILSAYQRKCIQSILKEEGEHIREMV
ļ		1	KQINDIRNHVNF
5944	167	3428	PSIATFTDEPEVLTEPPSATTTTTIGISATWITLAGSHGKRNNT
35			ITTTSSKRKNRKNKITPENVQIIFDDPLPISYSQPEKVNGESKS
	ļ	1	SSTSESGDSDNMRISSCSDESSNSNSSRKSDNHSPAVVTTTVSS
		1	KKQPSVLVTFPKEERKSVSGKASIKLSETISEGTSNSLSTCTKS
l		ļ	GPSPLSSPNGKLTVASPKRGQKREEGWKEVVRRSKKVSVPSTVI
			SRVIGRGGCNINAIREFTGAHIDIDKQKDKTGDRIITIRGGTES
		<b>{</b>	TROATOLINALIKOPOKBIDELIPKNRLKSSSANSKIGSSAPTT
1			TAANTSLMGIKMTTVALSSTSQTATALTVPAISSASTHKTIKNP
	1	1	VN\NVRPGFPVSFP\LAYPPPQFAHALLAAQTFQQIRPPRLPMT
		1	HEGGTEPPAQSTWGPPPVRPLSPARATNSPKPHMVPRHSNQNSS
ļ		1	GSQVNSAGSLTSSPTTTTSSSASTVPGTSTNGSPSSPSVRRQLF
1		1	VTVVKTSNATTTTVTTTASNNNTAPTNATYPMPTAKEHYPVSSP
[		1	SSPSPPAQPGGVSRNSPLDCGSASPNKVASSSEQEAGSPPVVET
			TNTRPPNSSSSSSSSSAHSNQQQPPGSVSQEPRPPLQQSQVPPP
			EVENTVPPLATSSAPVAVPSTAPVTYPMPQTPMGCPQPTPKMET
i		1	PATRPPPHGTTAPHKNSASVQNSSVAVLSVNHIKRPHSVPSSVQ
			LPSTLSTQSACQNSVHPANKPIAPNFSAPLPFGPFSTLFENSPT
<u> </u>			SAHAPWGGSVVSSQSTPESMLSGKSSYLPNSDPLHQSDTSKAPG
į.			FRPPLQRPAPSPSGIVNMDSPYGSVTPSSTHLGNFASNISGGQM
	[	l	YGPGAPLGGAPAAANFNRQHFSPLSLLTPCSSASNDSSAQSVSS
ł			GVRAPSPAPSSVPLGSEKPSNVSQDRKVPVPIGTERSARIRQTG
	1		TSAPSVIGSNLSTSVGHSGIWSFEGIGGNQDKVDWCNPGMGNPM
Ì	į	1	IHRPMSDPGVFSQHQAMERDSTGIVTPSGTFHQHVPAGYMDFPK
		,	VGGMPFSVYGNAMIPPVAPIPDGAGGPIFNGPHAADPSWNSLIK
		1	MVSSSTENNGPQTVWTGPWAPHMNSVHMNQLG
5945	1461	197	GVTHLFLFGKRKLRNGIAEDLKGQADFFFLLVSEAVVATGSPRA
			WLTCLILPLPGIIFSVLPKAMSRPLLITFTPATDPSDLWKDGQQ
Ì	ļ		QPQPEKPESTLDGAAARAFYEALIGDESSAPDSQRSQTEPARER
-	Ì	,	KRKKRRIMKAPAARAVAEGASGRHGQGRSLEAEDKMTHRILRAA
	1		QEGDLPELRRLLEPHEAGGAGGNINARDAFWWTPLMCAARAGQG
l			AAVSYLLGRGAAWVGVCELSGRDAAQLAEBAGFPBVARMVRBSH
	į.		GETRSPENRSPTPSLQYCENCDTHFQDSNHRTSTAFLLSLSQGP
		į	QPPNLPLGVPISSPGFKLLLRGGWEPGMGLGPRGEGRANP1PTV
j		†	LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW
	i	ļ	REERRREB\KDRAWERDLRTYMNLEP
5946	541	1666	ILGSYSSIQPERYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP
	l		SEGSPORVNSIDEV\BL\EHLQPDVLVHAVLRVVDF/TILTEAV
İ			YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG
	Ì		YIWBFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA
·			KFQKSAPSYVKISDLATHLEDKCSGVVLIKAQISKLAFPITASQ
1	1		KIALNAHSSLKSIPSSLPNIVYTGCAKCGLELETDENRIYKQCF
	'		SCLPFIMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA
			DCLNRVIVPSSRITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL
	1	1	DENSYPLQQDFSLLDFYPDIVKHGANARL
5947	3	1317	RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKBK
1			CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT
1	l		KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA
l		i	PPVQNQALARQYMOMLPKEKQPVAGSBGAQYRKKQLAKQLPAHD
]		1	QDPSKCHELSPREVKRMEQFVKKYKSEALGVGDVKLPCEMDAQG
l			PKQMNIPGGDRSTPAAVGAMBDKSAEHKRTQYSCYCCKLSMKEG
		1	DPATYAERAGYDKLWHPACFVCSTCHBLLVDMIYFWKNBKLYCG
i	į .	l .	RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI
]	1		LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN
İ		1	NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVBCKKRMS
5948	39	3370	YRERYPVSGGSVLRSALEVCNDFLSGLTEGSLLPEGFFSGPIDQ
1	]	1	GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM
	F		VEIETEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP
			PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRIVBY
	1	I	E V WARE A PRODUCTION OF THE PARTY OF THE PA

SEQ	Predicted	Predicted end	
ID			Amino acid segment containing signal peptide
NO:	beginning   nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E~
l MO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Nethionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			SPPSAPRRPPVYYKFIEKSARELDNEVRYDMDEEDYAWLEIVNE
İ		!	KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGEQQSLIDEDA
1	1	i	VCCICMDGECQNSNVILPCDMCNLAVHOBCYGVPY1PEGOWLC/
1	1		RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP
4		İ	E\VGFANTVFIBPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI
l	1	<b>!</b>	OCHKANCYTAFHVTCAOKAGLYMKMEPVKELTGGGTTFSVRKTA
Ì		į	
l .	Ì		YCDVHTPPGCTRRPLNIYGDVBMKNGVCRKESSVKTVRSTSKVR
1		1	KKAKKAKALABPCAVLPTVCAPYIPPQRLNRIANQVAIQRKKQ
1			FVERAHSYMLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM
1			KAAKEKLKYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA
1		<u> </u>	MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI
I	l		KHPMDFATMRKRLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV
1	l		FYRAAVRLRDQGGVVLRQARREVDSIGLREASGMHLPERPAAAP
1	[		RRPFSWEDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG
1			SRSKRAKLLKKE LALLRNKLSQQHSQPLPTGPGLEGFEEDGAAL
Į.			GPEAGEEVLPRLETLLOPRKRSRSTCGDSEVEEESPGKRLDAGL
	1		TNGFGGARSBQBPGGGLGRKATPRRRCASESSISSSNSPLCDSS
	· .		FNAPKCGRGKPALVRRHTLEDRSELISCIENGNYAKAAR!AAEV
1			COSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV
			PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFFDNKRSWQ
ı			WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL
1			SRVHGEPTSDLSDID
5949	39	3370	YRKRYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDO
3343	3,	3370	GNHYOMRRKGRCHRGSAARHPSSPCSVXHSPTRETLTYAOAORM
.1			_ · · · · <del>_</del> · · · · · · · · · · · · · · · · · · ·
1			VEIBLEGREHRISIPDPLBIILEDDLTAQEMSECNSNKENSERP
İ			PVCLRTKRHKNNRVKKKNRALPSAHGTPASASALPEPKVRIVZY
j			SPPSAPRRPPVYYKFIEKSAEBLDNEVBYDMDREDYAMLRIVNE
			KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGEQQSLIDEDA
			VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/
1			RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP
1			E\VGFANTVFIRPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI
	ļ .		QCHKANCYTAPHVTCAQKAGLYMKMBPVKBLTGGGTTFSVRKTA
ł	'		YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR
ļ			KKAKKAKKALAEPCAVLPTVCAPYIPPQRLNRIANQVAIQRKKQ
}			fverahsywllkrlsrngapllrrlqsslqsqrssqqrendrem
1			KAAKEKLKYWQRLRHDLERARLLIKLLRKREKLKREQVKVEQVA
			MBLRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI
			KHPMDFATMRKRLBAQGYKNLHEFERDFDLTIDNCMKYNARDTV
1			FYRAAVRLRDQGGVVLRQARREVDSIGLEEASGMHLPERPAAAP
			RRPFSWEDVDRLLDPANRAHLGLEBOLRELLDMLDLTCAMKSSG
l			SRSKRAKLLKKETALLRNKLSQQHSQPLPTGPGLEGFEEDGAAL
Į.			GPEAGEEVLPRLETLLQPRKRSRSTCGDSEVEEESPGKRLDAGL
1	1		TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSSNSPLCDSS
t			PNAPKCGRGKPALVRRHTLEDRSELISCIENGYYAKAARIAARV
1	l .		GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV
1			PGHHNGVTIPAPPLDVLKIGRHMOTKSDEKLFLVLFFDNKRSWO
1			WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL
]			SRVHGEPTSDLSDID
EREA	1166	202	
5950	TTPP	373	BSRS_TMSTSQPGACPCQGAASRPAILYALLSSSLKAVPRPRSR
}			CLCRQHRPVQLCAPHRTCREALDVLAKTVAFLRNLPSFWQLPPQ
l i			DQRRLLQGCWGPLFLLGLAQDAVTFEVAEAPVPSILKKILLEEP
1			SSSGGSGQLPDRPQPSLAAVQWLQCCLESFWSLELSPKE\YACL
į .			KGPILFNPDVPGIQAASHIGHLQQEAHWVLCEVLEPWCPAAQGR
L			LTRVLLTASTLKSIPTSLLGDLPFRP1IGDVDIAGLLGDMLLLR
5951	143	5449	WNVKPSLLVVQLFKF9DKEEHEQNDSISGKTGETGVBEMIATRK
1	!		VEODSKETVKLSHEDDHILEDAGSSDISSDAACTNPNKTENSLV
i			GLPSCVDEVTECNLELKDIMGIADKTENTLERNKIEPLGYCEDA
		•	ESNROLESTEFNKSNLEVVDTSTPGPESNILENAICDVPDQNSK
1			1
1		i	QLNAIBSTKIESHETANLQDDRNSQSSSVSYLESKSVKSKHTKP
]			VIHSKONMTTDAPKKIVAAKYEVIHSKTKVNVKSVKRNIDVPES
L			QQNFHRPVKVRKKQIDKRPKIQSCNSGVKSVKNQAHSVLKKTLQ

	digerace editryiska		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
i (ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L-Leucine, M=Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
!	amino acid	sequence	Codon, /=possible nucleotide deletion,
<b>}</b>	sequence	Degacine	\=possible nucleotide insertion)
ļ	bequence		DOTLVQIPKPLTHSLSDKSHAHPGCLKEPHHPAQTGHVSHSSQK
i .		}	_ <del>-</del> -
		'	QCHKPQQQAPAMKTNSHVKBELEHPGVEHFKEEDKLKLKKPEKN
I	İ		LQPRQRRSSKSFSLDEPPLFIPDNIATIRREGSDHSSSFESKYM
j .			WTPSKQCGFCKKPHGNRFMVGCGRCDDWFHGDCVGLSLSQAQQM
1			GEEDKEYVCVKCCAEEDKKTEILDPDTLENQATVEFHSGDKTME
ł			CEKLGLSKHTINDRIKYIDDIVKHKVKILKRESGEGRNSSDCRD
ļ	1		NEIKKWQLAPLRKWGQ?VLPRRSSEEK\$EKIPKESTTVTCTGEK
1			ASKPGTHEKQEMKKKKV\EKGVLNVHPAASASKPSADQIRQSVR
		j	HSLKDILMKRLTDSNLKVPREKAAKVATKIEKELFSFFRDTDAK
f		İ	YKNKYRSLMFNLKDPKNNILPKKVLKGEVTPDHLIRMSPEBLAS
ļ		· ·	KELAAWRRRENRHTIEMIEKEQREVERRPITKITHKGBIEIBSD
1			APMKEQBAAMEIQEPAANKSLEKPEGSEK\RKEEVDSMSKDTTS
, '	1	l	QHRQHLFDLNCKICIGRMAPPVDDLSPKKVKVVVGVARKHSDNE
1.		[	ABSIADALSSTSNILASEFFBEEKOBSPKSTFSPAPRPEMPGTV
	1 .		
1			EVESTFLARLNFIWKGFINMPSVAKFVTKAY?VSGSPBYLTEDL
	1	ĺ	PDSIQVGGRISPQTVWDYVEKIKASGTKEICVVRFTPVTEEDQI
ļ	1		SYTLLFAYFSSRKRYGVAANNMKQVKDMYLIPLGATDKIPHPLV
ł		1	PFDGPGLBLHRPNLLLGLIIRQKLKRQHSACASTSHIAETPESA
l		]	PPIALPPDKKSKIEVSTEEAPBEENDFFNSFTTVLHKQRNKPQQ
1	1	1	NLQEDLPTAVEPLMEVTKQEPPKPLRFLPGVLIGWENQPTTLEL
ľ	1		ANKPLPVDDILQSLLGTTGQVYDQ\AQSVMEQNTVKBIPFLNEQ
1 .	<u>'</u>	1	TNSKIBKTDNVEVTDGENKEIKVKVDNISESTDKSABIETSVVG
1		•	SSSISAGSLTSLSLRGKPPDVSTKAFLTNLSIQSKQBETVESKR
1		1	KTLKRQLQBDQENNLQDNQTSNSSPCRSNVGKGNIDGNVSCSBN
ł	]		LVANTARSPOFINLKRDPROAAGRSQPVTTBESKDGDSCRNGEK
1 .		İ	HMLPGLSHNKEHLTEQINVEEKLCSAEKNSCVQQSDNLKVAQNS
		• •	PSVENIQTSQAEQAKPLOEDILMQNIETVHPFRRGSAVATSHFE
i .	j '	i	VGNTCPSEFPSKSITFTSRSTSPRTSTNFSPMRPOOPNLOHLKS
1.			SPPGPPFPGPPNFPPQSMFGFPPHLPPPLLPPPGFG\FA\ONPM
}			VPWPPVV\HLP\GQPQRMMGPLSQASRYIGPQNFYQVKDIRRPR
			RRHSDPWGRQDQQQLDRPFNRGKGDRQRFYSDSHHLKRERHEKE
1			WEQESERHEREDESODEDERFERMANDESCHEICHER GEBERCHEREN WEGESERHERERSODEDERFERMANDESCHEICHER GEBERCHEREN WEGESERHERE WEGESERHERE WEGESERHERE WEGESERHERE WEGESTER
Ī			GKASRDSRNVDKKPDKPKSEDYBKDKEREKSKHREGEKDRDRYH
FOFO	7226	730	KDRDHTDRTKSKR .
5952	3226	639	PPARRSARDLPRALSMRAARPSGSWNGALCRLL\LVTL\AFLIF
I			ASDACKNVTLHVPSKLDAEKLVGRVNLKECFTAANLIHSSDPDF
I			QILEDGSVYTTNTILLSSEKRSFTILLSNTENQEKKKIFVFLEH
l	1		OTKVLKKRHTKEKVLRRAKRRWAPIPCSMLENSLGPFPLFLQQV
l	1		QSDTAQNYTIYYSIRGPGVDQEPRNLFYVERDTGNLYCTRPVDR
1	1		BOYESFRITAPATTPDGYTPELPLPLITKIEDENDNYPIFTEET
1			YTFT1FENCRVGTTVGQVCATDKDEPDTMHTRLKYS11GQVPPS
l			PTLFSMHPTTGVITTTSSQLDRRLIDKYQLKIKVQDMDGQYFGL
	]		QTTSTCIINIDDVNDHLPTFTRTSYVTSVEENTVDVEILRVTVE
l	.		DKDLVNTANWRANYTILKGNENGNFKIVTDAKTNEGVLCVVKPL
1	]		NYEEKQQMILQIGVVNEAPFSREASPRSAMSTATVTVNVBDQDE
1	]	,	GPECNPPIQTVRMKENAEVGTTSNGYKAYDPETRSSSGIRYKKL
[	<b>j</b>		TOPTGWVTIDENTGSIKVFRSLDRRAETIKNGIYNITVLASDQG
1			GRTCTGTLGIILQDVNDNSPFIPKKTVIICKPTMSSABIVAVDP
			DEPIHGPPFDFSLESSTSEVORMWRLKAINDTAARLSYONDPPF
			GSYVVPITVRDRLGMSSVTSLDVTLCDCITENDCTHRVDPRIGG
1			GGVCLGKWAILAILLGIALFFCILFTLVCGASGTSKQPKVIPDD
			LAQQNLIVSNTRAPGDDKVYSANGFTTQTVGASAQGVCGTVGSG
			IKNGGQETIEMVKGGHQTSESCRGAGHHHTLDSCRGGHTEVDNC
			RYTYSEWHSFTQPRLGEESIRGHTLIKN
5953	330	811	PLLCNPDPGWYWWVKQESEISKESQEMDARPKLDLGFKEGQTIK
· '			LCIGNITNKKGGASKPRTARGGGLSLLPPPPGGKVTIPPPSS/V
!			KLPSTNHVTPPSIPKSNHGGSDADILLDLDSPAPVTTPAPTPVS
			VSNDLWGDFSTASSSVPNQAPQPSNWVQF
5954	32	2130	PPPPPPKLANMADI, EAVI ADVSYLMAMBKSKATPAARASKRIVI.
2234		2130	PEPSIRSVMQKYLAERNEITFDXIFNQKIGFLLFKDFCLNEINE
	ì		
			AVPQVKFYERIKBYEKLDNBEDRLCRSRQIYDAYIMKELLSCSH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
		1	
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ı	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of		
i		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ī	amino acid	Bequence	Codon, /=possible nucleotide deletion,
i .	sequence	Ĭ	\=possible mucleotide insertion)
	-		PPSKQAVEHVQSHLSKKQVTSTLFQPYIEEICESLRGDIFQKFM
1	i	į.	ESDKFTRFCQWKNVBLNIHLTMNEFSVHRIIGRGGPGEVYGCRK
1	1		ADTGKMYAMKCLNKKRIKMKQGETLAINERIMLSLVSTGDCPFI
į.	ı	l .	
I	1	1	VCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSEKEMRFYA
1	ł .		TEILGLEHMHNRFVVYRDLKPANILLDEHGHARIS\DLGLACD
ì	ł		FSKKKPHASVGTHGYMAPEVLQKGTAYDSSADWFSLGCMLFKLL
	į	]	RGHSPFRQHKTKDKHEIDRMTLTVNVELPDTFSPELKSLLEGLL
Į.		1	QRDVSKRLGCHGGGSQBVKEHSFFKGVDWQHVYLQKYPPPLIPP
l .	l .		RGEVNAADAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERW
)	İ	l	
į.			QQEVTETVYEAVNADTDKIEARKRAKNKQLGHEEDYALGKDCIM
}	}	]	HGYMLKLGNPFLTQWQRRYFYLFPNRLEWRGEGESRQNLLTMEQ
i	]	1	ILSVEETQIKDKKCILFRIKGGKQFVLQCESDPEFVQWKKELNE
1	i	1	TPKEAQRLLRRAPKFINKPRSGTVELPKPSLCHRNSNGL
5955	1726	444	KREREFRLAVCPLRYPSAYESSPGTELRECGLCRSGQEFADCRR
		333	PANRODVLSGWINLPVLOLTKOPLKTPGRLDHGTRTAFIHHREO
1		1	
l	]	1	VWKRCINIWRDVGLFGVLNEIANSEBEVFBWVKTASGWALALCR
I		1	WASSLIGSLIPHLSLRSEDLIAEFAQVINWSSCCLRVFAHIPHT
!			NKFAVALLDDSVRVYNASSTIVPSLKHRLQRNVASLAWKPLSAS
i	1	1	VLAVACQSCILINTLDPTSLSTRPSSGCAQVLSHPGHTPVTSLA
j	1	1	WAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLLW
l .		ĺ	SPDGSKILATTPSAVFRVWEAQMWTCERWPTLSGRCQTGCWSPD
1	i	ì	GSRLLFTVIGEPLIYSLSFPERCGEGKG\ALEVQSQORLWQICL
1		l .	1
			RQQYRHQMVRRGLGERLTPWSGTPVGNVWLCL
5956	1705	139	GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAQKPFGA
		1	TYVWSSIINTLQTQVKVKKRRHRLKRHNDCFVGSEAVDVIFSHL
l	į.	ţ	IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT
l			FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR
l .	ì	}	SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL
ļ.	-		
i	·	i	LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK
1 .		<u> </u>	AYSDSQEDEWLSAAIDCSBYLPDQMVVBISRSFPEQPDRTDLVK
l		1	ELLFDAIGRYYSSREPLLNHLSDVHNGIAELLVNGKTEIALEAT
	ı		QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK
1	1	Ì	RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI
Í			VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE
	1	ł i	LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIBHFGD
5957	1479	451	ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK
1 2331	1 43/3	1 457	
1	1	Į	GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF
	1	1	SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIBNFV
l	1	ŀ	SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG
l	I	ł	PTVSNIRLAGLBYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIR
l	i	1	LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD
1	<b>J</b> .		TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPAERITEDHEKKS
l	1	l	KRIKKKLMBLSOPLLFHCVLLKRIIKHOSIOSFL
	<del></del>		
5958	1	3138	AAALGMLLNFPACQAFNLDVBKLTVYSGPKGSYFGYAVDFH1PD
l	l		ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
Ì		}	DITINNRKIRVNGTKEPIRPKSNQWFG\ATVKA\HKGKSCGPVAP
I	l		LLPTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP
}	1		EGOGYCOAGFSLDFYKNGDLIVGGPGSFYWOGOVITASVADIIA
ł .			NYSPKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSOO
l '	1		
[	ī.	1	ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV
!			VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL
			VSDVNSDGLDDVLVGAPLFMBRBFESNPRBVGQIYLYLQVSSLL FRDPQILTGTBTFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD
!			FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD
			FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIA IGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD
			FRDPQILTGTETFGEFGSAMAHLGDLNQDGYNDIA IGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAPGTGKVAVYRARPVVTVDAQLLLHPMIIN
			FRDPQILTGTETFGEFGSAMAHLGDLNQDGYNDIA IGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAPGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMABVQLD
			FRDPQILTGTETFGEFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAPGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMABVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSAQCQDFIVYLRD
			FRDPQILTGTETFGEFGSAMAHLGDLNQDGYNDIA IGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAPGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMABVQLD
			FRDPQILTGTETFGEFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAPGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETBFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE
			FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIA IGVPFAGKD QRGKULIYNGNKDGLNTKPPPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAPGTGKVAVYRARPVVTVDAQLLIHPMIIN LENKTCQVPDSMTSAACPSLRVCASVTGQSIANTIVIMBVQLD SLKQKGAIKRTLFLDNHQAHRVPPLVIKRQKSAQCQDPIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR
			FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIA IGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDLDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLHPMIIN LENKTCQVPDSMTSAACPSLRVCASVTGQSIANTIVLMABVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSAQCQDFIVYLRD ETBFRDKLSPINISLNYSLDBSTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHOVIIGDENHLMLIINAR NEGEGAYEAKLFVMIPEBADYVGIERNNKGFRPLSCEYKMENVT
			FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIA IGVPFAGKD QRGKULIYNGNKDGLNTKPPPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAPGTGKVAVYRARPVVTVDAQLLIHPMIIN LENKTCQVPDSMTSAACPSLRVCASVTGQSIANTIVIMBVQLD SLKQKGAIKRTLFLDNHQAHRVPPLVIKRQKSAQCQDPIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR

	ana di kacamatan bangara	- (Fil), 2	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
מז	beginning :	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1 1		i	P=Proline, Q=Glutamine, R=Arginine,
, ,	to first	amino acid	
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
i i	sequence		\=possible nucleotide insertion)
	Bequence		EPHKEEBYGPLVEHIYELHNIGPSTISDTILEVGWPFSARDEFL
ŀ	1	i	
}	ì	1	LYIFHIQTLGPLQCQPNPNINPQDIKPAASPEDTPELSAFLRNS
1 1	(	1	TIPHLVRKRDVHVVEFHRQSPAKILNCTNIECLQISCAVGRLEG
} i	i	į.	GESAVLKVRSRLWAHTFLQRKNDPYALASLVSFEVKKMPYTDQP
i !	1		AKLPEGSIAIKTSVIWATPNVSFSIPLWVIILAILLGLLVLAIL
	ł		
	l		TLALWKCGFFDRARPPQEDMTDREQLTNDKTPEA
5959	1	1166	GTSGYAAQQLPSLLKEREFHLGTLNKVFASQWLNHRQVVCGTKC
	J		NTLFVVDVQTSQITKIPILKDRBPGGVTQQGCGIHAIELNPSRT
	<b>!</b>	ľ	LLATGGDNPNSLAIYRLPTLDPVCVGDDGHKDWIFSIAWISDTM
! I	l	•	AVSGSRDGSMGLWEVTDDVLTKSDARHNVSRVPVYAHITHKALK
)	]	1	
t	l	1	DIPKEDTNPDNCKVRALAFNNKNKELGAVSLDGYFHLWKAENTL
1	l	1 .	SKLLSTKLPYCRENVCLAYGSEWSVYAVGSQAHVSFLDPRQPSY
1 1	}	1	NVKSVCSRERGSGIRSVSFYEHIITVGTGQGSLLFYDIRAQRFL
1. 1	i	ſ	BERLSACYGSKPRLAGENLKLTTG\KGWLNHDETWRNYFSDIDF
<b>!</b>		I	
	L		PPNAVYTHCYDSSGTKLFVAGGPLPSGLHGNYAGLWS
5960	2853	870	PVWSDGGPRPRRGPAVGAGAAHLSDPWAMTPGTANRATNPLNKB
	i		LDWASINGFCEQLNEDFEGPPLATRLLAHKIQSPQEWEAIQALT
1 1		}	VLETCMKSCGKRFHDEVGKFRFLNELIKVVSPKYLGSRTSEKVK
]	1	1	NKILELLYSWTVGLPEEVKLAEAYQMLKKQG\IVKSDPKLPDDT
1		1 .	TFPLPPPRPKNVIPEDEBKSKMLARLLKSSHPBDLRAANKLIKE
i l	Ì	ŀ	
<b>!</b>	<b>.</b>	1	MVQEDQKRMEKISKRVNAIEBVNNNVKLLTENVMSHSQGGAAAG
! i			SSEDL\MKEL\YQRCERMRPTLFPTGRVDTEDND\EALAEILQA
i	i .	ł	NONLTQVINLYKQLVRGEEVNGDATAGSIPGSTSALLDLSGLDL
	}		PPAGTTYPAMPTRPGRQASPEQPSASVSLLDDELMSLGLSDPTP
		i .	PSGPSLDGTGWNSPQSSDATEPPAPALAQAPSMESRPPAQTSLP
	1	į.	ASSGLDDLDLLGKTLLQQSLPPBSQQVRWEKQQPTPRLTLRDLQ
1 1	[	ł	
1	<b>t</b> .	1	NKSSSCSSPSSSATSLLHTVSPEPPRPPQQPVPTELSLASITVP
	•		LESIKPSNILPVTVYDQHGFRTLFHFARDPLPGRSDVLVVVVSM
l i	Ì	1	LSTAPQPIRNIVFQSAVPKVMKVKLQPPSGTELPAFNPIVHPSA
1	}	Ì	ITOVLLLANPOKEKVRLRYKLTPTMGDQTYNEMGDVDQFPPPET
		1	WGSL
		3.45	SGEPRPEPGNMATCIGEKIEDFKVGNLLGKGSFAGVYRAESIHT
5961	198	3147	
			GLEVAIKMIDKKAMYKAGMVQRVQNEVKIHCQLKHPSILELYNY
			FEDSNYVYLVLEMCHNGRMNRYLKNRVKPFSENEARHFMHQIIT
	t .	ł	CMLYLHSHGILHRDLTLSNLLLTRNMNIKIADFGLATQLKMPHB
	1	l .	KHYTLCGTPNYISPETATRSAHGLESDVWSLGCMFYTLLIGRPP
j	ŀ	1	PDTDTVKNTLNKVVLADYEMPTFLSIEAKDLIHQLLRRNPADRL
[	Į.	Į.	
]	1	B .	SLSSVLDHPFMSRNSSTKSKDLGTVEDSIDSGHATISTAITASS
		B	
1			STSISGSLFDKRRLLIGQPLPNKMTVFPKNKSSTDFSSSGDGNS
			STSISGSLFDKRRLLIGQPLPNKMTVFPKNKSSTDFSSSGDGNS FYTQWGNQETSNSGRGRVIQDABERPHSRYLRRAYSSDRSGTSN
			FYTOWGNOETSNSGRGRVIODABERPHSRYLRRAYSSDRSGTSN SOSQARTYTMBRCHSAEMLSVSKRSGGGKNEERYSPTONNANIF
			FYTOWGNOETSNSGRGRVIODABERPHSRYLRRAYSSDRSGTSN SOSOARTYTMERCHSAEMLSVSKRSGGGENEERYSPTONNANIF NFFKEKTSSSSGSFERPDNNQALSNHLCPGKTPFPFADPTPQTB
			FYTOWGNOETSNSGRGRVIODABERPHSRYLRRAYSSDRSGTSN SOSOAKTYTMERCHSAEMLSVSKRSGGGKNEERYSPTONNANIF NFFKEKTSSSSGFERPDNNQALSNHLCPGKTPFPFADPTPQTB TVQQWFGNLQINAHLRKTTEYDSISPNRDFQGHPDLQKDTSKNA
			FYTOWGNOETSNSGRGRVIODABERPHSRYLRRAYSSDRSGTSN SOSQARTYTMERCHSAEMLSVSKRSGGGENEERYSPTONNANIF NFFKEKTSSSSGFERPDNNQALSNHLCPGKTPFPFADPTPQTE TVQQWFGNLQINAHLRKTTEYDSISPNRDFQGHPDLQRDTSKNA WTDTKVKKNSDASDNAHSVKQQNTMKYWTALHSKPBIIQQECVF
			FYTOWGNOETSNSGRGRVIODABBRPHSRYLRRAYSSDRSGTSN SQSQAKTYTMBRCHSABMLSVSKRSGGGKNBERYSPTONNANIF NFFKEKTSSSSSFBRPDNNQALSNHLCPGKTPFPFADPTPQTB TVQQWFGNLQINAHLRKTTEYDSISPNRDFQCHPDLQRDTSKNA WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPBIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLRSITSPLVAHRLKPIRQKT
			FYTOWGNOETSNSGRGRVIODABERPHSRYLRRAYSSDRSGTSN SOSQARTYTMERCHSAEMLSVSKRSGGGENEERYSPTONNANIF NFFKEKTSSSSGFERPDNNQALSNHLCPGKTPFPFADPTPQTE TVQQWFGNLQINAHLRKTTEYDSISPNRDFQGHPDLQRDTSKNA WTDTKVKKNSDASDNAHSVKQQNTMKYWTALHSKPBIIQQECVF
			FYTOWGNOETSNSGRGRVIODABERPHSRYLRRAYSSDRSGTSN SQSQAKTYTMERCHSAEMLSVSKRSGGGKNEERYSPTOMAANIF NFFREKTSSSSSFERPDNNQALSHHLCPGKTPFPFADPTPQTE TVQQWFGNLQINAHLRKTTEYDSISPNRDPQCHPDLQKDTSKNA WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLESITSPLVAHRLKPIRQKT KKAVVSILDSEEVCVKLVKEYASQEYVKEVLQISSDGNTITIYY
			FYTOWGNOETSNSGRGRVIODABERPHSRYLRRAYSSDRSGTSN SQSQAKTYTMERCHSAEMLSVSKRSGGGENEERYSPTONNANIF NFFREKTSSSSSFERPONNQALSMILCPGKTPFPFADPTPQTB TVQWFGNLQINAHLRKTTEYDSISPNRDFQCHPDLQKDTSKNA WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLRSITSPLVAHRLKPIRQKT KKAVVSILDSEEVCVRLVKEYASQEYVKEVLQISSDGNTITIYY PNGG\RGPPLA\DRPPSPT\DNISR\YSF\DNLPEKYWRKYQYA
			FYTOWGNOETSNSGRGRVIODABERPHSRYLRRAYSSDRSGTSN SQSQAKTYTMERCHSAEMLSVSKRSGGGENERRYSPTONNANIF NFFREKTSSSSGSFERPONNQALSMILLCPGKTPFPFADDTPQTB TVQWFGNLQINAHLRKTTEYDSISPNRDFQCHPDLQKDTSKNA WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPBIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLRSITSPLVAHRLKPIRQKT KKAVVSILDSEEVCVRLVKEYASQEYVKEVLQISSDGNTITIYY PNGG\RGPPLA\DRPPSPT\DNISR\YSP\DNLPEKYWRKYQYA SRFVQLVRSKSPKITYPTRYAKCILMENSPGADFEVNFYDGVKI
			FYTOWGNOETSNSGRGRVIQDABBRPHSRYLRRAYSSDRSGTSN SQSQARTYTMBRCHSABMLSVSKRSGGGKNBERYSPTIDNAANIF NFFKEKTSSSSGSERPDNNQALSHHLCPGKTPFPFADPTPQTB TVQQWFGNLQINAHLRKTTBYDGISPNRDFQCHPDLQKDTSKNA WIDTKVKKNSDASDNAHSVKQQNTMKYWTALHSKPBIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLRSITSPLVAHRLKPIRQKT KKAVVSILDSERVCVBLVKEYASQBYVKBVLQISSDGMTITIYY PNGG\RGPPLA\DRPPSPT\DNISR\YSP\DNLPEKYWRKYQYA SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVNFYDGVKI HKTEDFIQVIEKTGKSYTLKSBSEVNSLKBBIKMYMDHANBGHR
			FYTOWGNOETSNSGRGRVIODABERPHSRYLRRAYSSDRSGTSN SQSQAKTYTMERCHSAEMLSVSKRSGGGENERRYSPTONNANIF NFFREKTSSSSGSFERPONNQALSMILLCPGKTPFPFADDTPQTB TVQWFGNLQINAHLRKTTEYDSISPNRDFQCHPDLQKDTSKNA WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPBIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLRSITSPLVAHRLKPIRQKT KKAVVSILDSEEVCVRLVKEYASQEYVKEVLQISSDGNTITIYY PNGG\RGPPLA\DRPPSPT\DNISR\YSP\DNLPEKYWRKYQYA SRFVQLVRSKSPKITYPTRYAKCILMENSPGADFEVNFYDGVKI
			FYTOWGNOETSNSGRGRVIQDABBRPHSRYLRRAYSSDRSGTSN SQSQARTYTMBRCHSABMLSVSKRSGGGKNBERYSPTIDNAANIF NFFKEKTSSSSGSERPDNNQALSHHLCPGKTPFPFADPTPQTB TVQQWFGNLQINAHLRKTTBYDGISPNRDFQCHPDLQKDTSKNA WIDTKVKKNSDASDNAHSVKQQNTMKYWTALHSKPBIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLRSITSPLVAHRLKPIRQKT KKAVVSILDSERVCVBLVKEYASQBYVKBVLQISSDGMTITIYY PNGG\RGPPLA\DRPPSPT\DNISR\YSP\DNLPEKYWRKYQYA SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVNFYDGVKI HKTEDFIQVIEKTGKSYTLKSBSEVNSLKBBIKMYMDHANBGHR
			FYTOWGNOETSNSGRGRVIODABERPHSRYLRRAYSSDRSGTSN SQSQAKTYTMERCHSAEMLSVSKRSGGGKNERRYSPTONAANIF NFFKEKTSSSGSFERPDNNQALSHHLCPGKTPFPFADPTPQTB TVQQWFGNLQINAHLRKTTEYDSISPNRDFQCHPDLQKDTSKNA WTDTKVKKNSDASDANAHSVKQQNTMKYMTALHSKPEIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLESITSPLVAHRLKPIRQKT KKAVVSILDSEEVCVELVKEYASQEYVKEVLQISSDGNTITIYY PNGG\RGPPLA\DRPPSPT\DNISR\YSP\DNLPEKYMRKYQYA SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVMPYDGVKI HKTEDFIQVIEKTGKSYTLKSESEVNSLKEBIKMYMDHANBGHR ICLALESIISBERKKTRSAPFFPIIIGRKPGSTSSPKALSPPPS VDSNYPTRORASFNRMYMHSAASPTQAPILNPSMVTN3GLGLTT
			FYTOWGNOETSNSGRGRVIODABERPHSRYLRRAYSSDRSGTSN SQSQAKTYTMERCHSAEMLSVSKRSGGGKNEERYSPTONAANIF NFFREKTSSSSGFERPDNNQALSHHLCPGKTPFPFADPTPQTB TVQQWFGNLQINAHLRKTTEYDSISPNRDFQCHPDLQRDTSKNA WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPBIIQQECVF GSDPLSEQSKTEGMSPPWGYQNRTLESITSPLVAHRLKPIRQKT KKAVVSILDSEEVCVELVKEYASQBYVKEVLQISSDGNTITIYY PNGG\RGPPLA\DRPPSPT\DNISR\YSP\DNLPEKYMRKYQYA SRFVQLVRSKSPKITYFTRYAKCTLMENSPGADFEVNFYDGVKI HKTEDFIQVIEKTGKSYTLKSBESVNSLKBBIKMYMDHANBGHR ICLALBSIISBKBRKTRSAPPFPIIIGRKPGSTSSPKALSPPPS VDSNYPTRDRASFNRMVMHSAASPTQAPILMPSMVTN3GLGLTT TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGMATQ\LTSGAVW
			FYTOWGNOETSNSGRGRVIQDABERPHSRYLRRAYSSDRSGTSN SQSQAKTYTMERCHSAEMLSVSKRSGGGKBERRYSPTDNNANIF NFFREKTSSSSGFBRPDNNQALSHHLCPGKTPFPFADPTPQTB TVQQWFGNLQINAHLRKTTEYDSISPNRDFQCHPDLQRDTSKNA WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPBIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLESITSPLVAHRLKPIRQKT KKAVVSILDSEEVCVELVKEYASQBYVKEVLQISSDGNTITIYY PNGG\RGPPLA\DRPPSPT\DNISR\YSP\DNLPEKYMRKYQYA SRFVQLVRSKSPKITYFTRYAKCTLMENSPGADFEVNFYDGVKI HKTEDFIQVIEKTGKSYTLKSBESVNSLKBBIKMYMDHANBGHR ICLALBSIISBKBRKTRSAPPFPIIIGRKPGSTSSPKALSPPPS VDSNYPTRDRASFNRMVMHSAASPTQAPILMPSMVTN3GLGLTT TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGMATQ\LTSGAVW VQFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENEKLPDYIKQ
			FYTOWGNOETSNSGRGRVIQDABBRPHSRYLRRAYSSDRSGTSN SQSQARTYTMBRCHSABMLSVSKRSGGGKNBERYSPTIDNAANIF NFFKEKTSSSGSFREDNNQALSHILCPGKTPFPFADPTPQTB TVQQWFGNLQINAHLRKTTEYDGISPNRDFQCHPDLQKDTSKNA WIDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLRSITSPLVAHRLKPIRQKT KKAVVSILDSERVCVBLVKEYASQBYVKBVLQISSDGRTITIYY PNGG\RGPPLA\DRPPSPT\DNISR\YSP\DNLPEKYWRKYQYA SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVNFYLGVKI HKTEDFIQVIEKTGKSTILKSESEVNSLKEBIKMYMDHANBGHR ICLALESIISBKBRKTRSAPPFPIIIGRKPGSTSSPKALSPPPS VDSNYPTRDRASFNRMWHSAASPTQAPILMPSMVTNSGLGLTT TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGMATQ\LTSGAVW VQFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENBKLPDYIKQ KLQCLSSILLMFSNPTPNFH
5962	20	2447	FYTOWGNOETSNSGRGRVIQDABBRPHSRYLRRAYSSDRSGTSN SQSQARTYTMBRCHSABMLSVSKRSGGGKNBERYSPTIDNAANIF NFFKEKTSSSGSFREDNNQALSHILCPGKTPFPFADPTPQTB TVQQWFGNLQINAHLRKTTEYDGISPNRDFQCHPDLQKDTSKNA WIDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLRSITSPLVAHRLKPIRQKT KKAVVSILDSERVCVBLVKEYASQBYVKBVLQISSDGRTITIYY PNGG\RGPPLA\DRPPSPT\DNISR\YSP\DNLPEKYWRKYQYA SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVNFYLGVKI HKTEDFIQVIEKTGKSTILKSESEVNSLKEBIKMYMDHANBGHR ICLALESIISBKBRKTRSAPPFPIIIGRKPGSTSSPKALSPPPS VDSNYPTRDRASFNRMWHSAASPTQAPILMPSMVTNSGLGLTT TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGMATQ\LTSGAVW VQFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENBKLPDYIKQ KLQCLSSILLMFSNPTPNFH
5962	20	2447	FYTOWGNOETSNSGRGRVIQDABBRPHSRYLRRAYSSDRSGTSN SOSQARTYTMBRCHSABMLSVSKRSGGGKNBBRYSPTONNANIF NPFKEKTSSSGSFBRPDNNQALSHILCPGKTPFPFADPTPQTB TVQQWFGNLQINAHLRKTTBYDGISPNRDPQCHPDLQRDTSKNA WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPBIJQGECVF GSDPLSEQSKTRGMSPPWGYQNRTLBSITSPLVAHRLKPIRQKT KKAVVSILDSBEVCVBLVKEYASQBYVKBVLQISSDGRTITIYY PNGG\RGPPLA\DRPPSPT\DNISR\YSP\DNLPEKYWRKYQYA SRFVQLVRSKSPKITYPTRYAKCILMENSPGADPEVNFYDGVKI HKTBDFIQVIBKTGKSTTLKSBSBVNSLKBLKMYMDHANBGHR ICLALESIISBKBRKTRSAPPFPIIIGRKPGSTSSPKALSPPPS VJSNYPTRDRASFNRMVHISAASPTQAPILMPSMVTNBGLGLTT TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGMATQ\LTSGAVW VQFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENEKLPDYIKQ KLQCLSSILLMPSNPTPNPH RVCSSSASTASQAVMADAWERIRRLAADFQRAGFAEATQRLSER
5962	20	2447	FYTOWGNOETSNSGRGRVIQDABBRPHSRYLRRAYSSDRSGTSN SQSQAKTYTMBRCHSABMLSVSKRSGGGKNBERYSPTONNANIF NFFKEKTSSSGSFERPDNNQALSHHLCPGKTPFPFADPTPQTB TVQQWFGNLQINAHLRKTTEYDGISPNRDPQCHPDLQRDTSKNA WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPBIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLRSITSPLVAHRLKPIRQKT KKAVVSILDSBEVCVBLVKEYASQBYVKBVLQISSDGRTITIYY PNGG\RGPPLA\DRPPSFT\DNISR\YSP\DNLPEKYWRKYQYA SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVWFYDGVKI HKTBDFIQVIBKTGKSYTIKSBSRVNSLKEBIKMYMDHANBGHR ICLALBSIISBKBRKTRSAPPFPIIIGRKPGSTSSPKALSPPPS VDSNYPTRDRASFNRMVMHSAASPTQAPILNPSMVTN3GLGLTT TASGTDISSNSLKDCLERSAQLLKSVFVKNVGMATQ\LTSGAVW VQFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENEKLPDYIKQ KLQCLSSILLMFSNPTPNFH RVCSSSASTASQAVMÄDAWERIRRLAADFQRAQFARATQRLSER NCIEIVNKLIAQKQLEVYHTLDGKEYITPAQISKEMRDBLHVRG
5962	20	2447	FYTOWGNOETSNSGRGRVIQDABERPHSRYLRRAYSSDRSGTSN SQSQAKTYTMERCHSAEMLSVSKRSGGGKNERRYSPTDNNANIF NFFREKTSSSSSFERPDNNQALSHHLCPGKTPFPFADPTPQTB TVQQWFGNLQINAHLRKTTEYDSISPNRDFQCHPDLQKDTSKNA WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLESITSPLVAHRLKPIRQKT KKAVVSILDSEEVCVELVKEYASQEYVKEVLQISSDGNTITIYY PNGG\RGPPLA\DRPPSPT\DNISR\YSP\DNLPEKYMRKYQYA SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVNFYDGVKI HKTEDFIQVIEKTGKSYTLKSESEVNSLKEBIKMYMDHANBGHR ICLALESIISBRERKTRSAPFPFIIIGRKPGSTSSPKALSPPPS VDSNYPTRDRASFNRMVMHSAASPTQAPILNPSMVTNSGLGLTT TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGMATQ\LTSGAVM VOFNDGSQLVVQAGVSSISYTSPNGQ\TTR\TGENEKLPDYIKQ KLQCLSSILLMFSNPTPNFH RVCSSSASTASQAVMADAWERIRRLAADFQRAQFAEATQRLSER NCIEIVNKLIAQKQLEVVHTLDGKEYITPAQISKEMRDELHVRG GRVNIVDLQQVINVDLIHIENRIGDIIKSEKHVQLVLGQLIDEN
5962	20	2447	FYTOWGNOETSNSGRGRVIQDABERPHSRYLRRAYSSDRSGTSN SQSQAKTYTMERCHSAEMLSVSKRSGGGKBERRYSPTDNAANIF NFFREKTSSSSSFERPDNNQALSHHLCPGKTPFPFADPTPQTB TVQQWFGNLQINAHLRKTTEYDSISPNRDFQCHPDLQKDTSKNA WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLESITSPLVAHRLKPIRQKT KKAVVSILDSEEVCVELVKEYASQEYVKEVLQISSDGNTITIYY PNGG\RGPPLA\DRPPSPT\DNISR\YSP\DNLPEKYMRKYQYA SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVMFYDGVKI HKTEDFIQVIEKTGKSYTLKSESEVNSLKEBIKMYMDHANBGHR ICLALESIISBEBRKTRSAPPFPIIIGRKPGSTSSPKALSPPPS VDSNYPTRDRASFNRMVMHSAASPTQAPILNPSMVTNSGLGLTT TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGMATQ\LTSGAVM VQFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENEKLPDYIKQ KLQCLSSILLMFSNPTPNFH RVCSSASTASQAVMADAWEEIRRLAADFQRAQFAEATQRLSER NCIEIVNKLIAQKQLEVVHTLDGKEYITPAQISKEMRDELHVRG GRVNIVDLQQVINVDLHHENRIGDIIKSRKHUQLVLGQLIDEN YLDRLAEEVNDKLQESGQVTISELCKTYDLPGNFLTQALTQRLG
5962	20	2447	FYTOWGNOETSNSGRGRVIQDABERPHSRYLRRAYSSDRSGTSN SQSQAKTYTMERCHSAEMLSVSKRSGGGKNERRYSPTDNNANIF NFFREKTSSSSSFERPDNNQALSHHLCPGKTPFPFADPTPQTB TVQQWFGNLQINAHLRKTTEYDSISPNRDFQCHPDLQKDTSKNA WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLESITSPLVAHRLKPIRQKT KKAVVSILDSEEVCVELVKEYASQEYVKEVLQISSDGNTITIYY PNGG\RGPPLA\DRPPSPT\DNISR\YSP\DNLPEKYMRKYQYA SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVNFYDGVKI HKTEDFIQVIEKTGKSYTLKSESEVNSLKEBIKMYMDHANBGHR ICLALESIISBRERKTRSAPFPFIIIGRKPGSTSSPKALSPPPS VDSNYPTRDRASFNRMVMHSAASPTQAPILNPSMVTNSGLGLTT TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGMATQ\LTSGAVM VOFNDGSQLVVQAGVSSISYTSPNGQ\TTR\TGENEKLPDYIKQ KLQCLSSILLMFSNPTPNFH RVCSSSASTASQAVMADAWERIRRLAADFQRAQFAEATQRLSER NCIEIVNKLIAQKQLEVVHTLDGKEYITPAQISKEMRDELHVRG GRVNIVDLQQVINVDLIHIENRIGDIIKSEKHVQLVLGQLIDEN
5962	20	2447	FYTOWGNOETSNSGRGRVIQDABBRPHSRYLRRAYSSDRSGTSN SQSQARTYTMBRCHSABMLSVSKRSGGGKNBERYSPTINNANIF NFFKEKTSSSGSFREPDNNQALSHHLCPGKTPFPFADPTPQTB TVQQWFGNLQINAHLRKTTEYDGISPNRDFQCHPDLQKDTSKNA WIDTKVKKNSDASDNAHSVKQQNTMKYWTALHSKPEIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLRSITSPLVAHRLKPIRQKT KKAVVSILDSERVCVBLVKEYASQBYVKBVLQISSDGRTITIYY PNGG\RGPPLA\DRPPSPT\DNISR\YSP\DNLPEKYWRKYQYA SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVNPYLGVKI HKTEDFIQVIEKTGKSYTLKSESEVNSLKEBIKMYMDHANBGHR ICLALESIISBKBRKTRSAPPFPIIIGRKPGSTSSPKALSPPPS VDSNYPTRDRASFNRMWHSAASPTQAPILMFSMVTNEGLGLTT TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGMATQ\LTSGAVW VOFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENBKLPDYIKQ KLQCLSSILLMFSNPTPNFH RVCSSSASTASQAVMADAWERIRRLAADFQRAQFAEATQRLSER NCIETVNKLIAQKQLEVYHTLDGKRYITPAQISKEMRDELHVRG GRVNIVDLQQVINVDLIHIENRIGDIKSBKHVQLVLGQLIDEN YLDRLABEVNDKLQESGQVTISELCKTYDLPGMFLTQALTQRLG RIISGHIDLDNRGVIFTSAFVARHKARIRGLFSAITRPTAVNSL
5962	20	2447	FYTOWGNOETSNSGRGRVIQDABERPHSRYLRRAYSSDRSGTSN SQSQAKTYTMERCHSAEMLSVSKRSGGGKBERRYSPTDNAANIF NFFREKTSSSSSFERPDNNQALSHHLCPGKTPFPFADPTPQTB TVQQWFGNLQINAHLRKTTEYDSISPNRDFQCHPDLQKDTSKNA WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF GSDPLSEQSKTRGMSPPWGYQNRTLESITSPLVAHRLKPIRQKT KKAVVSILDSEEVCVELVKEYASQEYVKEVLQISSDGNTITIYY PNGG\RGPPLA\DRPPSPT\DNISR\YSP\DNLPEKYMRKYQYA SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVMFYDGVKI HKTEDFIQVIEKTGKSYTLKSESEVNSLKEBIKMYMDHANBGHR ICLALESIISBEBRKTRSAPPFPIIIGRKPGSTSSPKALSPPPS VDSNYPTRDRASFNRMVMHSAASPTQAPILNPSMVTNSGLGLTT TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGMATQ\LTSGAVM VQFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENEKLPDYIKQ KLQCLSSILLMFSNPTPNFH RVCSSASTASQAVMADAWEEIRRLAADFQRAQFAEATQRLSER NCIEIVNKLIAQKQLEVVHTLDGKEYITPAQISKEMRDELHVRG GRVNIVDLQQVINVDLHHENRIGDIIKSRKHUQLVLGQLIDEN YLDRLAEEVNDKLQESGQVTISELCKTYDLPGNFLTQALTQRLG

		- 1, x	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G=Glycine,
<b>\</b>	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		PLKAACVGOGLVDOVBASVEBAISSGTWVDIAPLLPTSLSVEDA
1	]	]	AILLQQVMRAFSKQASTVVFSDTVVVSEKF\INDCTELFRELMH
1	ĺ		QKAEKEMKNNPVHLITERDLKQISTLESVSTSKKDKKDERRRKA
1	1	1	TEGSGSMRGGGGGNAREYKIKKVKKKGRKDDDSDDESQSSHTGK
	{		KKPEISPMFODEIRDPLRKHIODAPKEFISELABYLIKPLNKTY
l	}	}	LEVVRSVFMSSTTSASGTGRKRTIKDLQEEVSNLYNNIRLFEKG
l	ĺ	1	MKFFADDTQAALTKHLLKSVCTDITNLIFNFLASDLMMAVDDPA
ļ	<b> </b>	}	AITSEIRKKILSKISEETKVALTKUHNSINEKSIEDFISCLOSA
<b>,</b>	j	1	ARACDIMVKRGDKKRBRQILFQHRQALAEQLKVTEDPALILHLT
ĺ	ł	Į	SVLLFQFSTHSMLHAPGRCVPQIIAFLNSKIPEDQHALLVKYQG
l	<b>!</b>	[	LVVKQLVSQSKKTGQGDYPLNNBLDKEQEDVASTTRKELQELSS
		i .	SIKDLVLKSRKSSVTRE
5963	62	1130	PWNPQDFPGNRGLMG\QKGBIGPP\GQQGKKGAPGMP\GLMGSN
l	J	[	GSPGQPGTPGSKGSKGEPGIQGMPGASGLKGEPGATGSPGEPGY
1	1	1.	MGLPGIQGKKGDKGNQGEKGIQGQKGENGRQGIPGQQGIQGHHG
	Į	•	AKGERGEKGBPGVRGATGSKGESGVDGLMGPAGPKGQPGDPGPQ
1		ŀ	GPPGLDGKPGRBFSEQFIRQVCTDVIRAQLPVLLQSGRIRNCDH
ł	<b> </b> .		CLSQHGSPGIPGPPGPIGPEGPRGLPGLPGRDGVPGLVGVPGRP
	{	·	GVRGLKGLPGRNGEKGSQGFGYPGEQGPPGPPGPEGPPGISKEC PPGDPGLPGKDGDHGKPGIQGQPGPPGICDPSLCFSVIARRDPF
1	!		REGENT
5964	3	2147	SCRTRGRLSPLOPRBAGSSRGSRARSEPPRPGGMEEACQVQTTK
3304		2147	REDPHELRNIFLOYASTEVDGERYMTPEDFVQRYLGLYNDPNSN
	1	1	PKIVQLLAGVADQTKDGLISYQEFLAFESVLCAPDSMFIVAFQL
		4.4	FDKSGNGEVTFENVKEIFGQTIIHHHIPFNWDCEFIRLHFGHNR
		1	KKHLNYTEFTQFLQELQLEHARQAFALKDKSKSGMISGLDFSDI
	1	•	MVTIRSHMLTPFVEENLVSAAGGSISHQVSFSYFNAFNSLLNNM
			ELVRKIYSTLAGTRKDAEVTKEEFAQSAIRYGQATPLEIDILYQ
1	1	Ī	LADLYNASGRUTLADIERIAPLAEGALPYNLAELQRQQSPGLGR
	1	1	PIWLQIAESAYRFTLGSVAGAVGATAVYPIDLVKTRMQNQRGSG
	ł		SVVGBLMYKNSFDCFKKVLRYEGFFGLYRGLIPQLIGVAPBKAI
			KLTVNDFVRDKFTRRDGSVPLPAEVLAGGCAGGSQVIFTNPLSI VKTRLQVAGBITTGPRVSALNVLRDLGIFGLYKGAKACFLRDIP
1		·	FSA TYFPYYAHCKILLADBNGHVGGLNLLAAGAMAG\VPAASLV
l		1	TPADVIKTRLQVAARAGQTTYSGVIDCFRKIL\RBEGPSAFWKG
l	l	Į.	TAARVFRSSPOFG\VTLVTYELLQRGPYIDFGGLKPAGSBPTPK
	1	1	SRIADLPPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPSVA
l	1	i	VVQPKAAVAATQ
5965	1	1498	MVTWLYRFLPTSNMAAKLRSLLPPDLRLQFWLHARLQKCFLSRG
[			CGSYCAGAKASPLPGKMAMGLMCGRRBLLRLLQSGRRVHSVAGP
}	)	1	SQWLGKPLTTRLLFPAAPCCCRPHYLFLAASGPRSLSTSAISFA
1	1	1	evovoappvvaatpsptavpbvasgbtadvvotaaeosfaelgl
1	1	<b>{</b>	GSYTPVGLIQNLLBFMHVDLGLPWWGAIAACTVFARCLIFPLIV
		1	TGQREAARIINHLPEIQKF9SRIREAKLAGDHIKYYKASSEMAL
Į.	Į.	(	YOKKHGIKLYKPLILPVTQAPIFISFFLALREMANLPVPSLQTG
		1	GLWWFQDLTVSDPIYILPLAVTATMWAVLELGAETGVQSSDLQW
I	Į	ļ	MRNVIRMMPLITLPITMHFPTAVFMYWLSSNLFSLVQVSCLRIP
[	1	1	AVRTVLKI PORVVHOLDKLPPREGFLESFKKGWKNAEMTROLRE
İ	1	1	RECEMPINGLELAARGPLRQTFTHNPLLQPGKDNPPNIPSS\SSS
5966	100	1925	SSKPKSKYPWHDTIG RSKQVMARLTKRRQADTKAIQHLWAAIRIIRNQKQIANIDRITK
2366	102	1925	YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQK
1		1	GYWLPGDBIDWETENHDWYCFBCHLPGEVLICDLCFRVYHSKCL
			SDEFRERDSSSPWQCPVCRSIKKKNTNKQEMGTYLRFIVSRMKE
}	1	1	RAIDLNKKGKDNKHPMYRRLVRSAVDVPTIQBKVNEGKYRSYEB
1			FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHKL\DRLQLC
{	1	}	KNCPYLANARPDNWPCYPCIPNHELDWAKMKGFGFWPAKVMQKB
l		1	DNOVDVRFFGHHHORAWIPSENIQDITVNIHRLHVKRSMGWKKA
1	1		CDELELHORFLREGRPWKSKNEDRGEEEABSSISSTSNEOLKVT
	1	i	QEPRAKKGRRNQSVEPKKEEPBPETEAVSSSQEIPTMPQPIEKV
l	l	I	SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF
			<u> </u>

414

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide _	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P-Proline, Q=Glutamine, R=Arginine,
]	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ			
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			KDRMKSDHKRETERVVREALEKLRSEMBEEKRQAVNKAVANMQG
l .	Į.		EMDRKCKQVKEKCKEEFVEEIKKLATQHKQLISQTKKKQWCYNC
l		1	REEAMYHCCWNTSYCSIKCQQEHWHAEHKRTCRRKR
5967	102	1925	RSKOVMARITKRROADTKAIOHLWAAIEIIRNOKOIANIDRITK
330.		1	YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQB
1			GYWLPGDBIDWETENHDWYCFECHLPGEVLICDLCFRYYHSKCL
į .			1
ļ			SDEFRLRDSSSPWQCPVCRSIKKKNTNKQEMGTYLRFIVSRMKE
l	<b>{</b>	{	RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYBE
			FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DBLQLC
1		ſ	KNCFYLANARPDNWFCYPCIPNHELDWAKMKGFGFWPAKVMQKB
	ļ	1	DNQVDVRFFGHHHQRAVIPSENIQDITVNIHRLHVKRSMGWKKA
l			CDELRLHORFLREGRPWKSKNEDRGREEABSSISSTSNBOLKVT
{	İ	Į.	<b>QEPRAKKGRRNQSVEPKKEEPEPETEAVSSSQEIPTMPQPIEKV</b>
Ì	1		SVSTOTKKLSASSPRMLHRSTOTTNDGVCQSMCHDKYTKIFNDF
1		į.	
i		ļ	KORNKSDHKRETERVVREALEKLRSEMEEEKRQAVNKAVANMQG
1			EMDRKCKQVKBKCKEBFVBBIKKLATQHKQLISQTKKKQWCYNC
L			EBEAMYHCCWNTSYCSIKCQQEHWHAEHKRTCRRKR
5968	81	1288	VRFPRRGGAPPTVL'I'PGRQQGVFLGPQRPGSBPDIPARGQPHPP
}	1		RPVGVSTSAQAQVQPPAMHRRRLALGLGFCLLACTELSVLWVYL
	i	ł	ENWLPVSYVPYYLPCPBIFNMKLHYKREKPLQPVVWSQYPQPKL
]	1	]	LEHRPTQLLTLTPWLAPIVSEGTFNPBLLQHIYQPLNLTIGVTV
l	ļ.		PAVGN/HPLESAREFFWRGYRVHYYIFTDNPAAVPGVPLGPHRL
1			LSSIPIOGHSHWEETSMRRMETISOHIAKRAHREVDYLFCLDVD
1		ļ	MVFRNPWGPETLGDLVAAIHPSYYAVPRQQFPYERRRVSTAFVA
1		ì	DSBGDFYYGGAVFGGQVARVYEFTRGCHMAILADKANGIMAAWR
1		1	
i		ľ	EESHLNRHFISNKPSKVLSPEYLWDDRKPQPPSLKLIRFSTLDK
	<u> </u>	<u> </u>	DISCLRS
5969	1126	503	DVGFNIKRKRCDLDVFLESPRKPSGRRDRAPEKQRRIAANKCLC
ſ			TGVREGEPPS/TTSQKVKEAGRDFTYLIVVLFGISITGGLFYTI
ì	į	1	FKELFSSSPSKIYGRALEKCRSHPEVIGVFGBSVKGYGEVTRR
ŧ	l	į	GRRQHVRFTEYVKDGLKHTCVKFYTEGSEPGKQGTVYAQVKENP
ĺ	1	1	GSGRYDFRYIFVRIESYPRRTIIIEDNRSQDD
5970	316	4712	SODNIGHRLLORHGWKLGOGLGKSLQGRTDPIPIVVKYDVMGMG
]	1	1	RMEMKLDYAEDATERRRVLEVEKEDTEELRQKYKDYVDKEKAIA
1	1	ĺ	KALEDLRANFYCELCDKQYQKHQBFDNHINSYDHAHKQRLKDLK
(	Į	1	OREFARNVSSRSRKDEKKOEKALRRLHKLABORKQABCAPGSGP
ļ	ł	i	MFKPTTVAVDEEGERDKDESATNSGTGATASCGLGSEFSTDKG
ł	l .	}	1
	Î	1	GPFTAVQITNTTGLAQAPGLASQGISFG1KNNLGTPLQKLGVSF
)	]	ì	SPAKKAPVKLESIASVFKDHABEGTSEDGTKPDEKSSDQGLQKV
į	1	<u>į</u>	GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE
I		1	PEYYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES
1	1	1	KKGSSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS
l	1	1 .	KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA
]	]	}	GKESOEGPKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS
i	ļ	1	YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE
Į		1	PNRSKEVGGEKIVRSSGGRMDAPASGSACSGLNKOEPGGSHGSE
1	1	1	TEDTGRSLPSKKERSGKSHRHKKKKKHKKSSKHKRKHKADTEEK
		-	
1	1	]	SSKAESGEKSKKRKKKKKKKKKKKKSSAPADSKRGPKPEPPGSGSPA
ļ	!	Į.	PPRRRRAQDDSQRRSLPABEGSSGKKDEGGGGSSSQDHGGRKH
I			KGKLPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHQ
1	}	1	KSPSQYSKEKEKEDSGSEHSRSRSRSGRRHSSHRSSRRSYSSSS
			DASSDQSCYSRQR8YSDDSYSDYSDRSRRHSKRSHDSDDSDYAS
J	1	]	SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRGRSRS
1	Į.	1	SSCSRSRSKRRSRSTTAHSWORSRSYSRDRSRSTRSPSQRSGSR
	1	}	KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK
1	1	1	DDGRGDDSKATGPPSONSNIGTGRGSEGDCSPEDKNSVTAKLLL
1	1		EKIOSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS
ì	1	}	
ļ		Į.	LGNKPVLPLIGKLPATRKPNKKCRESGLERGEBQEQSETEEGPP
l	)	1	GSSDALFGHQFP\SEETTGPLLDPPPEESK3GEVTADHPVAPLG
i	1	1	PPAHPDCYLGDPTISHNYLPDPSDGNTLESLDSSSOPGPVESSL
1	1	1	LPIAPDLEHFPSYAPPSGDPSIESTDGAEDA\SLAPLESQPITF

PCT/US00/34263

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, FaPhenylalanine, GaGlycine,
J	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1 .	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	N=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
)	1	acquence	\=possible nucleotide insertion)
<b></b>	sequence	<u> </u>	<u> </u>
Į	ł	ł	TPEEMBKYSKLQQAAQQHIQQQLLAKQVKAFPASAALAPATPAL
Į		ľ	QPIHIQQPATASATSITTVQHAILQHHAAAAAAAIGIHPHPHPQ
1	ł	1	PLAQVHHIPQPHLTPISLSHLTHSIIPGHPATFLASHPIHIIPA
ł	1	1	SAIHPGPFTFHPVPHAALYPTLLAPRPAAAAATALHLHPLLHPI
ł	1 .	ł	FSGQDLQHPPSHGT
5971	53	2149	SFLYFVGVDMDNPIGNWDGRFDGVQLCSFACVESTILLHINDII
] 33.1	1	1	PESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDPGNRN
,	i	1	1
ļ	l .	1	RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTD
l	1		FDR3SPPLQPPPVNSLTTENRFHSLPFSLTKMPNTNGSIGHSPL
1	1	1	SLSAQSVMEELNTAPVQRSPPLAMPPGNSHGLEVGSLAEVKENP
1	1	i	PFYGVIRWIGQPPGLNEVLAGLELEDBCAG\CIDGTF/REGTRY
1	1	1	FTCALKKALFVKLKSCRPDSRFASLQPVSNQIERCNSLAIWEAY
Į.		1 77.	LSEVVEENTPTQKWEKEGLEIMIG\KKKGIQGHYNSCYLDSTLF
1	1		CLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTBIVNPLRIYG
I	j	1	YVCATKINKLRKILEKVEAASGFTSEEKDPEEFLNILPHHILEV
1	· ·		
1	1	1	BPLLXTRSAGQKVQDCYFYQIFMBKNBKVGVPTIQQLLEWSFIN
1	I	1	SNLKFAEAPSCLIIQMPRFGKDFKLFKKIPPSLRLNITDLLEDT
1	1	1	PRQCRICGGLAMYBCRBCYDDPDISAGKIKQPCKTCNTQVHLHP
)	1	1	KRLNHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHY
ı	Į.	\$	VAFVKYGKDDSAWLFFDSMADRDGGQNGFNIPQVTPCPBVGBYL
ļ.			KMSLEDLHSLDSRRIQGCARRLLCDAIYVPCTQSPTMSLYK
5972	440	1761	ILLAGSPSPRDQCSQRQSSGGDKELVTRGCTPSTAVVSPSAMTQ
			EPFREBLAYDRMPTLRRGRODPASYAPDAKPSDLQLSKRLPPCF
j	,	}	SHKTWVFSVLMGSCLLVTSGFSLYLGNVFPAEMDYLRCAAGSCI
<b>.</b>	Į.	<b>.</b> .	PSAIVSFTVSRRNANVIPNFQILFVSTFAVTTTCLIWFGCKLVL
	1	Ī	NPSAININFNLILLLLLELLMAATVIIAARSSEEDCKKKKGSMS
ł			DSANILDEVPFPARVLKSYSVVBVIAGISAVLGGIIALNVDDSV
ì			SGPHLSVTFFWILVACFPSAIASHVAABCPNKCLVBVLIAISSL
		1	TSPLLFTASGYLSFSIMRIVEMFKDY?PAIKPSYDVLLLLLLLV
[	•	Į.	
l		1	LLLQA/GPQHGHRHPVRALQGQCKAAGCILGHPERPAGAPGWGG
1			GQBPPEGVRQGESLESRRGANGPVTPRRGNRVAAPSLAPGMETH
i		l	NP
5973	65	- 2007	NGDGKDLFGHIWAWRSNGIISNFRRSPHAGMAEDEPDAKSPKTG
(		ł	GRAPPGGARAGRPTTLLQRLRGTISKAVQNKVEGILQDVQKFSD
ì		i	NDKLYLYLQLPSGPTTGDKSSEPSTLSNEEYMYAYRWIRNHLRE
1		1	HTDTCLPKQSVYDAYRKYCESLACCRPLSTANFGKIIREIFPDI
1	}	1	KARRLGGRGQSKYCYSGIRRKTLVSMPPLPGLDLKGSRSPEMGP
J	1	Į.	EVTPAPRDELVEAACALTCDWAERILKRSFSSIVEVARFLLOOH
l	[	l	LISARSAHAHVLKAMGLAEEDEHAPRERSSKPKNGLENPEGGAH
	l		ł .
1	1	Į.	KKPERLAQPPKDLEARTGAGPLARGERKKSVVESSAPGANNLQV
1	<b>1</b>	1	NALVARLPILLPRAPRSLIPPIPVSPPILAPRLSSGALKVATLP
	1	Ī	LSSRAGAPPAAVPIINMILPTVPALPGPGPGPGRAPPGGLTQPR
<b> </b>	1	I	GTENREVGIGGDQGPHDKGVKRTAEVPVSEASGQAPPAKAAKQD
1	1	1	IEDTASDAKRKRGRPLKKSGGSGERNSTPLKSAAAMESAQSSRL
1	I	I	PWETWGSGGEGNSAGGAERPGPMGEARKGAVLAQG\QGDGTVSK
		,	GGRGPGSQHTKEAEDKIPLVPSKVSVIKGSRSQKEAFPLAKGEV
Ī	[	l	DTAPQGNKDLKEHVLQSSLSQEHKDPKATPP
5974	4293	2200	LGLOMHTTSGRIHOAMVTSLNEDNESVTVENIENGDTKGK\RID
1 33/3	1 72.53	4200	LESIFSLNP\DL\VPDGEIRPSP\ETPPPPASSAKVNKIVKNRR
I	1	l	
1	(	Į.	TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNGSV\S
j	1	Į	DISPVQAAKKEFGPPSRRKSNCVKEVRKLQEKREKRRLQQQELR
1	<b>!</b>	1	BKRAQDVDATNPNYBIMCMIRDFRGSLDYRPLTTADPIDEHRIC
1	1	<b>S</b>	VCVRKRPLNKKBTQMKDLDVITIPSKDVVMVHEPKQKVDLTRYL
l	[		ENOTFREDYAFDDSAPNEMVYRFTARPLVETIFERGMATCFAYG
}	1	,	QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKK
1	l ·	I	LELOVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVVGLQE
[	1	1	
ļ .	4	<b>[</b>	REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR
l	I	I	KGKLHGKPSLIDLAGNERGADTSSADRQTRLEGABINKSLLALK
1	]	}	eciralgrnkphtppraskltqvlrdsfigensrtcmlatispg
4	1	ì	MASCENTINTLRYANRVKELTVDPTAAGDVRPIMHHPPNQI\DD
	ļ	!	LETQWGVGSSPQRDDLKLLCEQNEEKVSPQLFTFHEAVSQMVEM

Deginning corresponding corresponding corresponding corresponding corresponding to first amino acid askino acid residue of anino acid sequence sequ	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:   nucleotide   corresponding to first anino acid residue of anino acid residue of anino acid residue of anino acid sequence   first anino acid residue of anino acid sequence   first anino acid s				
Corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence   Peroline, Q-Glutamine, R-Arginine, S-Serim, T-Threcoline, V-Valline, S-Serim, T-Threcoline, V-Valline, S-Serim, T-Threcoline, V-Valline, S-Serim, T-Threcoline, V-Valline, S-Serim, T-Threcoline, V-Valline, S-Serim, T-Threcoline, V-Valline, S-Serim, T-Threcoline, V-Valline, S-Serim, T-Threcoline, V-Valline, S-Serim, T-Threcoline, V-Valline, S-Serim, T-Threcoline, V-Valline, S-Serim, T-Threcoline, V-Vall				
Contresponding		location	corresponding	
amino acid residue of anino acid sequence  Seq			to first	
residue of amino acid sequence (Codon, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide insertion)  8equence (Codon, A-possible nucleotide insertion)  8equence (Codon, A-possible nucleotide insertion)  8equence (Codon, A-possible nucleotide insertion)  8equence (Codon, A-possible nucleotide insertion)  8equence (Codon, A-possible nucleotide insertion)  8equence (Codon, A-possible nucleotide insertion)  8equence (Codon, A-possible nucleotide insertion)  8equence (Codon, A-possible nucleotide)  8equence (Codon, A-possible)  8equence (Codon, A-possible)  8equence (Codon, A-possible)  8equence (Codon, A-possible)  8equence (Codon, A-possible)  8equence (Codon, A-possible)  8equence (Codon, A-possible)  8equence (Codon, A-possible)  8equence (Codon, A-possible)  8equence (C			I -	
amino acida sequence Codon, /=possible nucleotide deletion Lyposatble nucleotide insertion SEQVEDINIAN/SESTRELEBRALIS/STERN/DIVIDE NATURE ALEQUITIO INTELBRUNGS/STRELEBRALIS/STERN/DIVIDE NATURE ALEQUITIO INTELBRUNGS/STRELEBRALIS/STERN/DIVIDE NATURE ALEQUITIO INTELBRUNGS/STRELEBRALIS/STERN/DIVIDE NATURE ALEQUITIO INTELBRUNGS/STRELEBRALIS/STERN/DIVIDE NATURE CONTROL INTELBRUNGS/STRELEBRALIS/STERN/DIVIDE NATURE CONTROL INTELBRUNGS/STRELEBRALIS/STERN/DIVIDE NATURE CONTROL INTELBRUNGS/STRELEBRALIS/STERN/DIVIDE NATURE CONTROL INTELBRUNGS/STRELEBRALIS/STERN/DIVIDE NATURE CONTROL INTELBRUNGS/STRELEBRALIS/STERN/DIVIDENCE LISTS STREET NATURE CONTROL INTELBRUNGS/STREET STREET STREET NATURE CONTROL INTELBRUNGS/STREET ST		1		
Sequence	1		I.	
BEQUIVEDIRAN PURS FRANLESSEGANSKUINENS PEAL	1		sequence	
5975 4293 2200 ILLGMITTSGRITHOUTSINEMDSTYPENTRINGFERGY ETD LESIFSIAP JOLA PUCKTEREN STEPPPASSAVMIKTUKENER LESIFSIAP JOLA PUCKTEREN STEPPPASSAVMIKTUKENER TVASI KIKUPPS JOHNVUSSARAPSOPPROPSASAVMIKTUKENER ERRADVDANINTER HOVIRDPESSAVMIKTUKENER ERRADVDANINTER HOVIRDPESSAVMIKTUKENER ERRADVDANINTER HOVIRDPESSAVMIKTUKENERGOVORISTAS USUVALKERES PESERKSKUKSVEKULGERGERED AGORIE ERRADVDANINTER HOVIRDPESSAVMIKTUKENERGOVORVUSTAS ERRADVDANINTER HOVIRDPESSAVAMIKTUKENERGOVORVUSTAS ERRADVATPET IS GENEROVIRTUKENERGOVORVUSTAS ERVIKUURDIVIKALDI GENEROTSOORSKIITALAARDVIKALLKANIVKE ERRADVATPET IS GENEROVARISTERGORGOVORVITAS ERVIKUURDIVIKALDI GENEROTSOORSKIITALAARDVIKALLAKONIVKE ERRADVATPET IS GENEROVARISTERGORGOVORVITASE ERVIKUURDIVIKALDI GENEROTSOORSKIITALAARDVIKALLAKONIVKE ERRADVATPET IS GENEROVARISTERGOVORVITASE ERVIKUURDIVIKALDI GENEROVARISTERGOVORVITASE ERVIKUURDIVIKALDI GENEROVARISTERGOVORVITASE ERVIKUURDIVIKALDI GENEROVARISTERGOVORVITASE ERVIKUURDIVIKALDI GENEROVARISTERGOVORVITASE ERVIKUURDIVIKALDI GENEROVARISTERGOVORVITASE ERVIKUURDIVIKALDI GENEROVARISTERGOVORVITASE ERRODVARISTERGOVORVITASE ERR		sequence		
S975   4293   2200   LILLOMITTSCRINGTONEONSTYTEMIN REGISTERY   LILLSTEINAPOLA PURCEITERS   NETPOPASSAYERI (VERRE TO VASI KRODPS   PROPERTING STEERING COMES   DISPUGANKERED PER RESINGUE CHELLOGICERE RELOGICERE RERADONARI PROPERTING STEERING COMES   DISPUGANKERED PER RESINGUE CHELLOGICERE RELOGICERE RERADONARI PRETINGUE CONTROLOGICE PER CONTROLOGIC PER CONTROLOGICE PER CONTROLOGICE PER CONTROLOGICE PER CONTROLOGICE PER CONTROLOGICE PER CONTROLOGICE PER CONTROLOGICE PER CONTROLOGICE PER CONTROLOGICE PER CONTROLOGICE PER CONTROLOGICE PER CONTROLOGICE PER CONTROLOGICE PER CONTROLOGICE PER CONTROLOGICE PER CONTROLOGICE PER CONTROLOGICE PER CONTROLOGICE PER CONTROLO				
LESTEPSIAP/DIA/PUCKETERS/NTPPPPASSAWMETUWARD TVANSTKINDROPS (IRRIVERS/NATPPPASSAWMETUWARD TVANSTKINDROPS) (IRRIVERS/NATPPPASSAWMETUWARD DISPUQAAKUEROPSERKSKUKSVEKULORKREKERIAQOMER ERRAQUVDAINPINTEIMONITEINGMIRDPROSIDERELITADDIDERELI VUVRREPIARKATUMKULDUTITIESCHWITHERGMATUTAAG GUSSGKITHINGOISPSGKONGUSSIGTIALARADUVELIKKUNKK LEUQVYATPEITISGKVPILIARKKKURULBOKQOVQUVGLQIE REVKUKURULKILIDIAGNISCADTSSADIQTILEGGARINKELLALK REKUKHEKESILIDIAGNISCADTSSADIQTILEGGARINKELLALK REKUKHEKESILIDIAGNISCADTSSADIQTILEGGARINKELLALK REKUKHEKESILIDIAGNISCADTSSADIQTILEGGARINKELLALK REKUKHEKESILIDIAGNISCADTSSADIQTILEGGARINKELLALK REKUKHEKESILIDIAGNISCADTSSADIQTILEGGARINKELLALK REKUKHEKESILIDIAGNISCADTSSADIQTILEGGARINKELALK REKUKHEKESILIDIAGNISCADTSSADIQTILEGGARINKESYOMEM REVVEDURAVVOISTIMILEGNISCADTSSADIQTILEGGARINKESYOMEM REGUVEDURAVVOISTIMILEGNISCADTSSADIQTILEGGARINKESYOMEM REGUVEDURAVVOISTIMILEGNISCADTSSADIQTILEGGARINGSVORTINGTSANICATION REGUVEDURAVVOISTIMILEGNISCADTSSADIATION REGUVEDURAVVOISTIMILEGNISCADTSTADIATION REGUVEDURAVVOISTIMILEGNISCADTSTADIATION REGUVEDURAVVOISTIMILEGNISCADTSTADIATION REGUVEDURAVVOISTIMILEGNISCADTSTADIATION REGUVEDURAVVOISTIMILEGNISCADTSTADIATION REGUVEDURAVVOISTIMILEGNISCADTSTADIATION REGUVEDURAVVOISTIMILEGNISCADIATION REGUVEDURAVVOISTIMILEGNISCADIATION REGUVEDURAVVOISTIMILEGNISCADIATION REGUVEDURAVVOISTIMILEGNISCADIATION REGUVEDURAVVOISTIMILEGNISCADIATIONALUTATIONALUTA PUTAVITARION REGUVEDURAVAVOISTIMILEGNISCADIATIONALUTA PUTAVITARIONALUTA PU	E025	4202	2200	
TV\ASIKIDPES\LDNEWUSSARARBEG\PPROFESAQONEST DISPUQAAKKEPOPSERKSHOKUSURTISERELQQQKILE EKRAQDVDATNIPNYKIMOHTERFEGSIOYRELITADPIDENTEL VVVERPLIMKERFOKKIOUTI TESKOVWMENEPTQKYDUTTYL ERQTPEFDYAFDDSAPHBWYKPTARPINYTITERGRATUTYAT GEGKTITHMOLOFGSGNQDCS KUTALARABPUHALKKOWYKK LELQVYATPERIYSEKVPULIMERKTULBYLDEKQQVQVWKIQE RVVKCVEDULKLIDIGNSCRISTGQTSANAHISSRSHAVPQITIAR KOKLBERTSILDIAGNSRGADTSSARARTILERUMEKVQVQVWKIQE RVVKCVEDULKLIDIGNSCRISTGQTSANAHISSRSHAVPQITIAR KOKLBERTSILDIAGNSRGADTSSARAPTRIEDBALKKILALAK ECTRALGRINDHIPPRASKUTQVIARBSI GENSBRUTHETUDG HASCESSTIJERIGNSKYNSPRALGESSAKANPERPERA EGOVVEDDRANVPOSITIARRATILERUMEVONIN VATULE EGOVEDDRANVPOSITIARRATILERUMEVONIN VATULE EGOVEDDRANVPOSITIARRATILERUMEVONIN VATULE EGOVEDDRANVPOSITIARRATILERUMEVONIN VATULE EGOVEDDRANVPOSITIARRATILERUMEVONIN VATULE ALIEKKETULESBURTCPTCIQNOVSPRALGESSAKANPERPERA HIPPTSSSTIPPASISSILISKOSSIAPPUSGRESSARAVPUTI ATVELSUBISKEDEPT PIPPEPRI LIQRALDERMESPISKQODPL HIPPTSSSTIPPASISSILISKOSSIAPPUSGRESSARAVPUTI ATVELSUBISKEDEPT PIPPEPRI LIQRALDERMESPISKQODPL HIPPTSSSTIPPASISSILISKOSSIAPPUSGRESSARAVPUTI ATVELSUBISKEDEPT PIPPEPRI LIQRALDERMESPISKQODPL HIPPTSSSTIPPASISSILISKOSSIAPPUSGRESSARAVPUTI ATVELSUBISKEDEPT PIPPEPRI LIQRALDERMESPISKQODPL HIPPTSSSTIPPASISSILISKOSSIAPPUSGRESSARAVPUTI ATVELSUBISKEDEPT PIPPEPRI PIPPERPEPTORMOLISKERTSSTYTT APPLISHBERYSPROGRESHERMESPISKGTSSITIATA IMBERGOTUVPIJEPTPULPEPHILLEDPROPPPOPPEPPPPPPPPPPPPPPPPPPPPPPPPPPPP	23/2	4293	2200	
DISPUQAAKKEPOPSERKSNOVERUSLOGKREERRELOOGUE  RERRODVOANDENS LICHTEN SERGIOVPRILITADE PIDERIEL  VUVERREPLANKETOMKOLOVIT I ESKOVWHIEPERGAVOLTENS  OTGGESTITHMOCDESGRODCS KUITALAARDUPIALKKENYKKI  LELOVVATPPELY SEKVEVILAIR RETKLERVLEERGVOVVALOR  REVRCVEDVILKI I DI CONSCRISOOTSAAAHSISRSKAVPOITILRE  KOKAHSE PSI LIDIAONISRADITSAARDUPIALKKENYKKI  LELOVVATPPELY SEKVEVILAIR RETKLERVLEERGVAT LERGAS LIKSILLAIR  RECRALGINKUPI PPRASKLIQVINES I EIGISSIR SEKNIKOVATILERE  KOKAHSE PSI LIDIAONISRADITSSA DROTTE LEGAS LIKSILLAIR ECARALGINKUPI PPRASKLIQVINES I EIGISSIR SEVATOVATO  LETOMOVOSS PRODULGILGOR MEEROVAD PRASEDVET MINESPANOL VINE  BEROVEDDIRAVEOSI BRILDENKALERI EERDVINDING VALTULE  LEROMOVOSS PRODULGILGOR MEEROVAD PRASEDVET MINESPANOL VINE  EROVEDDIRAVEOSI BRILDENKALERI EERDVINDING VALTULE  LEROMOVOSS PROMUKALERI EN VINESPANOL AND PREDENSA PROPUTI  ATUSISVISS SESENDO I DEBLACLI CROIMITIAVVIPCCORSYS VILESESS SESENDO I DEBLACLI CROIMITIAVVIPCCORSYS VILESESS SESENDO I DEBLACLI CROIMITIAVVIPCCORSYS VILESESS SESENDO I DEBLACLI CROIMITIAVVIPCCORSYS VILESESS SESENDO I DEBLACIA LICHOMITIAVVIPCCORSYS VILESESS SESENDO I DEBLACIA LICHOMITIAVVIPCCORSYS VILESESS SESENDO I DEBLACIA LICHOMITIAVVIPCCORSYS VILESESS SESENDO I DEBLACIA LICHOMITIAVVIPCCORSYS VILESESS SESENDO I DEBLACIA LICHOMITIAVVIPCCORSYS VILESESS SESSESSES SERVED PROPUPL MIPPYTSSSTIPLASSI SISLINSOS SILAPPUSORDES SARAPUPDIT  ATVSISVISS KSOGE PREDISIALING LAPPUSORDES SARAPUPDIT  ATVSISVISS KSOGE PREDISIALING LAPPUSORDES SARAPUPDIT  ATVSISVISS KSOGE PREDISIALING LAPPUSORDES SARAPUPDIT  ATVSISVISS KSOGE PROPUP POLIVEP PUPPITUL PROPUP POPPOP POPPOP POPPOP POPPOP POPPOP POPPOP	1	ĺ		,
EKRAĞUVDATNINIYELIKOHTROFROSILDIYELITADƏ FIDERLIS  VÜVKREPLINKERJÖNKÜLÜNT TİL ESKUVWMERBEÇIKUDLTEYL  EKÇITREFDYAFDDSAPRBIYTEFTARPIJAYET I FERGMATTEYLÜ  EKÇITREFDYAFDDSAPRBIYTEFTARPIJAYET I FERGMATTEYLÜ  GÖRGKTİTIYMÜLÖ FÖĞGKÜDÜN KÜTALARADUY HALKKONYKK  LELQYYAFTPETY SÇKYPÜLİMERTILLEDÜKQÜQÜVÜKÜLĞE  REVEKUVEDÜLLÜL GÖRSCETSÖQTSARAHSISBESHAYPÇI TILBER  KÖKLHER FISILDIAGNISERADTSSADRƏTELBÜRAĞULALIK  ECTRALGINKPHTPFRASKLIQVILDE GERSEKTCHIATISDİ  BÜRÜMER KÖKLHER FISILDIAGNISERADTSSADRƏTELBÜRAĞULALIK  ECRAFILDIAGNISERADTYAĞUNDE HERBEYRÜLÜDÜK ÇÜLÜMER FÜRÜMER BÖYÜVEDÜRÜMER FÜRÜM				
VCVRRPLINKETONKIDUTTIESKUVWHIEPRQUVUDTIESK ENOTREPDYATDESAPBRWYTETAPRIVETIESKRATCPAYG OTGGGRTHYMCOPSGRONDCSKITYALAARDUFINLKKURVINKEL LELGVYATPEETYSKKVPILIMRKTRUAVLEBGROVUVUTLOB REVEKCURUVLKLIDIGNSCCTSCOTSANARSSESKAVPOTILER KOKLHELPSILIDLAGNSRCADTSAROOTRIBGAB INKGLIALR RCKRHGEPSILIDLAGNSRCADTSAROOTRIBGAB INKGLIALR RCKRALGENSILIDLAGNSRCADTSAROOTRIBGAB INKGLIALR RCKRALGENSTLULAGNSRCADTSAROOTRIBGAB INKGLIALR RCKRALGENSTLULAGNSRCADTSAROOTRIBGAB INKGLIALR RCKRALGENSTLULAGNSRCADTSAROOTRIBGAB INKGLIALR RCKRALGENSTLUTATIAKYARVKALTVUTAAGAVETMIRPKRYAL LETQVEVORRAVYQSSIRMLEBOKKALBATEEVYDVUDSIYATLIBO LETQMGVOSSPGRONKALBATEEVYDVUDSIYATLIBOV REROVESDERAVYQSSIRMLEBOKKALBATEEVYDVUDSIYATLIBOV REROVESDERAVYQSSIRMLEBOKKALBATEEVYDVUDSIYATLIBOV REROVENDERAVYGSSIRMLEBOKKALBATEEVYDVUDSIYATLIBOV RCHETALLESDERICKONTSARAALATPITIALRAAVGKEEPP PUSHMEVROPRIMKALDPITALRAATIPITAVIGKACHYTERAA RCHETALLESDERICKTOPTCQGNONDSTALARUTTURALGAVINFINDE TOTTKRLIKRQLESPEPPI IPPERPILIQRALGPIMREDI SRQODH HIPVTSSTTIPASSISSISSOKALAPPUSINFARDISGAROOTPUTI ATVELSVESKESGEFRUSTSISSISSICALAPPUSINFARDISG RCHERHSKKLGVINSPPOLIRAGOLIAPPUSINFARDISG RCHERHSKKLGVINSPPOLIRAGOLIAPPUSINFARDISGAROOTPUTI ATVELSVESKESGEFRUSTSISSISSISSOKALAPPUSINFARDISG RCHERHSKKLGVINSPPOLIRAGEGULIPTTOPUVENTARDOGG RRUGHERISKKLGVINSPPOLIRAGEGULIPTTOPUVENTARDOGG RRUGHERISKKLGVINSPPOLIRAGEGULIPTTOPUVENTARDOGG RRUGHERISKKLGVINSPPOLIRAGEGULIPTTOPUVENTARDOGG RRUGHERISKKLGVINSPPOLIRAGEGULIPTTOPUVENTARDOGG RRUGHERISKKLGVINSPPOLIRAGEGULIPTTOPUVENTARDOGG RRUGHERISKKLGVINSPPOLIRAGEGULIPTTOPUVENTARDOGG RRUGHERISKKLGVINSPPOLIRAGEGULIPTTOPUVENTARDOGG RSHERPSPERSREPYSGSSYSSSSYTISGSRGGTERSSYSSSPPY RYISGSRSPOLIRAGEGULIPTTOPUVENTARDOGGSPOPP QOX PPARAYSVPDROFPPARAILTTOWARSRGSHUTHRENGESSSPPYR RYISGSRSPOLIRAGEGURINGRAGGERINGRAGHATERISSSSPPYR RYISGSRSPOLIRAGEGURINGRAGGERINGRAGHATERISSSSPPYR RYISGSRSPOLIRAGEGURINGRAGGERINGRAGHATERISSSSPPYR RYISGSRSPOLIRAGEGURINGRAGGERINGRAGHATERISSSSPPYR RYISGSRSPOLIRAGEGURINGRAGGERINGRAGHATERISSSPPYR RYISGSRSPOLIRAGEGURINGRAGGERINGRAGHATERISTUD SREENITARDOGGRAFINGRAGHATERISTUD SREENITA	ľ			
REQUERPOYADDSAPHEMYRETARELANDVETTEREGRATCHAYG  OTGGGGTTHMOGOPSGNOGOPSGNIZHALANDVETTEREGRATCHAYG  OTGGGGTTHMOGOPSGNOGOPSGNIZHALANDVETHALKUNYKK  LELQVYATPPEITSGKOVPHLIBRKYKURULEDGKQQVOVGLQE  REVKCVEDVLKLID IGNGCTEGOGTSANISHSSRSHAVPQILIRR  KOKLHGKPSLIDLAGNEGDTSSADRQTRLEGABINKBLLALK  ECTRALGANKPHTPPRAGKLTQVLRGSPISHSTROHATISFG  MASCRITIATTERARKVERELTVDPTAGGUVRFUHHEPPRQL UD  LETQMOVGSSPQRDULKLLCEGNREEVSPQLITTHRAVSGWYRM  REVOVEDKRAVPGSSTRALDGEGGASKQINFREPRAL  SOYTE  20 2949 VHHILITAVSVVINLDILIRLAGOMSIKTHAVVLGVLKRAVLASF  PEVSHMEVKDPINKGGAMLTATGKALLETPIDA KRAYLAGKERPP  PLIPESBSSSGEEDDIP IDBLICLICKCHIMTAVVLGVLKRAVLASF  PEVSHMEVKDPINKGGAMLTATGKALLETPIDA KRAYLAGKERPP  PLIPESBSSSGEEDDIP IDBLICLICKCHIMTAVVLGVLKRAVLASF  BEGUNDALLAGUNG STATLAGOMSIKTHAVVLGVLKRAVLASF  REGRESSEDDIP IDBLICLICKCHIMTAVVLGVLKRAVLASF  REGRESSENDIP IDBLICLICKCHIMTAVVLGVLKRAVLASF  REGRESSENDIP IDBLICLICKCHIMTAVVLGVLKRAVLASF  REGRESSENDIP IDBLICLICKCHIMTAVVLGVLKRAVLASF  REGRESSENDIP IDBLICLICKCHIMTAVVLGVLKRAVLASF  REGRESSENDIP IDBLICLICKCHIMTAVVLGVLKRAVLASF  REGRESSENDIP IDBLICLICKCHIMTAVVLGVLKRAVLASF  REGRESSENDIP SPEPLI ILGGGLLHGOLIP TTOPPUR INTARPOGC  GESLEATPUR VLORTINGSPEPPE I PEPPER ILGGGLLHGOLIP TTOPPUR INTARPOGC  GESLEATPUR VLORTINGSPEPPE I PEPPER ILGGGLLHGOLIP TTOPPUR INTARPOGC  GESLEATPUR VLORTINGSPESCHYSSIS STRASSIS STRASSIS STRASSIS  REGRESSENDIP SEGRIF INTERLETHUS SCOVETARISTIC PTY  APPLERBERY REGRILLAGESKKKOKLDER TUDEPARKENSTER SERSESTERS  REGRESSENDIP SEGRIF INTERLETHUS SCOVETARISTIC PTY  APPLERBER SERSES STRASSIS TRASSIS STRASSIS STRASSIS  REGRESSENDIP SEGRIF INTERLETHUS SCOVETARISTIC PTY  REGRESSENDIP SEGRIF INTERLETHUS SCOVETARISTIC PTY  REGRESSENDIP SEGRIF INTERLETHUS SCOVETARISTIC PTY  REGRESSENDIP SEGRIF INTERLET SERSER TRASSIS STRASSIS STRASSIS  REGRESSENDIP SEGRIF SEGRIF INTERLET SERSER STRASSIS STRASSIS  REGRESSENDIP SEGRIF SEGRIF INTERLET SERSER STRASSIS STRASSIS  REGRESSENDIP SEGRIF S			•	
LELQVIATFFELTSGRUPDLINKTKILEPJGROGOVOUGLOGE   REVICURDULELD IGNOSTESOGYSANAISSESHAYPQILIER    GKILHEKPELIDIAGNERGADTSSADROTTLEGABINKSILALK     ECTRALGRINKPHITPAGAKITQVIADGF JGENSKTCHIATISEG     HASCERTIATTARARNEELTVDPTAGAGURYELIHHEPPRQL UD     LETQHOVGSSPQEDDLIALLEGQNEREUSPQLETHRANSGWEM     EROVEDHRANVPGSSTRALBKALLERTESUDVDUDSTATQLE     EROVEDHRANVPGSSTRALBKALLERTESUDVDUDSTATQLE     EROVEDHRANVPGSSTRALBGREENDOVDUSTATQLE     EROVEDHRANVFGSTRALGGREENSPQLETHRANSGWEM     EROVEDHRANVUNDITIELROKKALSHALLERDUDVDUSTATQLE     ALLEGELDILTELROKKASPRALGEREGOASKQINPREPRAL     ALLEGELDILTELROKKASPRALGEREGOASKQINPREPRAL     ALLEGELDILTELROKKASPRALGEREGOASKQINPREPRAL     ALLEGELDILTELROKKASPRALGEREGOASKQINPREPRAL     ALLEGELDILTELROKKASPRALGEREGOASKQINPREPRAL     ALLEGELDILTELROKKASPRALGEREGOASKQINPREPRAL     ALLEGELDILTELROKKASPRALGEREGOASKQINPREPRAL     ALLEGELDILTELROKASPRALGEREGOASKQINPREPRAL     ALLEGELDILTELROKASPRALGEREGOASKQINPREPRAL     ALLEGELDILTELROKASPRALGEREGOASKQINPREPRAL     ALLEGELDILTELROKASPRALGEREGOASKQINPREPRALIC     ALLEGELDILTELROKASPRALGEREGOASKQINPREPRESAR     ALLEGELDILTELROKASPRALGEREGOASKQINPREPRESAR     ALLEGELDILTELROKASPRALGEREGOASKGINPREPRESAR     ALLEGELDILTELROKASPRALGERING     ALLEGELDILTELROKASPRALGERING     ALLEGELDILTELROKASPRALGERING     ALLEGELDILTELROKASPRALGERING     ALLEGELDILTELROKASPRALGERING     ALLEGELDILTELROKASPRALGERING     ALLEGELDILTELROKASPRALGERING     ALLEGELDILTELLTICAS RESERVENTENTENTAR     ALLEGELDILTELLTICAS RESERVENTENTENTAR     ALLEGELDILTELLTICAS RESERVENTENTENTAR     ALLEGELDILTELLTICAS RESERVENTENTENTAR     ALLEGELDILTELLTICAS RESERVENTENTENTAR     ALLEGELDILTELLTICAS RESERVENTENTENTAR     ALLEGELDILTELLTICAS RESERVENTENTENTENTAR     ALLEGELDILTELLTICAS RESERVENTENTENTENTENTAR     ALLEGELDILTELLTICAS RESERVENTENTENTENTENTENTENTENTENTENTENTENTENTE	l	)		
REVICUED/LIGHT SCOTS ANABISSRSHAP TO ILLIR  BEKLHEKEPLIDLAGNERGADTS SANDGYSTELDIKS LLALL  ECITALGRIK DET PARKLT OVLÆDES FORDIST TOTT SANDGYSTELDIK SILLALL  ECITALGRIK DET PARKLT OVLÆDES FORDIST TOTT SANDGYSTELDIK SILLALL  ECITALGRIK DET PARKLT OVLÆDES FORDISTAL SENDEN SKALLENDE SENDEN STATILE  LETOMOVES SEQUEDIK LLEGEMBERS SQLETTERRAVS GNYFRE PARKLT OVLÆDES FORDISTAL SENDEN SKALLENTES STONDAY TATULE  ALLEGKID LITERARN VESTBALDE BEKKALLENTES STONDAY TATULE  ALLEGKID LITERARN VESTBALDE BEKKALLENTES STONDAY TATULE  ALLEGKID LITERARN VESTBALDE BEKKALLENTES STONDAY TATULE  ALLEGKID LITERAR SKALLENG VAR FALLENG SK		į		QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLNLKKPNYKK
RSKLHEKPSLIDLAGNERGADTSANDRYIGENETONIATISPE BCTRALIGNIKPHTPPRASELTOVIRDSPIGENETONIATISPE MASCRATLATIRYANRVRELTVDPTAGDVRPIMHHPPNQI\DD LETQMGVGSSPQRDDLKLLCSQMEREVSPQLFTTHRASGGWFM ERGVVEDHRAVPOSSTRMEDDRALLEMERSGGWFMHHPPNQI\DD LETQMGVGSSPQRDDLKLLCSQMEREVSPQLFTTHRASGGWFM ERGVVEDHRAVPOSSTRMEDDRALLEMERSGGWFMPRAL AILLOKIDILTELRDKVKSFRAALGERGASKQINFKPRAL AILLOKIDILTELRDKVKSFRAALGERGASKQINFKPRAL VHHILHITWSVVAVLDILTIRLAGQMGIKTALIOVGJLKRAYLOK ERGTATLLESDRHTCPTCIQNDVSPPAALGERGASKQINFKPRAL VHENERSSSSSERDDP PDBLICLICKUNTAVILOVGLCKRSKCPP PEVSMMEVRUDPNMKGMMINTGXXAIPTIDA\RAYAIGKEKKPP PEVSMMEVRUDPNMKGMMINTGXXAIPTIDA\RAYAIGKEKKPP PEVSMMEVRUDPNMKGMMINTGXXAIPTIDA\RAYAIGKEKCPP PEVSMEVRUDPSPPELBICLICKUNTAVILOVICCONSYCD BCTRTALLESDRHTCPTCIQNDVSPDAILIANKFLRQAVNNYKNE TGYTRALLRGQLSPPPIP PEPP PEP LIGRALDVSTESSILOTA AIPVISSSTHPAPSISSLTSNQSSLAPPVSGNPSSAPAPVPDIT ATVSISVISERSGGPFRIDSHKLIPAAALASEHSKSTSILITA LMBEKNYLVYPVISTPSLLIGSGLHEGGLIPPORTNTARPCGG REGMENSKLAYLUSPPQOJERGERSCKSTSINGSTARPTSPTTTTQ APPLISRBRYPVPROPRUPVPDPPP PEPP PEPR PIRTURETRETRETRYKKITY APPLISRBSPYPRORRIKEREKKKSKLIPPORTNTARPCGG GQSLPATVPVPVPDPPPPP PEPP PIRTURETRYNTATIVAGGGTRAGGGSPPPPP RAMENNSPSPPPPRGRAKEREKKKSKLIPPORAKEMSTSTYSSSS RSHSHSYSRSPPPPRRGRAKERKKSKLIPPORAKEMSTSTYSSSS RSHSHSYSRSPPPPRRGRAKERKKSKLIPPORAKEMSTSTYSSSS RSHSHSYSRSPPPPRRGRAKERKKSKLIPPORAKEMSTSTYSSSS RSHSHSYSRSPPPPRRGRAKERKKSKLIPPORAKEMSTSTYSSSS RSHSHSYSRSPPPPRRGRAKERKKSKLIPPORAKEMSTSTYSSSS RSHSHSYNSPPPPRRGRAKERKKSKLIPPORAKEMSTSTYSSSS RSHSHSYNSPPPPRRGRAKERKKSKLIPPORAKEMSTSTYSSSS RSHSHSYNSPPPPRRGRAKERKKSKLIPPORAKEMSTSTYSSSS RSHSHSYNSPPPPRRGRAKERKKSKLIPPORAKEMSTSTYSSSS RSHSHSYNSPPPPRRGRAKERKKSKLIPPORAKEMSTSTYSSSS RSHSHSYNSPPPPRRGRAKERKSKNAPGGGRANGHKRHKKRKKT KGEREGGLIPPORAKEMSPPPRRGRAKERSTSTYSSSSS RSHSHSYNSPPPPRRGRAKERKKSKNAPGGGRANGHKRHKKRHKRK KGEREGGLIPPORAKEMSPPPRRGRAKERSTSTARPORATGMYSSTT PVARBERSPRAMGGGGRANGHKRHKMRKHRKHRKKT PVARBERSPRAMGGGGRANGHTANIATIONALOKATERILKV ALPPRORATIONALOKATATATATATATATATATATATATATATATATATATAT				LELQVYATFFEIYSGKVFDLINRKTKLRVLEDGKQQVQVVGLQB
RCTRALGRIKPHTPPRASKLTQVLARGS FIGERISTORIATISPE MASCRATLETT.RXANINVERLEVADTAAGUSTHHHPPROI.)DD LETQWGUGSPQRIDIKLLCSQMEREVSPQLFTFHRAVSGWYRM ERQVVEDHRAVFQSSTRWLEDEKALLEWTESVDTUDYSTATQLE ERGVVEDHRAVFQSSTRWLEDEKALLEWTESVDTUDYSTATQLE ERGVVEDHRAVFGSSTRWLEDEKALLEWTESVDTUDYSTATQLE BALDEKELD LITERLEKUKSPRAALGEREGASKQINPKRPRAL  5976  20 2949 VHHIHLITRUSVVWLIDITLRIAQQMGIKTALDVGLJKRAVLGKEPP PLYSEBESSSERDDP PDELLCLICKOINTDAVUTECCHSYCO BCITCTALLESSBETTCPTCGMOVSPDALLANKFLRQAVNINPKNE TOYTKRLRKQLPSPPPIPPPRILIGNILQPLMRGSPISRQQDFL MIPVTSSSTHPAPSISLITSNQSSLAPPVSGNPSSARPVEDIT ATVSISVISEBESDPTCPTGLGQGLLEGGLIPTTGPVRITARPCGC RPGWEISHKLKSTVSDPQIFRGERSCYRSISHGRRHESERSQPT GGSSLPATDVEVDVPDPPPPLAPPPHTLATPSPOVPPDPSPPOPPP GQP\PPAAVSVPDPGPPPAPANISTPWSGAVGTAISMTTPTTQ APPLSREBPYBEQRILKEBEKKKSKLDBFTNDFAKEMSSSPYK RKRRSPGSRSSPYSPPPRGRGKSKRWTRSGRSSSTSPTTPTTQ APPLSREBPYBEQRILKEBEKKSKLDBFTNDFAKEMSSSPYK RKRRSPGSRSSPYPPRGRGKSKRWTRSGRSSTYSRSSS RSHSRSYSRSPYPPRGRGKSKRWTRSGRSSTYSRSSS RSHSRSYSRSPYPPRGRGKSKRWTRSGRSSTYSRSSS RSHSRSYSRSPYPPRGRGKSKRWTRSGRSSPYKSTSS RSHSRSYSRSPYPPRGRGKSKRWTRSGRSSPYKSTSSPYSSSSS RSHSRSYSRSPYPPRGRGKSKRWTRSGRSSTYSKSSSSPYKSSSSPYKSKSSTSSSPYKSKRSSTYSKSSSSPYKSKSSSPYKSKSSSPYKSSSSPYKSKSSSTYSSSSSPYKSKRSSTYSKSSSSPYKSKSSSPYKSKSSSSPYKSKSSSPYKSKSSSPYKSKSSSPYKSKSSSPYKSKSSSPYKSKSSSPYKSKSSSPYKSKSSSPYKSKSSSPYKSKSSSPYKSKSSSPYKSKSSSPYKSKSSSPYKSKSSSPYKSKSSSSPYKSKSSSPYKSKSSSSPYKSKSSSSPYKSKSSSSPYKSKSSSSPYKSKSSSSPYKSKSSSSPYKSKSSSSSSSS	I			
HASCERTIATIRYARRYKELTUDPTAAGDVRPIMHEPROIT ND LETQWSUGSSPQRDDLKLLCRQNEEEVSPQLTHHERVSQWVEM ERQWYEDRRAYPGBSTRMLEDBKALLEWTERVDYDDGYYATQLE AILLOKIDILTELRDKYKSFRAALGERGASKQINKRPRAL AILLOKIDILTELRDKYKSFRAALGERGASKQINKRPRAL HINDRYSSSSERDDP I PERDILGILCKUMTALOVGILKRAY LIKE PUSHMEVRDPMKGAMILTNYGKKAIPTIDA\RAYAIGKERCPP HINDRESSSSERDDP I PEDELGILCKUMTAVIPCCHOSKYL BCIRTALLESDEHTCPTCHQNDVSPDALIANKFLRQAVNNPRNE TOTTKILKRQIPSPPP I PPRPILIQRALQPLARESPI ERQOPEI MIPVTSSSTHPAPSI ISSILTSQSLLAPPURPTNITARPCGG REGHENSNILSYLVSPPQOLIRGERSCYRSINKGHERSBAPAPUDIT ATVSISVISEKSDOPPRIDSNIKLLPAALASEISKGISSI AITTA LIMERKGYUVPVIGTPSLLGGGLLEGGLI PPROPRIPTNITARPCGG REGHENSNILSYLVSPPQOLIRGERSCYRSINKGHERSCAPP GQP\PPAGYSVPPPGPPPPUPPPPPPLPPPRIPTNITARPCGG REGHENSNILSYLVSPPQOLIRGERSCYRSINGKERSKERSINTPPTTQ APPLSRBEPYREGRRIKKEERKKKSKLDEFTMDPAKELMFYKLVI KERRESPGRASSSPYSSSSSTTSSSSSTTSRSSSTTSRSSYSSSS RESISSSSSPSPYSRSSSSTTSSSSSTTSRSSSTTSRSSSSSSTSSSST				
LETQWOVEDREADURALLCEQUEREVSPOLETHRRAYSOWURM ERQVYZDRIKAPVORST RWLEDRKALLEMTERVDYDVDUSYATOLE 5976  20 2949  VHILHILTRUSVVINIDITERIAQMOSTKYLLEMTERVDYDVDUSYATOLE PEVSIMBEVINDENMIKGAMITYMIKYATYTIDA\RAYATGKREKPP PLEERSSSEEDDP 1PDELICLICKOIMTDAVTICCONSYCO BETRATLLESSILESDHITCPTECKONDVSPOALIANKFERQAVNNYKNE TGYTKRLRKQLFSPPPT1PPRPLICRILGKULQPLMRSETSRQODPI. MIPPTSSSTPAPSISSLTSNOSSLAPPVSORPSSAPAPVPDIT ATVSISVHSEKSOOPPRISINKTLEPAALSEHIKSTSSIAITA LMESKOYVPVLETPSLIGGSLLHEGGLIPTTGPVRITARPCGG RPOMEHSKKLGYLVSPPOGJIREGRERGYRSTSHSKRISSSIAITA LMESKOYVPVLETPSLIGGSLHEGGLIPTTGPVRITARPCGG RPOMEHSKKLGYLVSPPOGJIREGRERGYRSTSHSKRISTSSIAITA LMESKOYVPVLETPSLIGGSLHEGGLIPTTGPVRITARPCGG RPOMEHSKKLGYLVSPPOGJIREGRERGYRSTSHSKGSSTTRATSYSSGSY RSSPSTSPYSGSSYSSYSSSSSTTSSSSSTTRASSYSSGS RSSPSSSSSTRASSYSSGSSTTSSSSSTTRASSYSSGSSTTRASSYSSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSYSGSSTTRASSTRASSTRASSTRASSTRASSTRASSTRASS	1	]		
EROVVEDHRAVPORSITRILERKIRENDYDVDGYTATQLE ALILGKID LITHLARVKVSPRALAGEROJAKQINPKRPRAL 5976  20  2949  VHHILHTRVSVVVNLDI LITLAQOMGIKTINIVIG\LKRA\LEF PEVSIMEVKDPRIMKGAMLINTICKYAIPTIDA\LARVAICKREKPP PEVSIMEVKDPRIMKGAMLINTICKYAIPTIDA\LARVAICKREKPP PEVSIMEVKDPRIMKGAMLINTICKYAIPTIDA\LARVAICKREKPP PEVSIMEVKDPSSSERDDPI PDEBLICLICKOLIMTIAVVIECGISYCD ECIRTALLESDEHTCPTCHONDVSPDALIANKFIRGAVNINFKRIE TGYTKILKRO\LESDEHTCPTCHONDVSPDALIANKFIRGAVNINFKRIE TGYTKILKRO\LESDEHTCPTCHONDVSPDALIANKFIRGAVNINFKRIE TGYTKILKRO\LESDEHTCPTCHONDVSPDALIANKFIRGAVNINFKRIE TGYTKILKRO\LESDEHTCPTCHONDVSPDALIANKFIRGAVNINFKRIE TGYTKILKRO\LESDEHTCPTCHONDVSPDALIANKFIRGAVNINFKRIE TGYTEILKRO\LESDEHTCPTCHONDVSPDALIANKFIRGAVNINFKRIE TGYTEILKRO\LESDEHTCPTCHONDVSPDALIANKFIRGAVNINFKRIE TGYTEILKRO\LESDEHTCPTCHONDVSPDALIANKFIRGAVNINFKRIE THE MERKOVQOVPVIGTPSLAGGSLIGHCIDAMSTATSPTGY GOP\PPACTYSVPVPUPPPPPLYPPPHITTDEVENTIARPCGG REGELERYVPVPUPPPPPLYPPPPTITTDEVENTIARPCGG REGELERYVPVPUPPPPPLYPPPPPPPPPPPPPPPPPPPPPPPPPPP				
ALLEGKID LITELRINKVKSPRAALGERGASKQIIPKIPRAPAL  5976  20  2949  VHHILITRVSVVUNDII ILRIAQMGIKTKILVIJCIG\LKRA\LEF PEVSMEVKDPMMKAALINTICKAAIPTIDA\KAVAICKEKEPP PLPERESSSERDDPI DDELLCLICKOIMTDAVVITCCGRSYCD BCIRTAL LESDEHTCPTCHONVSPDALIANKTERQANMIKRE GCIRTAL LESDEHTCPTCHONVSPDALIANKTERQANMIKRE TGYTKRLRKGLESPPPP LIPPRPLIQRILQPLMESPISRQDDPI MIPVTSSTHPAPSISSLISNQSSLAPPVSOMPSSAPAPVPDIT ATVSISVHSEKSDCPPREDINKILFAAALASEHSKITSS IAITA IMEEKGYQVPVIGTFSLLGGSLLHEQLIPTTGVPRINTARPGGG REGMENSIKIGYUSPPOQIRRGERSCYRS IMEGRHHSERGRT GGESLPATDVFVVDVDPPPLYPPPPDFPDRARILFPTQ APPLSREEPYREQRILEEBKKKSKLDEFTNDFAKRIMEYKKIQ KERRESPERSKSPYSGSSYSRSSYTYSKSSGSTTRSRYSKSES RSHSHSYSKSPYPYREGKGKSKINVKSRSSHOTHSRSRSSPYR RYHSRSRSPOAFRGGSINVKSNVPGGETERSTYNKREVPPPYM KAYYGKSVDPENPPEKSERVEHERSKRSHWKYKYGVAAAAORP PSANRENPSPERFI,PLNIRNSPPTRGREDVVGGQSHRSRNIGS NYPEKLSARDGHMQKDMTKSKKRSRARPGDKKKHKKRIKRKR KGERSEGINDFLLETERSKEPTOVEKRYKYKYGVAAAORP PSANRENPSPERFI,PLNIRNSPPTRGREDVVGGQSHRSRNIGS NYPEKLSARDGHMQKDMTKSKKRSRARPGDKKKHKKRIKRKR KGERSEGINVELLETERSKEPTOVEKRYKYKYKYAAAORP PVENDEPHDABSITYKGVSKKOKRRBDRPKKKGNKHKKRIKRKR KGERSEGINVELLETERSKEPTOVEKRYKYKYKYAAAORP PVENDEPHDABSITYKGVSKKOKRRBDRPKKKGNKTKRRNIGSAV SKENTIVEPAGRGGEVYKYKREKMERSKENTGLVLYKKYGYGRGKSE BELFORGGINKENVYKYKYGKOMEYSDLELEAI IERDEDGGGKS BELFORGGINKHKYSL\EPPICKTERSPANTONIOLISKPKRESETYBLL TILNHHLPLRRMKKSL\EPPICKTERSPANTONIOLISKPKRESETYBLL TILNHHLPLRRMKKSL\EPPICKTERGENDEDGGGWV DTYHNTGITGITEAVKEITLENKINIRLQDCSALCEREREDEDG BAADHBEVERSGLLETDRATLDTRIVERACKAKTDAGGERDAILQ TRYTYLLYTYNKYYQTPRIMLFGYDBGCFLYKHMINTSIGOBW VKKTYTIKNHPHJEPPPMGSVBFCRHAEWKKI INTVAEGGGEL GWMYLLIFLKFVQAVIPTIENDVATREFTM PVERSERPERAMDEGGSELTANPRECTICKELLGOALMGMH VKKTYTIKNHPHJEPPPPMGSVBFCRHAEWKKI INTVAEGGGEL GCHTYLLEFLKFVQAVIPTIENDVATSGRRLEMGITSIGOBW VKKTYTIKNHPHJEPPPPMGSVBFCRHAEWKKI INTVAEGGGEL GCHTYLLEFLEGRAGCPFCAPALOLERSHAEMKHAHMINGQVVRINGW ASSVITTPVDPOPTTSELVOPNOATPVLENFSTLRQRADPVSPP LQUSGLCWRLKVYPDGRSVURGYVLSEVSLEGAGLPETSKYEYR VEMUNGSCNDPTRNITRIRGRASDFEVGEGGGWNETHRILLANGSTLLT GETELLESLLGBURGDVANGGVURGYVLSUFLEGAGLPETSKYEYR VEMUNGSCNDPTRNITRIRGRASDFE	1			
5976  2949  VIHIHLITRYSVUVNIDITIELIAGOMETKTINIUTGUKERALGKEKPP PEVSWMEVKDPMMKAMLITRYGKYAIPTIDA\EAYAIGKKEKPP PEVSWMEVKDPMMKAMLITRYGKYAIPTIDA\EAYAIGKKEKPP PLEREPSISSEDDPI POBELLCLICKOIMTAWVIPCGNSYCD BCIRTALLESDBHTCPTCHQNDVSPDALIAMKELRQAVMPRENE TGTYRELREGUESPPEPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	i I			
PEVSIMEVALDPAMKGAMI.TNYGKYA I ET TIDA KANAIGKKEKEP PIPEEPSSSEEDDP I PDBLICLICKUMTDAVVIPCCGNSYCD BCIRTALLESDBHTCPTCHQMDVSPDALTANKFI.KQAVNINFRUB TGYTKRI.RKQLESPEPFI PPER PILQRILQPILMSPI SRQQDPI. MIPVTSSTHPAPSI SISJISNOSSIAPPVSGDPSSAPPVPDIT ATVSISVHSEKSGFPRISDIKILPANALASEHSKGTSSIA.TA IMBEKGYQVPVIGTPSILGQSLLHGQI.PTTGPVRINTARPGGG RPGWEHISINI.GYILVSPPQQIRRGESCYRS I MRGHHISERSQRT GGSLPATPVPVPPPPPLYPPPHTLDI.PPGVPPPQPSPQPPP GQPV.PPAGYSVPPPGFPPPAPANITSWSGQOTAHENTI.PTTQ APPLSREEPYRRQRILKEBEKKSKILDBFTNDPAKERMEYKYIQ KERREFSRSKSPYSGSSYSRSYTYSKSRSGSTSRSYSYSRSFS RSHSRSSSRSPPYPRGRGKSRNYRSGRSSHGYHRSRSSPPYR RYHSRSRSPQAFRGGSYNKRNVPQGSTEREYTHNYREVPPPYDM KAYYGRSVDFIDPPEKERYRWKRYKYIQWAAGAQPR PSANRENPSPBRFI-DAIRINSPPTRGRRDDYVGCQSHESINIGS NYPEKLSARDGHNQXDNTKSKEKESRAPPGDGKGKIKHKKHRKRR KGESESGFILNPELLETSRKSREEPTGVERNKTDSLYVLPSRDDAT PVRDEPMDABSITPKGVSRKVDKRRRDKPRKRAKGDKTKRKNRGSAV SKRNIVKPAKOPGEKVOG (VVRDALLLALLA)LKKPKETTKDL TILMHILPLRRNKKSI\EPP\EKLTINQOK\TPRIKTSQRGKSB BGLPQRCQIRKANN  5977 1363 1336 FIEDRGQVISHPGCLISHSINHTLHPGAGVAAGPATGW/REKKY ANLPTIKACDPLVYKNOMPCYKRCKGMETSDELAAI IEDDGGGGWW DTYHNTGITGITRAVKSI\EPP\EKLTINQOK\TPRIKTSQRGKSB EGLPQRCQIRKANN  5978 160 3213 RDGAREWGGCQSPLTWAPGFFTRFDLATTSGRRLEGGYTAEPAGKQ RPRREPEAMDSGSVSSIABVFRCFICMKKKIRKTRKMED SHAWLIFLERKAGCPHCRAPLOLIRE GGHTFKPLAETYBQHVYKVNBEVAKLIRKURBALCPHCSKLCC FSCITRKHITERRAGCPHCRAPLOLIRELISLOQUEVERNV GGHTFKPLAETYBQHVYKVNBEVAKLRIKLMSLISLOQUEVERNV GGHTFKPLAETYBQHVYKVNBEVAKLRIKLMSLISLOQUEVERNV ASVUTHOVPOPPSTERUPSTANKRURSTILMFQQVHRKWM ASVUTTPVP POPTSERUPSTANKRURSTILMFQQVHRKWM ASVUTTPVP POPTSERUPSTANKRURSTILMFQQVHRKWM ASVUTTPVP POPTSERUPSTANKRURSTILMFQQVHRKWM ASVUTTPVP POPTSERUPSTANKRURSTILMFQQVHRKWM ASVUTTPVP POPTSERUPSTANCHNESTILKGNADVSPSP LQVGCLWRLKVYPOGNGVVRGYYLSVPLEISAGLPETSKYEYR VENNIGGCNDTTKNI IRBFRSDFEUGECGWINTFFILDLLANKG ALSVETTPVP POPTSERUPSTANTFFILMSTANGLISLIALLANG VENDOGRADATULREFURSPETFFORMSTANGLISLIALLANG VENDOGRADATULREFURSPETFFORMSTANGLINGFTSLILLANGG	5976	20	2949	
BCCRTALLESDRITCPTCHQNDVSPDALIANKFLKQAVNNYRNE TGYTKRLRKQLPSPPPP LIPRNLQPILMRSPISRQDDPL MIPVTSSSTHPAPSISSITSNQSSLAPPVSGHPSSAPAVPUDIT ATVSISVHSEKSGPFRISDNKLLPANALASEHSKGTSSIAITA IMBEKGYQVPVIGFFSLLGQSLLHGQLIPTTGPVRINTARPGGG ROWENSINLGYILVSPPQQIRRGERSCYRSIMEGHISERSQRT GGSLPATPVPVPPPPPLYPPPHTLDLPDGYPPPQPSPQPPP GQPVPPAGYSVPPPGPPPAPANLTSWSGYGTHANTITTTY APPLSRBEPYREQRILKEERKKSKLDBFTNDFAKELMEYKKIQ KRRRSPFSRSSPYSGSSYSRSSYTYSKSRSSITRSRSYSRSSS RSSIRSSYSSSPYPRYRGRGKSKINTYPWSGGYTHANTITTTY APPLSRBEPYREQRILKEERKKSKLDBFTNDFAKELMEYKKIQ KRRRSPFSRSSPYSGSSYSRSSYTYSKSRSSITRSRSYSRSSS RSSIRSSYSRSPYPRRGRGKSKINTYPWSSGYGTHANSTSTERTYPNYRWPPPYDM KAYYGRSVDFRDPPKREYRRWEKKYRWYKGYAAGAQPR PSAMRENTSPBRFIPLINTRNSPFTEGREDVYGGGSHRSNIGS NYPEKLSARDGINQXDMYKSKEKKSRNAPGOKGNKHKKHRRR KGESSEPLINPBLLETTSKESEBPTGVBGNKTDSLFVLDSRDDAT PVRDEPMDABSITPKSVSEKDKRBRDKPKAKGDKKTKRNDGSAV SKRENIVEPAKGPGEKVDGJDVBDLLDLINLQLKKPRETTFNL TILMHILPLRRNKKSLJSPP EKILTINDQK\TPRNTTSGRGSAV SKRENIVEPAKGPGEKVDGJDVBDLLDLINLQLKKPRETTFNL TILMHILPLRRNKKSLJSPP EKILTINDQK\TPRNTTSGRGELKVK AYLPTGKGPLVSKHPGCLSLHSINHTLHPGAGVAAGPATGW/REYLT PULKSSKPKETGVITPREFVAADGHLVHHCDTWQMATGRELKVK AYLPTGKGPLVTKNVPCYRCKQMEYSDELBAIIEDDGDGGRV DTYHNTGITGITEAVKSITILBRNDNITLDQCSALCEBERDEDGG BAADMBEYEEGGLLEFTDBATLDTRKLVBACCAGKTDAGGRDAILQ TRYYDLYTTYDHYYQTPRLMLFGYDGROPDLYSHMMEDISQDH VKTVTILRHPHLLPPPPMCSVHECHRAFWKKIITHVADGGGEL GVHMYLLIFLKHPVQAVIPTIEYDTYRHTM  5978  160 3213 ROGARRWGGCGSFLTWARGFYRRFDLATTSGRRLAGGTAEPAGRQ RPREPERANDGGGVSTLAWRGVTLATGGRRLAGGTAEPAGRQ GYFTPLAATTGGRRLAGVARBENTQQLDTLQ LCSLTKHEENERDCCBMHHKLSVPCWTCKKCICQCALWGGMH GGTTFPLAATTGGVTKVRBEVAKLRRLAGELTHMQVHYSEP LQVGCLCWELKVVPOGRSVVRGYYLSVELBISAGLIPSTSKYER VEMVHQSCLOPPTKNITRFTRADFFVIGEKGWYNFFFRIDLANGRM ASSVTTPVPOPPTSELVPSTLASTFVILRHESTILRWRDDLTSHTSKYER VEMVHQSCNDPTKNITRFTRADFFVIGEKGWYNFFFRIDLANGR VEMPQCDTVTRNITRRFTRADFFVIGEKGWYNFFFRIDLANGR VEMPQCDTVTRNITRRFTRADFFVIGEKGWYNFFFRIDLANGR VEMPGCGCWYNFFFRIDLANGR			-5-15	
TGYTKLIRKQLespeppipperplorriopembesparapoped mipvessthappsislespesgepsarapopedia mipvessthappsislespesgepsarapopedia mipvessthappsislespesgepsarapopedia atvesses persentile production in the production of the p				PLPEEPSSSSEEDDPIPDELLCLICKDIMTDAVVIPCCGNSYCD
MIPVTSSSTÜRAPSISSLTSNQSSLAPPVSGMPSSAPAPUPDIT ATVSISVHSEKSGGPFRDSMKILPAALASEHSKGTSSLATTA. IMERKGYQVPVLGTPSLLGGGLHGGLIPTTGPVRINTARPGG RPGWEHSNKLGYLVSPPQQIRRGERSCYRSINGGHISERSQRS CGPSLPATPVPVPVPPPPPLYPPPPHTLPIPPPPQPSPPQPPPQPPPQPPPQPPPQPPPPQPPPQPPP				
ATVSISVESKSDGPPRDSDNKILPAALASEHSKGTSSIAITA  IMEEKGYQVPVIGTESLIGGSLIHGGLIPTTGPVINTAPPGGG RGWEHSNKIGYIVSPPQQIRESECYRSINGREHBERSQRT GGESLPATPVFVDVDPPPDLYPPPDTTDPUTTAPPGGST GGPSLPATPVFVDVDPPPDLYPPPPTTDPUTTAPPGGSP GQP\PPAGYSVPPPGFPPAANLSTPWSSGVTAHSNTIPTTQ APPLSREFYTREGRILKEEKKKSLUBFTNDFAKELMEYKKTQ KRRRGFSRSKBPYSGSSYSRSSYYTSKGRSGSTRSRSYSKSFS RSHSRSYSRSPYPSGSSYSRSSYYTSKGRSGSTRSRSYSKSFS RSHSRSYSRSPPYPRRGRGKSRNYRSRSRSGSTRSRSYSKSFS RYHSRSRSPQAFRGQSPKRRNVPQGETERSYFNRYRSVPPPYDM KAYYGRSVDFRDPPKERVRWEKKYREWYKKYYKGYAAGAQPR PSANRENFSPBRFIPLNIRNSPFTGRREDYVGGQSHRSRNIGS NYPEKLSARDGHNQKONTKSKEKSSRNAPGUGKONKHKKHRKR KGESSGFLNPELLBTSRSRSPDTOVEBNKTDSLFVLPSRDDAT PVRDEPDDASSITPKSVSKEKDKRRRDLYKAGDKTRKNDGSAV SKKENIVKPAKGPQEKUDG\DVROLLDLAN\QOK\TPRNTTSQRGKSB GGLPQRCQIRKANN  5977 1363 1336 FLEDRGQVISHPQCLSLHSINHILHPGAGVAAGPATGW/REYLT PVLKESKFYKKTGYITPERFVAAGDHLVHHCPTMQMATGRELKVK AYLPTGKOFLVTKNVPCYRRCKQMEYSDELBAI IEDDGGGGWV DTYHNTGITGITEAVKEITLENKUNIBLQDCSALCEBREBEDEG EAADMSYKESGLLEFDERTLDTRKIVBACKAKTDAGGRIAILQ TRYDLYITYDKYYQTPRLMLFGVDBQROPLTVBHMYEDISQDH VKKTVTIRHHPHLPPPPMCSVHPCRHAEVMKKIIBTVABGGGEL GVMMYLLIFLKFVQAVIFTIEYDTTRHFUM PDGARRWGGCGSPLTWAPGFYRRFDLATSGRRLRGQTAEPAGRQ RPRRBBEAMDGGVSSLAEVFRCTICHEKLRDARLCPHCSKLCC FSCLTRWLITEQRAQCPHCRAFLQLRELWNCKAICHGGMTLAG GGHTFKPLARITRGRAVTAVMMHIARLDTQLLKKLITLMGGRTSLT QETELLESLLQEVEHQLRSCSKSELISKSSLLMMPQQVHRKPM ASFVTTPVDPDPTSSLUVSYNDSATFVLENSTLRQRADPUYSPP LQVGCLCWRLKVYPDGNGVURGYYLSVFLUSLAGLPETSKYEYR VEMVHQSCNDPTKNI IRBFRASDPEVGECWGYNRFFRLDLLANGG YLMPQNDTVILRPQVRSTFPRASSPRUEGWGNRFFRLDLLANGG YLMPQNDTVILRPQVRSTFPRASSRDLEWNRIPELDLLANGG				
IMBEKGYUPVIGTPSILIGGSLLHIGQIL PTTGPVRINTARPCGG RGWEHSNKIGYILVSPPQQIRRGERSCYRS IMBGRIHISERSQRT GGSSLRATPVFVVDVPPPDITPDPPGVPPPDGYPPPDGFPPPP GQP\PPAGYSVPPPGFPPPARNISTPWSSGVTAHISTT-DTTQ APPLSREPYREQRIKKEEKKKSKLDEPTNDPAKRIMEYKKIQ KRRRGFSRSKSPYSGSSYSRSSYTYSKSRSGSTRGRSYSKSFS RSHSBSYSRSPYPRGGGKSRNYRSSRSGGTRGRSYSKSFSS RSHSBSYSRSPPYPRGGGKSRNYRSSRSHGYHRSRSRSPPYR RYHSRSRSPQAFRGGFRRNVPVGGSTERRYPRYREVPPPYDM RAYYGRSVDFRDPPEKERYREWERKYREWYRKYYKGYAAGAQPR PSANRENFSFBRFI-PLNIRNSPFTEGREDYVGGGSHRSENIGS NYPEKLSARDSHMOKUMTKSKEKRSRNAPGOKGNHKKRKRRR KGERSEGYLNPEILETSRKSREPTGVERNKTDSLFVLPSRDDAT PVEDDEPMDABSITFKSVBEKDKRRRKDKAKGDKTRKNDGSAV SKKENIVKPAKGPGEVUGG DVRDLLDLINLOKKPKERETFYDL TILNHHLPLRRMKKSL\EPP\EKLTINQQK\TPRNTSQRGKSB BGLFQRCQIRKANN  5977 1363 1336 FLEDGGGVISHFQCLSLHSINHTLHPGAGVAAGPATGW/REYLT PVLKESKPKSTGVITDREPVAAGDHLVHHCPTWQWATGRELKVK AYLPTGKGFLVTKNVCYKRCKQMSYDBLRAI IEBDDGDGGWV DTYHTGITGITTAVKSITLERNDINTRLODCSALGERERBGBBG EAADNBSYEESGLLETDBATLDTRKLVBACKAKTDAGGBDA ILQ TRTYDLYITYDKYYQTPRLWLFGYDBQROPLJVEHMYEDISGDH VKKTVTIENHEPHPPPPROXHECRAEVMKKIISTVARGGCEL GVEMYLLIFIKEYQAVIPTIEYDYTRHFTM  5978 160 3213 RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEPAGRQ RPRREPEANDEGSVESIASWFRCFICMEKLRDARLCPHCSKLCC FSCIRRWILTEDRAQCPHCRAPLQLRSLWCRMABEWTQQLDTLQ LCSLIKHLEDRAGCRESHREVRGVARABEWTQQLDTLQ LCSLIKHEENBKDKCENHHEKLSVFCWTCKKCICHQCALWGGMH GGFTFFPLAEI'YSQHTVKNUBEVAKLRRLRDARLCPHCSKLCC FSCIRRWILTEDRAQCPHCRAPLQLRSLWCRMABEWTQQLDTLQ CEAURIAKDRRVRSIRRAVEWMIARLTSLUNGRWABEWTQQLDTLQ GGTFFFLEI'YSQHTKVMESVAKLRRLRBARLCPHCSKLCC FSCIRRWICHDRSCXSSESLISKSSEILMMFQQVHRKPM ASSVTTPVPPDFPTSELVDSYDSATFVLENFSTLRQRADPVYSPP LQVGGLCWRLKVVPDGNGVVRGYYLSUBLGAGLPETSKYER VEMVHQSCNDPTKNIIRBPASDFFEUGEWGYNRFPFRLDLLANGG VLMPQGCNDPTKNIIRBPASDFFUGGWYNRFPFRLDLLANGG VLMPQGCNDPTKNIIRBPASDFFUGGWYNRFPFRLDLLANGG VLMPQGCNDPTKNIIRBPASDFFUGGWYNRFPFRLDLLANGG VLMPQGCNDPTKNIIRBPASDFFUGGWYNRFPFRLDLLANGG VLMPQGCNDPTKNIIRBPASDFFUGGWYNRFPFRLDLLANGG VLMPQGCNDPTKNIIRBPASDFFUGGWYNRFPFRLDLLANGG VLMPQGCNDPTKNIIRBPASDFFUGGWYNRFPFRLDLLANGG				
RPGWEHSINKI,GYLVSPPQQIRRGERSCYRSINRGRHHSERSQRT CGPSLPATPVPVPPPPLYPPPPLYPPPPTQPFQFFQFT GQP\PPAGYSVPPEGFPPAPAILSTPWUSSGVQTAHSINT.PTTQ APPLSRBPYREQRRILEBEKKKSKLDBPYNDPAKEIMEYKKIQ KERRESFSRSYSPYSGSSYSRSSYTYSKSRSGSTRSSYSKSSS RSHESGYSRSPYPPRRGRGKSRNYRSRSRSHGYHRSFSRSSPPYR RYHSERSPQAFFQQSFNKENVPQGSTERRYPMRYKRYYKGYAAGAQPR RYHSERSPQAFFQQSFNKENVPQGSTERRYPMRYKRYYKGYAAGAQPR PSANRENFSPERFI,PLNIRNSPTTEGREDYVGQQSHRSENIGS NYPEKLSARDGHAQKUNTKSKERSRAPGDCKGNHKKHRKRR KGERSEGFLNPELLBTSRKSRBPTGVBENKTDSLFVLPSRDDAT PVRDBFMDABSITYKSVBEKDKRRRDKPKAKGDKTRKRDGSAV SKERNIVKPAKGPQEKVDG\DVRDLLDLNL\QLKFRYBETPKDL TILNHHLPLRRMKKSL\EPP\ENLTLAQK\TPRNKTSQRGKS BGLFQRCQIKKANN  5977 1363 1336 FLEDRGQVLSHFQCLSLHSINHILHPGAGVAAGPATGW/REYLT PVLKESKFKRTGVITPBEFVAAGBHLVHCPTWGMATGKELKVK AVLPTKKPILVTRNVPCYKRCKGMBYSDELBAIIBDDGGGWV DTYHNTGITGITEAVKEITLENKDNIRLQDCSALCEBEBCDEGG EAADMBEYEESGLLETDBATLDTRKIVACKAKTDAGGBDAILQ TRYTDLYITYDLYITYDLYYTVRLFCYKDRQKQTFWHMYSDSIQDH VKKTVTIENHEHLPPPPMCSVHPCRAEKAKTDAGGBDAILQ TRYTDLYITYDLYITYDLYYTYDFRWLFCYDRGRQBLTYMHMYSDSIQDH VKKTVTIENHEHLPPPPPMCSVHPCRAEKAKTDAGGBDAILQ TRYTDLYITYDLYTTYDLYTYTYDFFWLFYDRGRQBLTYMHMYSDSIQDH VKKTVTIENHEHLPPPPPMCSVHPCRAEKAKTDAGCBDAILQ GUMYLLLIFLKFVQAVIPTIETDYTTHFFM  5978 160 3213 RDGARRWGGCOGSDITVANGFYPRFDLATSGRRLRGGTAEPAGGQ GRARRWGGCOSDITVANGFYPRFDLATSGRRLRGGTAEPAGGQ GGHTFKPLARIYBQWGCRHHEKLSVPCMTCKKCICHQCALWGGMH GGHTFKPLARIYBQWGCRHHEKLSVPCMTCKKCICHQCALWGGMH GGHTFKPLARIYBQWRGVPREVALRIKLMELISLVQUFVRRW EAVRNAKDRRVRSIRRAVRMIARLLDTDLKNLITIMGQKTSLT QETELLESLLQEVBHQLRSCSKSELISKSSRILMMFQQVHRKPM ASSVTTPVPPDFPTSBLVDSYDSATFVLRMFSTLRQRADPVYSPP LQVGGLCWRLKVVPDORGVURGYYLSVILBLSAGLPFTSKYSTR VEMVHQSCNDPTKNITRBPASDFFUGGWYNRFPFILDLLANGG YLMPQMDTVILRPQVRSDFFFQKSRDQHHYITQLEAAGTSYLQQ YLMPQMDTVILRPQVRSDFFFQKSRDQHYNTYDLLEAAGTSYLQQ				
GGPSLPATPUPUPUPPPLYPPPHTLPLPPGUPPPQGPPQGPP GQP\PPAGYSUTPPGFPPAPANISTPWSGVQTAHISTT.PTTQ APPISRREPYREQRILLEERKKKKLIDEPTNIPAKHEMSYKKTQ KERRESPSRSKPYSGSSYSRSSYTYSKSRSGSTRSRSYSKSFS RSHSRSYSRSPYSGSSYSRSSYTYSKSRSGSTRSRSYSKSFS RSHSRSYSRSPYPRRORGKSRIVATSRSRSHGYHKSRSRSPPYR RYHSRSRSPQAPRGGS PMKRNVPQGSTERSFYNDRYREVPPYDM RAYYGRSVDFRDPPKERYREWERKYREWYKKYYKGYAAGAQPR PSANREMFSPBRFIPLNTRNSPFTGRREDYUGGSHRSRNIGS NYPPKLSARDGHNQKDWTYSKEKRSBPTGVERNKTDSLFVLDSRDDAT PVRDBPHDABSITYKBVSEKNERSRDPGKGNKHKKHRKRR KGERSEGILMPELLETSRKSREPTGVERNKTDSLFVLDSRDDAT PVRDBPHDABSITYKBVSEKNKRBRDRPKAKGDKYKKRNDGSAV SKKENIVKPAKGPQEKVDG/DVRDILLDLNL\QLKKPKEBTPKDL TILMHILPLRRMKKSL\SPP\EKKTINQOK\TPRWKTSQRGKSR BGLPQRCQIRKANN  5977 1363 1336 FLEDRGQVISHFQCLSLHSINHTLHPFAGVAAGPATGW/REYLT PVLKESKPKBTGVITPREPVAAGDHLVHHCPTWQMATGEELKVK AYLPTGKQPLVTKNVPCYKRCKQMEYSDELEAIIREDDGDGGWV DTYHNTGITGITTRAVKEITLENKDNIRLQDCSALCERREDEBDG EAADNBSYESSGLLEFVBRATDTRKIVRACKAKTDAGGRDAIQ TRTYDLYITYDKYYQTPRLWLPGYDBGRQPLTVEHMYEDISQDH VKKTVTIENHEHLPPPPMCSWHPCHABEVMKKIITVABGGGEL GVHMYLLIFLKPVQAVIPILBYDYTRHFM  5978 160 3213 RDGARRWGGCQSPLTWARGFYRRPDLATSGRRLRGQTAEPAGRQ RPREPBRAMDEQSVES LAEVPRCPICMEKLADARLCPRCSKLCC FSCIRRLTEQRAQCPHCRAPLVKKIITLMGOKTSLT CSCHTKPLARIYBQHVTKVNEEVAKLRRKLMBLISLVQEVERNV EAVRNAKDBRVREIRNAVBMIARLDTQLKNKLITLMGQKTSLT GETELLESLLGEVBHQLESCSKSKLISKSSEILMMPGQVHRRPM ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQUGGICWRLKVYPDGGMSVVRGYYILENFSTLRQRADPVYSPP LQUGGCWRLKVYPDGGMSVVRGYYILENFSTLRQRADPVYSPP LQUGGCWRLKVYPDGGMSVVRGYYILENFSTLRQRADPVYSPP LQUGGCWRLKVYPDGGMSVVRGYYILENFSTLRQRADPTSKYETSYR VEMWHQSCNDPTKNIIREPRASDPEVGECWGYNRPFRLDLLANEG YLNEQNDTVULLRPQVRSPTFYPGXSRDCHWYTTQLEBAQCTSYLYQ	1 .		•	
GQP\PPAGYSVPPPGFPPAPANLSTPWSSGVQTAHENTIPTTQ APPLSRBEPYREQRILKEEHKKSKLDBFTMDFAKKLMSYKKIQ KERRRSFSRSPYGSSSYYRSSSYTYSKSSGSTRSSFYSKSS RSHERSYSRSPYSGSSYRSSSYSKSSTYRSSSSTRSSFSYSSSS RSHERSYSRSPPYPPRRGRGSRNYRSRSGSTRSSFSYSSSS RSHERSYSRSPPYPPRRGRGSRNYRSRSRSHGYHRSRSPPYR RYHSRSRSPQAFRGQSPMKRNVPQGSTERRYFNRYREVPPYDM KAYYGRSVDFEDPPFKEHEYRKHRYRFKYRKYKYYGYAAGAQPR PSANRENFSPEPFPPLNIRNSPFTRGREDYVGQSHRSRNIGS NYPEKLSARDCHNQKDNYKSKEKESRNAPGDGKGMKHKKHRKRR KGERSEGI-HPELLISTSKESRPTOVERNKTDSLPV1-BSRDAT PVRDEPMDABSITPKSVSEKDKRBRDKPKAKGDKYKRNDGSAV SKRENIVKPAKGPQGKVDG\DVRDLLDLNI\QLKKPKEETPKDL TILNHHLPLRRMKSSL\BPP\EKLTLHOQK\TPRNKTSQRGKSB BGLFQRCQIRKANN  5977 1363 1336 FLEDRGGVLSHFQCLSLHSINHTLHPGKGVAAGPATGW/REYLT PVLKESKPKETGVITPBEPVAAGDHLVHCPTWQWATGBELKVK AYLPTGKQFLVTKNVPCYKRCKQMEYSDELBAI IREDDGDGGWV DTYHNTGITGITRAVKEITLENKDNIRLQDCSALCEBREDEDEG EAADMBEYEESGLLETDBATLDTRKIVBACKAKTDAGGEDAILQ TRYYDLYITYDKYTQTPRLMLFGYDSGQPLTVEHMYEDISQDH VKKTVTIENHEHLPPPPMCSVHPCRHASVMKIIHTVAEGGGEL GVHMYLLIFLKFVQAVIPTIEYDYTRFTM  SPARBARDEGGSPLTWARGFYRRFDLATSGGRLRGQTAEPAGRQ RPREPEAMDEGSVESIAEVFRCPICMEKLRDARLCPHCSKLCC FSCIRNLTEQRAQCPHCRAPLQLREDVNCRWAEBVTQQLDTLQ LCSLTKHEEMBKOKCRSHHRKLSVPCWTCKKCICHQCALMGGMH GGHTFKPLAEIYBQHVTKVNEEVAKLRRKLMELISLVQEVERNV EAVRINAKDERVREITRNAVBMIARLDTQLKNKLITLMGQKTSLT QBTELLESLLQEVEHQLRSCSKSELISKSSELLMMPQQVHRRPM ASFVTTPVPPDFFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQUSGLCWRLKVYPDGGKSVURGYYISVFLEISAGLPBTSKYEYR VEMWHQSCNDPTKNI IRBFRASDPEVGECWGYNRPFRIBLLANGG YLLNEQONDTVILLRPQVRSPTPFQXSRDQCWGYNRPFRLDLLANGG YLLNEQONDTVILLRPQVRSPTPFQXSRDQCWYNRPFRLDLLANGG	!	}		
APPLSRBEPYREQRRLKEEEKKKSKLDEFTNDFAKELMEYKKIQ KRRREFFERSKEPYSGSSYSTSSTYTYSKSRSGSTRSRSYSRSFS RSHSRSYSFSPYPRGGGKSRYRSRSGSTTSRSYSRSFS RSHSRSYSFSPYPRGGGKSRYRSRSGSTTSRSYSRSFS RSHSRSYSFSPYPRGGGKSRYRSRSGSTGSTSRSYSRSFS RYHSRSRSPQAFRQQSPNKRNVPQGETEREYFNRYREVPPPYDM RAYYGRSVDFRDPFKKERYREMEKYYKGYAAGAQPR PSANRENFSPERFI,PLNIRNSPFTRGRREDYVGGQSHRSRNIGS NYPEKLSARDGHNQKONTKSKEKSRNAPGDGKGNKHKKHRKRR KGERSEGFLNPELLFTSRKSRBEPTGVBRNTTDSLFVLPSRDAT PVRDEPPMDABSITYKBVSEKDKRRRDKPKAKGDKTKRKNDGSAV SKRENIVKPAKGPGPERVOG\DVRDLLDLNI\QLKRPKEFTPRDL TILNHHLPLRRMKKSL\EPP\EKLTLNQQK\TPRNKTSQRGKSB BGLFQRCQIRKANN  FLEDRGQVLSHFQCLSLHSINHTLHPGAGVAAGPATGW/REYLT PVLKESKFKETGVITFBEFVAAGDHLVHHCPTWQWATGEELKVK AYLPTGKQFLVTKNVPCYRRCKQMEYSDELBAIIEDDGGGWV DTYHNTGITGITRAVKEITLENKDNIRLQDCSALCEBREDEGG EAADMBEYESGGLLETDRATLDTRKTVRACKAKTDAGGGDAILQ TRYDLYITJRYYQTPRIMLFGYDBQRQPLTVBHMYEDISQDH VKKTVTIENHPPPPPKCSVHPCRHAEVMKKIIETVAEGGGEL GVMYLLIFLKFVQAVIPTIEVDYTRHFTM  S978  160  3213  RDGARRWGGCQSFLTWAPGFYRRFDLATSGRRLRGQTAEPAGRQ RPRREPEAMDEQGVES IABVFRCFICMBKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPCFICMBKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPCFICMBKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPCFICMBKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPCFICMBKLRDARLCPHCSKLCC GGHTFKPLARTYBQHVTKVNBEVAKLRRLIMBLISLVQEVERNV EAVRNAKDERVRBTRNAVEMBLARLDTQLKNKLITLINGQKTSLT QBFELLESLLQEVEBIGLESCSKSBLISKSSBILMFQQVHRRPM ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWRLKVYPDGRGYVRGYYLSVFLELSAGLPBTSKYEYR VEWNHQSCNDPTKNIIRSPADPFEVGECWGYNRFFRILDLLANEG YLNPQNDTVILRRPQNRSPFFFQKSROGYNRFFRILDLLANEG		i ,		l
KERRSPSRSBYYSGSYSRSSYTYSKSRSGSTRSYSRSFS RSISRSYSRSPYPRRGROKERRYYRSRSRSHYHRSRSRSPYR RYHSRSRSPQAFRGQSPIKRNVPQGETERBYPRRYREVPPPYDM KAYYGRSVDFEDPFKKEKYREWEKKYYKGYAAGAQPR PSANREWFSPRFIPININSPPTEGREDYVGGSHRSRIGS NYPEKLSARDGHNQKDNTKSKEKRSRAAPGDGKGNKHKKHRKR KGERSEGFLNPELLETSRSRBPTGVBENKTDSLFVLPSRDDAT PVRDEPMDAESITYKSVEEKDKRERDKPKAKGDKTKRKNDGSAV SKRENIVKPAKGPQERVDG\DVRDLLDLIN\QUKYPERETPRDL TILNHHLPLRMKKSL\EPP\EKLTLNQQK\TPRNKTSGRKSS SKRENIVKPAKGPQERVDG\DVRDLLDLIN\QUKYPERETPRDL TILNHHLPLRRMKKSL\EPP\EKLTLNQQK\TPRNKTSGRKSS BGLFQRCQIRKANN  5977 1363 1336 FLEDRGQVLSHFQCLSLHSINHTLHPGAGVAAGPATCW/REYLT PVLKESKFKETGVITPREFVAAGDHLVHHCPTMQWATGSELKVK AYLPTGKQPLVKNNVPCYKRCKQMEVSDELBAIIEDDGDGGWV DTYHNTGITGITEAVKEITLERKDNIRLDQDCSALCEEREDEDEG EAADMBEYEESGLLETDRATLDTRKIVRACKAKTDAGGBDAILQ TRTYDLYITYDLYYQTPRLWLFGYDBQRQPLTVEHMYEDISQDH VKKTVTIENHFHLPPPPMCSVHFCRIAEVWKKIIETVABGGGEL GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM  5978 160 3213 RDGARRWGGCQSPLTWAFGFYRRFDLATSGRRLRGQTAEPAGRQ RPRREPEAMDEQSVESIAEVFRCFUCMEKLRDARLCPHCSKLCC FSCIRRWLTEGRAQCPHCRAPLQLRELVNCRWABEVTQOLDTLQ LCSLTKHEENEKDKCENHHEKLSVFCWTCKKCICHQCALWGMH GGGTTKFLARIYRGRVTKVNBEVAKLRRLMBLISLVQEVKRNV EAVRNAKDERVREIRNAVEMILARLDTQLKNKLITLMGQKTSLT QRTELLESLLQEVERIGLESCSKSELISKSSEILMMPQQVHRKPM ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWRLKVYPDGNGVVRGYYLSVFLELSAGLPBTSKYEYR VEMVHQSCNDPTKNIIRFRASDPFKVGEGWYNFFFRLDLILANEG YLNPQNDTVILRFQVRSFTFFQKSRDQHNYITQLEAAQTSYLQQ	!			1
RYHSRSRSPQAFRGQSPNKRNVPQGETERBYFNRYREVPPPYDM KAYYGRSVDFRDFFBKERYRBWBKRYREWYBKYYKGVAAGAQPR PSAMRENFS PERFI.PLNIRNSPFTRGREDYVGGQSHRSRNIGS NYPEKLSARDGENQKDMTKSKEKBSENAPEGDRGNKHKKHRKRR KGERSEGFLNPELLBTSRKSRBPTGVERNKTDSLFVLPSRDDAT PVRDBPMDABSITFKSVBRKDKRRRDKPRKAKGDKTKRNDGSAV SKKENIVVPAKGPQERVDG\DVRDLLLDLNL\QLKKPKEBTPKDL TILNHHLPLRRMKKSL\EPP\EKLTLNQQK\TPRNKTSQRGKSB BGLPQRCQIRKANN  5977 1363 1336 FLEDRGQVLSHFQCLSLHSINHILHPGAGVAAGPATCW/REYLT PVLKESKPKRTGVITPBEFVAAGDHLVHHCPTWQWATGEBLKVK ANLPTGKQFLVTKNVPCYKRCKQMEYSDELBAI IBEDDGDGGWV DTYHNTGITGITBAVKEITLBRKDNIRLQDCSALCBBRDGBGWV DTYHNTGITGITBAVKEITLBRKDNIRLQDCSALCBBRDGBGWV DTYHNTGITGITBAVKEITLBRKDNIRLQDCSALCBBRDGBGGWV TRTYDLYITYDKYVQPPRLMLFGYDBQRQPLTVBHWEDISQDH VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIBTVAEGGGEL GVHMYLLIFLREVQAVIPTIEYDTTRHTTM  5978 160 3213 RDGARRWGGCQSPLTWAPGFYRFDLATSGRRLRGQTAEPAGRQ RPRREPRAMDEGSVESIABVFRCPICMBKLRDARLCPHCSKLCC FSCIRRWLTBCRAQCPHCRAPLQLRBLVNCRMABBVTQQLDTLQ LCSLTKHEENBKDKCBNHHEKLSVPCWTCKKCICHQCALWGGMH GGHTFKPLABITYBQRVTKVNBEVAKLRIKLMBLISLVQEVBRNV EANVANADERVRBIRNAVBMIARLDTQLLNKLITLMGQKTSLT QKTELLBSLLQEVBHQLRSCSKSELISKSBILMMFQQVIBKPM ASPVTTPVPPDPTSBLVPSYDSATFVLENFSTLRQRADPVYSPP LQUGGLCWRLKVYPDGNGVVRGYYLSVPLBLSAGGLPETSKYEYR VEMVHQSCNDPTKNIIRBPASDPEVGBCWGYNRFFRLDLLANBG YLNEQNDTVLILRPQVRSPTFPGXSRDCHWYITQLBRAQTFYIQQ	1 1			
RAYYGRSVDFRDPFKERYREWERKYYKGYAAGAQPR PSANRENES PERTI, PLNITINS PTEGEREDYVGGQSHRSRIIGS NYPEKLSARDGHNQKDYKKKEKRSRNAPGDGKGNKHKKHRKRR KGERSEGFILNPELLETSRKSREPTGVERNKTDSLPVLPSRDDAT PVRDEPMDAES ITFKEVSEKDKRERDKYKAGDKTKRNDGSAV SKKRNIVKPAKGPQEKVDG\DVRDLLDLINL\QLKRPKEETPKDL TILNHHLPLRRMKKSL\BPP\EKLTLNQK\TPRNKTSQRGKSE BGLPQCQITKANN  5977 1363 1336 FLEDRGQVLSHFQCLSLHSINHTLHPGAGVAAGPATCW/REYLT PVLKESKPKETGVITPEBPVAAGDHLVHHCPTWQWATGEELKVK AYLPTGKQFLVTKNVPCYKRCKQMEYSDELEAI IEEDDGDGGWV DTYHNTG ITGITEAVKE ITLENKDNIRLQDCSALCEBERDEDGG EAADMBEYEESGLLETDEATLDJTRKLVBACKAKTDAGGRDAILQ TRTYDLYITYDKYYQTPRLWLFGYDBQRQPLTVEHMYEDISQDH VKKTVTI ENHPHLPPPENCSVHPCRHAEVMKKI IETVAEGGGEL GVHMYLLIFLKPVQAVIPTIEYDYTRHFTM  5978 160 3213 RDGARRWGGGGSUTWAAGFYRRFDLATSGRRLRGQTAEPAGRQ RPRREPEAMDEQSVES LAEVFRCPICMEKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPLQLRBLVNCRWAEBEVTQQLDTLQ LCSLTKHEENBKOKCENHHBKLSVFCMTCKKCICHQCALWGGMH GGHTFKPLAEI YBQUYTKVNBEVAKLRKKLMBLISLVQEVERNV EAVRNAKDERVERI YRBUTKVNBEVAKLRKKLMBLISLVQEVERNV CHYNAKDERVERI RNAVBMH LARLDTQLKNKLITLMGQKTSLT QBTELLESLLQEVEHQLRSCSKSELISKSSRILMMFQQVHRKPM ASFVTTTEVPPDFTSBLVPSYDSATFVLRNFSTLARGRADPVYSPP LQVSGLCWRLKVYPDGMGSVVRGYYLSVFLELSAGLPETSKYSIR VEMVHQSCNDPTKNI IRBFASDFEVGBCWGYNRFFRLDLILANGG YLNPQNDTVILIRFQVRSPTFPQKSRDQHWYITQLEAAQTSYIQQ				RSHSRSYSRSPPYPRRGRGKSRNYRSRSRSHGYHRSRSRSPPYR
PSANRENFS PERFI, PLNIRNS PFTRGREDY VGGQSHRSRNIGS NYPEKLSARDGHQKDTYKSKEKRSRAPGDGKGNKIKKKRKRR KGEBEGFLNPELLETSRKSREPTGVEBNKTDSLFVLPSRDDAT PVADBPMDABS ITFKSVBEKDKRERDKPKAKGDKTRKNDGSAV SKKENIVKPAKGPQEKVDG\DVRDLLDLNL\QLKKPKEETPKDL TILNHHLPLRMKKSL\EPP\EKLTLNQQK\TPRNKTSQRGKSE BGLFQRCQIRKANN  5977 1363 1336 FLEDRGQVISHFQCLSLHSINHTLHPGAGVAAGPATGW/REYLT PVLKESKFKETGVITPEEFVAAGDHLVHHCPTWQWATGEELKVK AYLPTGKQFLVTKNVPCYKRCKQMEYSDELBAI IBEDDGDGGWV DTYHNTGITERAVKEITLENKONIRLQDCSALCEBEREDEGG EAADMBEVEESGLLETDEATLDTRKTVBACKAKTDAGGRDAILQ TRTYDLYITYDKYYQTPRLWLPGYDBQRQPLTVEHMYEDISQDH VKKTVTIENHPHLPPPEMCSVHPCRHAEVMKKIIBTVAEGGGEL GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM  160 3213 RDGARRWGGCQSPLTWAFGFYRFFDLATSGRRLRGQTAEPAGRQ RPRREPRAMDEGOSVESLABVFRCFICMEKLRDARLCPHCSKLCC FSCIRWLTEQRAQCPHCRAPLQLRBLVNCRWAEBEVTQQLDTLQ LCSLTKHEEDBKDKCENHHEKLSVFCMTCKKCICHQCALWGGMH GGHTFKPLAEIYEQHVTKVNBEVAKLRKRLMBLISLVQEVERNV EAVNRAADDERVBEIRNAVBMHTARLDTQLNKLLITLMGQKTSLT QBTELLESLLQEVEHQLRSCSKSELISKSSEILMMFQQVHRKPM ASFVTTTVPPDFTTSELVPSYDSATFVLENFSTLAGRADPYYSPP LQVSGLCWRLKVYPDGMGVVRGYYLVFLELSAGLPETSKYEYR VEMVHQSCNDPTKNIIREFASDFEVGECWGKNRFFRLDLLLANGG YLNEQADTVILLRFQVRSPTFFQKSRDQHWYLTQLEAAQTSYLQQ	1 1			
NYPEKLSARDGHNQKDNTKSKEKBSRNAPGDGKGNKHKKHRKRR KGERSEGFINPELLETSRKSREPTOVBENKTDSLFVIPSRDDAT PVRDEPMDABSITPKSVSEKDKRRRDKPKAKGDKTKRKNDGSAV SKKENIVKPAKGPQEKVDG\DVRDLLDLINL\QLKKPKERTPKDL TILNHHLPLRRMKISL\REP\EKLTINQOK\TPRNKTSQRGKSE BGLFQRCQIRKANN  5977 1363 1336 FLEDRGQVLSHFQCLSLHSINHTLHPGAGVAAGPATGW\REYLT PVLKESKPKETGVITPBEPVAAGDHLVHHCPTWQWATGBELKVK ANLPTGKQFLVTKNVPCYKRCKQMEYSDELGAI IREDDGDGGWV DTYHNTGITGITEAVKEITLENKUNIRLQDCSALCEBEBEDEGG EAADMBEYEBSGLLBTDBATLDTRKIVRACKAKTDAGGRDAILQ TRTYDLYITYDKYYQTPRLWLFGYDBQRQPLITVBHMYEDISQDH VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIKTVAEGGGEL GUMYLLIFLKYQAVIPTIEYDVTRHFTM  5978 160 3213 RDGARRWGGCQSFLTWAPGFYRRFDLATSGRRLRGQTAEPAGRQ RPREPBAMDEQSVESIABVFRCPICMEKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPLQLRBLVACKMAEBVTQQLDTLQ LCSLTKHEENBKDKCBNHHEKLSVFCWTCKKCICHQCALWGMH GGGTKFKLAEIYRQHVTKVNBEVAKLRRLMBLISLVQEVBRNV EAVRNAKDBRVREIRNAVBMMIARLDTQLKNKLITLMGQKTSLT QBTELLESLLQEVEHQLRSCSKSELISKSSEILMMFQQVHRKPM ASSVTTEVPPDFTSELVESYDSATFVLENFSTLRQRADFVYSPP LQVSGLCWRLKVYPDGNGVVRGYYLSVPLELSAGLPETSKYE'R VEMVHQSCNDPTTNIIRFSADPEVGECMGYNSPFRLDLLANBG YLNPQNDTVILRPQVRSPTPFQKSRDQHWYITQLEBAQTTSYIQQ	]			
KGERSEGFLNPELLETSRKSREPTGVERNKTDSLFVLPSRDDAT PVRDEPMDABS ITFKSVSEKOKRRRDRYKAKGOKTKRRNDGSAV SKKENIVKPAKGPGEKVDG\DVRDLLDLL\QLKKFKEETFKDL TILNHHLPLRRMKKSL\EPP\EKLTLNQQK\TPRKTSQRGKSE BGLFQRCQIRKANN  5977 1363 1336 FLEDRGQVLSHFQCLSLHSINHTLHPGAGVAAGPATGW/REYLT PVLKESKFKETGVITPERFVAAGDHLVHHCPTWQWATGERLKVK AYLPTGKQPIVTKNVPCYKRCKQMEYSDELEAI IBEDDGDGGWV DTYHNTGITGITEAVKEITLENKDNIRLQDCSALCEBERBLEDGG EAADMBEYEESGLLETDBATLDTRKIVEACKAKTDAGGEDAILQ TRTYDLYITYDKYYQTPRLWLFGYDBQRQPLTVEHMYEDISQDH VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIBTVAEGGGEL GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM  5978 160 3213 RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEPAGRQ RPRREPEAMDEQSVESIABVFRCPICMEKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPLQLRBLWURGNAEBVTQQLDTLQ LCSLTKHEENEKDKCENHHBKLKSVFCWTCKKCICHQCALWGGMH GGHTKFLABIYBQHVTKVNBEVAKLRKLMELISLVQEVERNV EAVRNAKDERVREIRNAVEMMIARLDTQLKNKLITLMGQKTSLT QBTELLESLLQEVBHQLRSCSKSELISKSSEILMMFQQVHRKPM ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWRLKVYPDGNGVVRGYYLSVFLELSAGLPFTSKYEYR VEMVHQSCMDDTWIIRFQDRGVVRGYYLSVFLELSAGLPFTSKYEYR VEMVHQSCMDDTWIIRFQDRSVDRATFFRLDLLANGG				
PVRDEPMDAESITFKSVSEKDKRERDKPKAKGDKTKRKNDGSAV SKKENIVKPAKGPQEKVDG\DVRDLLDLNL\QLKKPKERTPKDL TILNHHLPLRRMKKSL\EPP\EKLTLNQQK\TPRNKTSQRGKSE EGLFQRCQIRKANN  1363 1336 FLEDRGQVISHFQCLSLHSINHTLHPGAGVAAGPATGW/REYLT PVLKESKFKETGVITPREFVAAGDHLVHHCPTWQWATGEELKVK AYLPTGKQFLVTKNVPCYKRCKQMEYSDELEAIIEDDGDGGWV DTYHNTGITGITEAVKEITLENKONIRLQDCSALCEBEBDEDGG EAADMBEYEESGLLETDEATLDTRKIVRACKAKTDAGGRDAILQ TRTYDLYITYDKYYQTPRLWLFGYDBQRQPLIVBHMYEDISQDH VKKTVTIENHPHLPPPFMCSVHPCRHAEVMKKIIBTVAEGGEL GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM  5978 160 3213 RDGARRWGGCQSPLTWADGFYRRFDLATSGRRLRGQTAEPAGRQ RPRREPBAMDEQSVESIABVFRCFICMEKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPLQLRBLVNCRWAEBVTQQLDTLQ LCSLTKHEENBKDKCENHHEKLSVFCWTCKKCICHQCALWGGMH GGHTFKPLABIYBGHVTKVMEEVAKLRKKLMELISLVQEVERNV EAVRNAKDERVREIRNAVEMMIARLDTQLKNKLITLMGQKTSLT QRTELLESLLQEVBHQLRSCSKSELISKSSBILMMFQQVHRKPM ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWRLKVYPDGNGVVRGYYLSVFLBLSAGLPETSKYEYR VEMVHQSCMDDTKNIIREPASDFEVGRGWNRFFRIDLILANGG YLNFQNDTVILRFQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ	1 1			l · · · · · · · · · · · · · · · · · · ·
SKKENIVKPAKGPQEKVDG\DVRDLLDLNL\QLKKPKEBTPKDL TILNHHLPLRRMKKSL\EPP\EKLTLNQQK\TPRNKTSQRGKSE BGLFQRCQIRKANN  1363  1336  FLEDRGQVLSHFQCLSLHSINHILHPGAGVAAGPATGW/REYLT PVLKESKPKRTGVITPBEFVAAGDHLVHHCPTWQWATGRELKVK AYLPTGKQPLVTKNVPCYKRCKQMEYSDELBAI IEEDDGDGGWV DTYHNTGITGITEAVKBITLENKDNIRLQDCSALCEBEBDBDGG EAADMBEYEESGLLETDBATLDTRKIVBACKAKTDAGGEDAILQ TRTYDLYITYDKYYQTPRLWLFGYDBQRQPLTVEHMYEDISQDH VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIETVAEGGEL GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM  5978  160  3213  RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEPAGRQ RPRREPEAMDEQSVBSIABVFRCFICMEKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPLQLRELVNCRWAEBVTQQLDTLQ LCSLTKHEENBKDKCENHHEKLSVPCWTCKKCICHQCALWGGMH GGHTFKPLABIYBQHVTKVMEEVAKLRKKLMELISLVQEVERNV EAVRNAKDERVREIRNAVBMMIARLDTQLKNKLITLMGQKTSLT QBTELLESLLQEVEHQLRSCSKSELISKSSEILMMFQQVHRKPM ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWRLKVVPDGNGVVRGYYLSVFLBLSAGLPBTSKYEYR VEMVHQSCMDPTKNIIREPASDPEVGRCWGNNFFFRLDLLANGG YLNFQNDTVILRPQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ	1	1		
TILNHHLPLRRMKKSL\EPP\EKLTLNQQK\TPRNKTSQRGKSE BGLFQRCQIRKANN  1363  1336  FLEDRGQVLSHFQCLSLHSINHTLHPGAGVAAGPATGW/REYLT PVLKBSKFYKBTGVITPBEFVAAGDHLVHHCPTWQWATGBELKVK AYLPTGKQFLVTKNVPCYKRCKQMBYSDELBAI IBEDDGDGGWV DTYHNTGITGITEAVKEITLENKDNIRLQDCSALCEBEBDDEG EAADMBEYEESGLLBTDBATLDTRKIVBACKAKTDAGGRDAILQ TRTYDLYITYDKYYQTPRLWLFGYDBQROPLIVEHMYEDISQDH VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIBTVAEGGGEL GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM  5978  160  3213  RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEPAGRQ RPRREPEAMDEQSVESIABVFRCPICMEKLRDARLCPHCSKLCC FSCTRRWLTEQRAQCPHCRAPLQLRELVNCRWAEBVTQQLDTLQ LCSLTKHEENBKKDKCBNHHEKLSVFCWTCKKCICHQCALWGGMH GGHTFKPLABIYBQHVTKVMBEVAKLRKKLMBLISLVQEVBRNV EAVRNAKDERVRIRNAVBMMIARLDTQLKNKLITLMGQKTSLT QBTELLESDLQEVBHQLRSCSKSELISKSSBILMMFQQVHRKPM ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWRLKVYPDGNGVVRGYYLSVFLBLSAGLPBTSKYEYR VEMVHQSCMDDTKNIIREPASDPEVGRCWGNNFFRLDLLANGG YLNFQNDTVILRFQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ		i		
BGLFQRCQIRKANN  1363  1336  FLEDRGQVLSHFQCLSHSINHTLHPGAGVAAGPATGW/REYLT  PVLKESKFRRTGVITPEFFVAAGDHLVHHCPTWQWATGRELKVK  AYLPTGKQPLVTKNVPCYKRCKQMEYSDELBAI IEEDDGDGGWV  DTYHNTGITGITEAVKBITLENKDNIRLQDCSALCEERBDEDEG  EAADMBEYEESGLLETDBATLDTRKLVBACKAKTDAGGRDAILQ  TRTYDLYITYDKYYQTPRLWLFGYDBQRQPLTVEHMYEDISQDH  VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIBTVAEGGGEL  GVEMYLLIFLKFVQAVIPTIEYDYTRIFTM  5978  160  3213  RDGARRWGGCQSPLTWADGFYRRFDLATSGRRLRGQTAEPAGRQ  RPRREPEAMDEQSVESIABVFRCPICMEKLRDARLCPHCSKLCC  FSCIRRWLTQRAQCPHCRAPLQLRBLVNCRWAEBVTQQLDTLQ  LGSLTKHEENBKDKCENHHEKLSVFCMTCKKCICHQCALWGGMH  GGHTFKPLAEIYBQHVTKVNBEVAKLRRKLMELISLVQEVERNV  EAVRNAKDERVRBIRNAVEMMIARLDTQLKNKLITLMGQKTSLT  QBTELLESSLLQEVEHQLRSCSKSBLISKSBRILMMFQQVHRKPM  ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP  LQVSGLCWRLKVYPDGNGVVRGYYLSVFLBLSAGLPBTSKYEYR  VEMVHQSCMDPTKNIIREPASDFEVGRGWNRFFRIDLLANGG  YLNFQNDTVILRPQVRSPTPFQKSRDQHWYITQLEAAQTSYIQQ				
PVLKESKPRETGVITPERFVAAGDHLVHHCPTWQWATGEELKVK AYLPTGKQPLVTKNVPCYKRCKQMEYSDELEAI IEEDDGDGGWV DTYHNTGITGITEAVKEITLENKUNIRLQDCSALCERERDEDGG EAADMBEYEESGLLETDBATLDTRKIVRACKAKTDAGGRDAILQ TRTYDLYITYDKYYQTPRLWLFGYDBQRQPLTVBHMYEDISQDH VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIBTVAEGGEL GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM  5978 160 3213 RDGARRWGGCQSPLTWADGFYRRFDLATSGRRLRGQTAEPAGRQ RPRREPBAMDEQSVESIABVFRCFICMEKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPLQLRBLVNCRWAEBVTQQLDTLQ LCSLTKHEENBKDKCBNHHEKLSVFCWTCKKCICHQCALWGGMH GGHTFKPLABEIYBQHVTKVMEEVAKLRKLMELISLVQEVERNV EAVRNAKDERVREIRNAVBMHIARLDTQLKNKLITLMGQKTSLT QBTELLESDLQEVBHQLRSCSKSBLISKSSBILMMFQQVHRKPM ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWRLKVYPDGNGVVRGYYLSVFLBLSGLPBTSKYEYR VEMVHQSCMDPTKNIIREPASDFEVGRCWGNNFFRIDDLLANGG YLNFQNDTVILRFQVRSPTFFQKSRDQHWYITQLEBAQTSYIQQ				
AYLPTGKQPLVTKNVPCYKRCKQMEYSDELEAI IBEDDGDGGGWV DTYHNTG ITGITRAVKE ITLENKUNIRLQDCSALCEBERDEDGG EAADMBEYEESGLLETDBATLDTRKIVBACKAKTDAGGEDAILQ TRTYDLYITYDKYYQTPRLWLFGYDBQRQPLTVEHMYEDISQDH VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIETVAEGGEL GVHMYLLIFLKFVQAVIPTIEYDYTRFTM  5978 160 3213 RDGARRWGGCQSPLTWADGFYRFDLATSGRRLRGQTAEPAGRQ RPRREPRAMDEQSVESIABVFRCFICMEKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPLQLRELVNCRWAEBVTQQLDTLQ LCSLTKHEENBKDKCENHHEKLSVPCWTCKKCICHQCALWGGMH GGHTFKPLABEIYBQHVTKVMEEVAKLRKKLMELISLVQEVERNV EAVRNAKDERVREIRNAVEMMIARLDTQLKNKLITLMGQKTSLT QETELLESDLQEVEHQLRSCSKSELISKSSEILMMFQQVHRKPM ASSVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWRLKVYPDGNGVVRGYYLSVFLBLSGLPETSKYEYR VEMVHQSCMDDTTNIIREPASDPEVGRCWGYNRFFRIDLILANGG YLNEQNDTVILRPQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ	5977	1363	1336	FLEDRGQVLSHFQCLSLHSINHILHPGAGVAAGPATGW/REYLT
DTYHNTGITGITEAVKEITLENKDNIRLQDCSALCEBERDEDEG EAADMBEYEESGLLETDBATLDTTKIVEACKAKTDAGGEDAILQ TRTYDLYITYDKYYQTPRLWLFGYBOROPLTVEHMYEDISQDH VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIETVAEGGGEL GVHMYLLIELKPVQAVIPTIEYDYTRHFTM  5978 160 3213 RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEPAGRQ RPRREPEAMDEQSVESIAEVFRCPICMEKLRDARLCPHCSKLCC FSCTRRWLTEQRAQCPHCRAPLQLRELVNCRWAEBVTQQLDTLQ LCSLTKHEENEKOKCENHHEKLSVFCWTCKKCICHQCALWGGMH GGHTFKPLABEIYRQHVTKVMEEVAKLRKKLMELISLVQEVERNV EAVRNAKDERVREIRNAVEMMIARLDTQLKNKLITLMGQKTSLT QETELLESDLQEVEHQLRSCSKSELISKSSEILMMFQQVHRKPM ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWRLKVYPDGNGVVRGYYLSVFLBLSAGLPETSKYEYR VEMVHQSCMDDTTNIIREPASDPEVGECWGVNRFFRLDLLANGG YLNFQNDTVILRFQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ	[	1		
EAADMBBYEESGLLETDBATLDTRKIVEACKAKTDAGGEDAILQ TRTYDLYITYDKYYQTPRLWLFGYDBQRQPLTVEHMYEDISQDH VKKTVTIEMHPHLPPPFMCSVHPCRHAEVMKKIIETVAEGGGEL GVHMYLLIFLKFVQAVIPTIEYDYTRFFTM  5978 160 3213 RDGARRWGGCQSPLTWAPGFYRFFDLATSGRRLRGQTAEPAGRQ RPRREPEAMDEGSVESIAEVFRCPICMEKLRDARLCPHCSKLCC FSCTRRWLTEQRAQCPHCRAPLQLRELVNCRWAEBVTQQLDTLQ LCSLTKHEENBKDKCENHHEKLSVFCWTCKKCICHQCALWGGMH GGHTFKPLAEIYBQHVTKVNEEVAKLRKLMELISLVQEVERNV EAVRNAKDERVREIENAVEMMIARLDTQLKNKLITLMGQKTSLT QKTELLESLLQEVENQLRSCSKSELISKSSEILMMFQQVHRKPM ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWLKVYPDGNGVVRGYYLSVFLELSAGLPETSKYEYR VEMVHQSCMDPTKNIIRFFASDFEVGECWGYNRFFRLDLLANGG YLNFQNDTVILRPQVRSPTPFQKSRDQHWYITQLEAAQTSYIQQ		Į		
TRTYDLY ITYDKYYQTPRLWLFGYDBQRQPLTVEHMYEDISQDH VKKTVTI ENHPHLPPPPMCSVHPCRHAEVMKKI I ETVAEGGGEL GVEMYLLI FILKFVQAVIPTI EYDYTRIFTM  5978 160 3213 RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEPAGRQ RPRREPEAMDEQSVES I AEVFRCPI CMEKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPLQLRBLVNCRWAEBVTQQLDTLQ LCSLTKHEENBKDKCENHHEKLSVFCMTCKKCI CHQCALWGGMH GGHTFKPLAEI YBQHVTKVNEEVAKLRKLMELISLVQEVERNV EAVRNAKDERVREI RNAVEMMI ARLDTQLKNKLI TLMGQKTSLT QRTELLESILQEVENGLRSCSKSBLISKSSBILMMFQQVHRKPM ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWRLKVYPDGNGVVRGYYLSVPLBLSAGLPETSKYEYR VEMVHQSCMDPTKNI I REPASDFEVERCWGYNRFFRIDLILANGG YLNFQNDTVILRPQVRSPTPFQKSRDQHWYITQLEAAQTSYIQQ	[	i		<del></del>
VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIBTVAEGGGEL GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM  5978  160  3213  RDGARRWGCQSPLTWADGFYRRFDLATSGRRLRGQTAEPAGRQ RPRREPEAMDEQSVES LAEVFRCPICMEKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPLQLRBLVNCRWAEBVTQQLDTLQ LCSLTKHEENBKDKCENHHEKLSVFCMTCKKCTCHQCALWGGMH GGHTFKPLABIYBQHVTKVNBEVAKLRRKLMELISLVQEVERNV EAVRNAKDERVRBIRNAVEMMIARLDTQLKNKLITLMGQKTSLT QRTELLESSLQEVEHQLRSCSKSBLISKSSBILMMFQQVHRKPM ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWRLKVYPDGNGVVRGYYLSVFLBLSGSLPBTSKYEYR VEMVHQSCMDPTKNIIREPASDFEVGECWGYNRFFRIDLLANGG YLNFQNDTVILRFQVRSPTPFQKSRDQHWYITQLEAAQTSYIQQ	}	1		· · · · · ·
GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM  5978  160  3213  RDGARRWGGCQSPLTWADGFYRRFDLATSGRRLRGQTAEPAGRQ RPRREPRAMDEQSVESIABVFRCFTCMEKLRDARLCPHCSKLCC FSCIRWLTEQRAQCPHCRAPLQLRBLVNCRWAEBVTQQLDTLQ LCSLTKHEENBKDKCENHHEKLSVPCWTCKKCICHQCALWGGMH GGHTFKPLABEIYBQHVTKVMEEVAKLRKLMELISLVQEVERNV EAVRNAKDERVREIRNAVEMMIARLDTQLKNKLITLMGQKTSLT QBTELLESDLQEVEHQLRSCSKSELISKSSEILMMFQQVHRKPM ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWRLKVVPDGNGVVRGYYLSVFLBLSGGLPETSKYEYR VEMVHQSCMDPTKNIIREFASDFEVGECWGVNRFFRLDLLANGG YLNFQNDTVILRFQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ		l		
7978 7978 7978 7978 7978 7978 7978 7978		İ		
RPRREPEAMDEQSVESIABVFRCFICMEKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPLQLRELVNCRWAEBVTQQLDTLQ LCSLTKHEENBKDKCENHHEKLSVFCWTCKKCICHQCALWGGMH GGHTFKPLABIYEQHVTKVMBEVAKLRRLMELISLVQEVBRNV EAVRNAKDERVREIRNAVEMMIARLDTQLKMKLITLMGQKTSLT QBTELLESLLQEVEHQLRSCSKSELISKSSEILMMFQQVHRKPM ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWKLKVYPDGNGVVRGYYLSVFLBLSAGLPBTSKYEYR VEMVHQSCNDPTKNIIRBFASDFEVGECWGYNRFFRLDLLANGG YLNFQNDTVILRFQVRSPTPFQKSRDQHWYITQLEAAQTSYIQQ	5978	160	3213	
FSCIRRWLTEQRAQCPHCRAPLQLRELVNCRWAEBVTQQLDTLQ LCSLTKHEENBKDKCENHHEKLSVPCWTCKKCICHQCALWGGMH GGHTFKPLABIYBQHVTKVMBEVAKLRRKLMBLISLVQEVBRNV EAVRNAKDBRVRBIRNAVBMMIARLDTQLKMKLITLMGQKTSLT QBTELLESLLQEVBHQLRSCSKSBLISKSSBILMMFQQVHRKPM ASFVTTPVPPDFTSBLVPSYDSATFVLBNFSTLRQRADPVYSPP LQVSGLCWKLKVYPDGNGVVRGYYLSVFLBLSAGLPBTSKYEYR VEMVHQSCNDPTKNIIRBFASDPEVGBCWGYNRFFRLDLLANGG YLNFQNDTVILRPQVRSPTPFQKSRDQHWYITQLEAAQTSYIQQ				
LCSLTKHEENBKDKCENHHBKLSVFCWTCKKCICHQCALWGGMH GGHTFKPLABIYBQHVTKVNBEVAKLRKLMBLISLVQEVBRNV EAVRNAKDBRVRBIRNAVBMMIARLDTQLKNKLITLMGQKTSLT QBTELLESLLQEVBHQLRSCSKSBLISKSSBILMMFQQVHRKPM ASFVTTPVPPDFTSBLVPSYDSATFVLBNFSTLRQRADPVYSPP LQVSGLCWLKVYPDGNGVVRGYYLSVFLBLSAGLPBTSKYEYR VEMVHQSCNDPTKNIIRBPASDPBVGBCWGYNRFFRLDLLANGG YLNFQNDTVILRPQVRSPTPFQKSRDQHWYITQLBAAQTSYIQQ		1		
GGHTFKPLABIYBQHVTKVNBEVAKLRRKLMBLISLVQEVBRNV EAVRNAKDBRVRBIRNAVBMMIARLDTQLKNKLITLMGQKTSLT QBTELLBSSLLQEVBHQLRSCSKSBLISKSBRILMMFQQVHRKPM ASFVTTPVPPDFTSELVPSYDSATFVLBNFSTLRQRADPVYSPP LQVSGLCWRLKVYPDGNGVVRGYYLSVFLBLSAGLPBTSKYEYR VEMVHQSCNDPTKNIIRBPASDPEVGRCWGYNRFFRIDLLANGG YLNFQNDTVILRFQVRSPTPFQKSRDQHWYITQLBAAQTSYIQQ		1		
EAVRNAKDERVREIRNAVEMMIARLDTQLKNKLITLMGQKTSLT QETELLESSLQEVEHQLRSCSKSELISKSSEIIMMFQQVHRKPM ASFVTTEVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWRLKVYPDGNGVVRGYYLSVFLELSAGLPETSKYEYR VEMVHQSCMDDTKNIIREPASDPEVGECWGYNRFFRIDILLANEG YLNFQNDTVILRFQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ				· · · · · · · · · · · · · · · · · · ·
QBTELLESJLQEVEHQLRSCSKSELISKSSEILMMFQQVHRKPM ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWRLKVYPDGNGVVRGYYLSVYLBLSAGLPBTSKYEYR VEMVHQSCNDPTKNIIRBFASDFEVGECWGYNRFFRLDLLANEG YLNPQNDTVILRPQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ		. 1	i	-
LQVSGLCWRLKVYPDGNGVVRGYYLSVFLBLSAGLPETSKYEYR VEMVHQSCNDPTKNIIRBFASDFEVGECWGYNRFFRLDLLANEG YLNFQNDTVILRFQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ		j		
VEMVHQSCNDPTKNIIRBFASDFEVGECWGYNRFFRLDLLANEG YLNFQNDTVILRFQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ			,	ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP
YLNEQNDTVILREQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ	1	1	j	-
		ĺ		, and the second second second second second second second second second second second second second second se
INNLKERLTIELSRTQKSRDLSPPONHLSPQNDDALETRAKKSA		ŀ		
	LL		<u></u>	INNLKERLTIELSRTQKSRDLSPPONHLSPQNDDALETRAKKSA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotice	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
	T	<del>                                     </del>	CSDMLLER\GPYSAS\VRBAKEDEEDEEKIQNEDYHEELSDGDL
1	]	1	DLDLVYEDEVNQLDGSSSSASSTATSNTBENDIDERTMSGENDV
}	i .	l	BYNNMELBEGELMEDAAAAGPAGSSHGYVGSSSRISRRTHLCSA
]		1	ATSSLLDIDPLILIHLLDLKDRSSIENLWGLQPRPPASLLQPTA
1		!	SYSRKOKOQRKQQAMWRVPSDLKMLKRLKTQMAEVRCMKTDVKN
1	į i	l	TLSEIKSSSAASGDMQTSLFSADQAALAACGTENSGRLQDLCMB
l	Į i		LLAKSSVANCYTRNSTNKKSNSPKPARSSVAGSLSLRRAVDPGE
1			NSRSKGDCQTLSEGSPGSSQSGSRHSSPRALIHGSIGDILPKTE
	ĺ	1	DRQCKALDSDAVVVAVFSGLPAVEKRRKMVTLGANAKGGHLEGL
1			QMTDLENNSETGELQPVLPEGASAAPEEGMSSDSDIECDTENEE
1	[. I	(	CEEHTSVGGFHDSFMVMTQPPDEDTHSSFPDGEQIGPEDLSFNT
			DBNSGR
5979	212	3665	LPDMIMYLWLKLLAFGFAFLDTEVFVTGQSPTPSPTDAYLNASE
1	i	ļ	TTTLSPSGSAVISTTIATTPSKPTCDEKYANITVDYLYNKETK
	. 1		LFTAKLNVNENVECGNNTCTNNEVHNLTECKNASVSISHNSCTA
1			PDKTLILDVPPGVEKVPVHCCS\QVEQPDSTIWLKWKNIETSTC
		ļ	DTQNITYRFQCGNMIFDNKRIKLENLEPEHEYKCDSEILYNSHK
] .	Į į		FTNASKIIKTDFGSPGEPQIIFCRSEAAHQGVITWNPPQRSFHN
			FTLCYIKETEKDCLNLDKNLIKYDLQNLKPYTKYVLSLHAYIIA
			KVQRNGSAAMCHFTTKSAPPSQVWNMTVSMTSDNSMHVKCRPPR
	į į		DRNGPHERYHLEVEAGNTLVRNESHKNCDFRVKDLQYSTDYTFK AYFHNGDYPGEPFILHHSTSYNSKALIAFLAFLIIVTSIALLUV
			LYKIYDLHKKRSCNLDEQQKLVERDDEKQLMNVEPIHADILLET
			YKRKIADEGRIFLAEFQSIPRVFSKFPIKEARKPFNQNKNRYVD
	ļ		ILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAOGPR
]	·		DETVDDYWRMIWEQKATVIVMVTRCEEGNRNKCAEYWPSMEEGT
[ ' ]			RAFGECCCKDLTKHKRCP\DYIIQKLNIVNKKEKATGREVTHIQ
	<b>!</b>		PTSWPDHGVPBDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGR
			TGTYIGIDAMLEGLEAENKVDVYGYVVKLRRQRCLMVQVEAQYI
			LIHQALVEYNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAE
			FORLPSYRSWRTQHIGNOE\ENKSKNRNSNVIPYDYNRVPLKHE
			LEMSKESEHDSDESSDDDSDSERPSKYINASFIMSYWKP\EVMI
		•	AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWG
			EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ
			YTNWSVEQLPAEPKELISMIQVVKQKLPQKNSSRGNKHHKSTPL
			LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP
		'	GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD
	1	'	KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP
5980	3	7763	ASPALNQGS
2280	3	2363	DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI
[	<u> </u>		PEBDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP
	1	i	VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN
	ļ	İ	CGAPGODTKAOSMLVEOSEKLRHLSTFSHOVLOTRLVDAAKALN
1 1	' <u> </u>	ì	LVHCHCLDIFINQAFDMORDLQITPKRLEYTRKKENELYESIMN
]	İ		IANRKQBEMKDMIVETLNTMKEELLDDATNMBPKDVIVPENGBP
! I	ł		VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL
}	·		ERCLOSLEKSODVSVHITSNYLKOILNAAYHVEVTFHSGSSVTR
[	!		MLWEQIKQIIQRITWVSPPAITLEWKRKVAQBAIBSLSASKLAK
	j		SICSOFRTRLNSSHEAFAASLROLEAGHSGRLEKTEDLWLRVRK
<u>i</u>	ĺ		DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN
	[		WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG
	1		SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL
j i			DVVBGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA
	ł		MMSGSIVGTP1HMAPELFTGKYDNSVDVYAPGILFWYICSGSVK
	1		LPBAFERCASKDHLWNNVRRGARPERLPVFDEBCWQLMEACWDG
	Ì		DPLKRPLLGIVQPMLQGIMNRLCKS\NSBQPNRGLDDST
5981	1	2519	GRKHSAAMERPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRL
	ì		DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP
			G\EDEBCGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV
		]	ILVLTTFHVPLVIMTFGQSKLYRSEDYGKNFKDITDLINNTPIR
	<del></del>		

	·		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding to first	to first	L-Leucine, M-Methionine, N-Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	sequence	sequence	Codon, /=possible nucleotide deletion,    -possible nucleotide insertion)
<u> </u>	sequence		TEPGMAIGPENSGKVVLTAEVSGSSRGGRIFRSSDFAKNFVOTD
1	}	į	LPFHPLTQMMYSPQNSDYLLALSTENGLWVSKNFGGKWEEIHKA
i	ļ	ł	VCLAKWGSDNTIPPTTYANGSCKADLGALELWRTSDLGKSPKTI
{	1		GVKIYSFGLGGRFLFASVMADKDTTRRIHVSTDQGDTWSMAQLP
1			SVGQEQFYSILAANDDMVFMHVDEPGDTGFGTIFTSDDRGIVYS
ì	<u>'</u>		KSLDRHLYTTTGGETDFTNVTSLRGVYITSVLSEDNSIQTMITF
			DQGGRWTHLRKPENSECDATAKNKNECSLHIHASYSISQKLNVP
1	}		MAPLSEPNAVGIVIAHGSVGDAISVMVPDVYISDDGGYSWTKML
ı	1		EGPHYYTILDSGGIIVAIRHSSRPINVIKFSTDEGQCWOTYTFT
1	ŧ		RDPIYFTGLASEPGARSMNISIWGFTRSFLTSQWVSYTIDFKDI
!	ł		LBRNCEEKDYTIWLAHSTDPKDYEDGCILGYKEQFLRLRKSSVC
			QNGRDYVVTKQPSICLCSLEDFLCDFGYYRPENDSKCVEQPELK
1	İ		GHDLBFCLYGREEHLTTNGYRKIPGDKCQGGVNPVREVKDLKKK
1			CTSNFLSPEKQNSKSNSVPIILAIVGLMLVTVVAGVLIVKKYVC
1			GGRFLVHLYSVLQQH\AEA\NGVDGVDALDTASHTNKSGYHDDS
			DEDITE
5982	56	2316	ATR⊇PRGSSWCRQFSRTASAAPGRSNMLRIPVRKALVGLSKSPK
ſ	İ		GCVRTTATAASNLIEVFVDGQSVMVBPGTTVLQACRKVGMQIPR
1			FCYHERLSVAGNCRMCLVEIEKAPKVVAACAMPVMKGWNILTNS
			EKSKKAREGVMEFLLANHPLDCPICDQGGECDLQDQSMMFGNDR
1			SRFLEGKRAVEDKNIGPLVKTINTRCIQCTRCIRPASEIAGVDD
i	,		LGTTGRGNDMQVGTYIEKMFMSELSGNIIDICPVGALT9KPYAF
1			TARPWETRKTESIDVMDAVCSNIVVSTRTGEVMRILPRMHEDIN
j			EEWISDKTRFAYDGLKRQRLTEPMVRNEKGLLTYTSWEDALSRV AGMLQSFQGKDVAAIAGGLVDAEALVALKDLLNRVDSDTLCTRB
1			VPPTAGAGTDLRSNYLLNTTIAGVEEADVVLLVGTNPRYEAPLF
			NARIRKSWLHNDLKVALIGSPVDLTYTYDHLGDSPKILQDIASG
l	,		SHPFSQVLKEAKKPMVVLGSSALQRNDGAAILAAVSSLAQKIRM
İ			TSGVTGDWKVMNILHRIASQVAALDLGYKPGVKAIRKNPPKVLP
			LLGADGGCITRQDLPKDCFIIYQGHHGDVGAPIADVILPGAAYT
1			EKSATYVNTEGRAQQTKVAVTPPGLAREDWKIIRALSETAGMTL
j .			PYDTL\DQVRNRLEEVSPNLVRYDDIEG\ANYPQQANELSKLVN
1			QQLLADPLVPPQLTMKDFYMTDSISRASQTMAKCVKAVTEGAQA
			VEEPSIC
5983	248	1763	BARGDGGRRHRASGRRAGRGKP\AGLKSQGQRAVPKRAVARGG
			RQ\YSAAIALLEPAGSBIADDLSILYSNRAACYLKEGNCSGCIQ
			DCNRALELHPPSMKPLLRRAMAYETLEQYGKAYVDYKTVLQIDC
			GLQLANDSVNRLSRILMELDGPNWREKLSLIPAVPASVPLQAWH
			PAKEMISKQAGDSSSHRQQGITDEKTFXALKERGNQCVNDKNYK
			DALSKYSECLKINNKECAIYTNRALCYLKLCQFEEAKODCDQAL
			QLADGNVKAFYRRALAHKGLKNYQKSLIDLNKVILLDPSIIRAK MFLEFUTDILNIKTARFARFERFERBYIFIA DEVNEYKERDOGDA
			MELBEVTRLINLKOKTAPFNKEKERRKIEIQEVNEGKERPGRPA GEVSTGCLASEKGGKSSRSPEDPEKLPIAKPNNAYEFGQIINAL
			STRKDKEACAHLLAITAPKOLPMFLSNKLEGDTFLLLLIQSLKNN
			LIEKDPSLVYQHILYLSKAERFKMMLTLISKGQKELIEOLFEDL
			SDTPNNHFTLEDIQALKRQYEL
5984	755	1193	SSVCMACTYVSNLGKKORSVSFLASGLMRVSTGPELRLHHSFVL
[			TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG
			SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY
			FHHSLRSISRFSSG
5985	22	1408	RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSBRGDSGR
	ļ	[	RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE
]	ļ		FAVEYFTRLREARAPASVLPAATPRQSLGHPPPBPGPDRVADAK
}	Ì	ļ	GD9ESEEDRDLEVPVPSRFNRRVSVCAETYNPDEBEEDTDPRVI
]	ļ	ŀ	HPKTDBQRCRLQBACKDILLFKNLDQBQLSQVLDAMFBRIVKAD
			EHVIDQGDDGDNFYVIBRGTYDILVTKDNQTRSVGQYDNRGSFG
			ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM
	}		PESFIESVPLLKSLEVSERMKIVDVIGBKIYKR/DGBRIITQGE
[ ]	ì		K\ADSFYIIESGEVSILIRSRTKSNKDGGNQEVELARCHKGQYP
	ļ	I	GELALVTNKPRAASAYAVGDVKCLVMDVQAPERLLGPCMDIMKR
LI			nishyeeqlvkmfgssvdlgnlgq

Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Prediction   Predicted   Pre			Predicted end	
Not   location   location   corresponding to first   amino acid   residue of   saino acid   residue of   saino acid   residue of   saino acid   residue of   saino acid   residue of   saino acid   sequence   Sectine, G-Giltraine, R-Arginine, S-Sectine, 3-Unknown, *-Stop   Coden, /-possible mucleotide deletion,   sequence   Sectine, 7-Threonine, V-Naline,   w-Tryptophan, Y-Typtopian, X-Typtopian, X-Typtophan, Y-Typtopian, X-Typtop	_	i .		
location   corresponding   coffice   first   control cold   coffice   first   control cold   cold	1		*	
corxesponding to first anison acid maino acid residue of aniso acid residue of aniso acid residue of aniso acid aniso acid aniso acid aniso acid aniso acid aniso acid aniso acid aniso acid sequence  5986 1806 484 BASE PROPERTY OF THE PROP	NO:	I .		
to first enidue of anino acid amino acid amino acid amino acid anino acid amino acid amino acid amino acid amino acid acquence  5986  1806  484  484  1806  484  1806  484  1806  484  1806  484  1806  1806  484  1806  484  1806  1806  484  1806  1806  484  1806  1806  1806  1806  1806  484  1806  1807  1806  1806  1806  1806  1806  1806  1806  1806  1806  1806  1806  1806  1806  1806  1806  1806  1806  1806  1807  1806  1807  1806  180	1	location	corresponding	
anino acid		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
enino acid	ľ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
metion acidd sequence  5986  1806  484  Sequence  484  Secuence  4	1	amino acid	residue of	
autho actid sequence 1806 1806 1806 1806 1806 1806 1806 1806	ı			• • • • • • • • • • • • • • • • • • • •
Sequence   N=possible mucleotide insertion				
S986   1896	1		sequence	
SPECKERDSPREGEPPERLGLIGALIAMPEDGWRGSPUPRESSLAPPDASI LISMYCSIGDHYAQELPQUSDLIGANEREREPGER, JACQHSPLERE EHYTCUGSILDRENG/VSSILLUSTRAWEREREPGER, JACQHSPLERE EHYTCUGSILDRENG/VSSILLUSTRAWEREREPGER, JACQHSPLERE EHYTCUGSILDRENG/VSSILLUSTRAWEREREPGER, JACQHSPERE SEKGLVLQLIGSYQRHACHAWURGPRAVATKRIVLAMDLOTTIK; QNELLOQUANDWARGURUNTUPRER, VHERSSPPY/ORDKITTSTOG VERNTRANDIPSRELLLIPHILLEVRIMGILGSUPRESSPPY ORDKITTSTOG VERNTRANDIPSRELLLIPHILLEVRIMGILGSUPRESSPPY ORDKITTSTOG VERNTRANDIPSRELLLIPHILLEVRIMGILGSUPRESSPPY ORDKITTSTOG VERNTRANDIPSRELLLIPHILLEVRIMGILGSUPRESSPPY ORDKITTSTOG VERNTRANDIPSRELLLIPHILLEVRIMGILGSUPRESSPPY ORDKITTSTOG VERNTRANDIPSRELLLIPHILLEVRIMGILGSUPRESSPPY ORDKITTSTOG VERNTRANDIPSRELLIPHILLIPHILLEVRIMGILGSUPRESSPPY ORDKITTSTOG GLIRETPRISSPLDDIGGLIGALIAMEROWARGEPOPPHERD GLIRETPRISSPLDDIGGLIGALIAMEROWARGEPOPPHERD GLIRETPRISSPLDDIGGLIGALIAMEROWARGEPOPPHERD GLIRETPRISSPLDDIGGLIGALIAMEROWARGEPOPPHERD GLIRETPRISSPLDDIGGLIGALIAMEROWARGEPOPPHERD GLIRETPRISSPLDIGGREGALIAMEROWARGEPOPPHERD GLIRETPRISSPLDIGGREGALIAMEROWARGEPOPPHERD GLIRETPRISSPLDIGGREGALIAMEROWARGEPOPPHERD GRANDIAMEROWARGEN GRANDIAMEROWARGEN GRANDIAMEROWARGEPOPPHERD GLIRETPRISSPLDIGGREGALIAMEROWARGEPOPPHERD GRANDIAMEROWARGEN		1		
GLRNTPKSPLDDIGGLLSCTLPMGFGGGGGGGGGGLAPDIASI LISNYCS GGHPAGEPLAGSLIAM PLAST LISTTEVERKLEDI PGGSF5TP SEKELVOLGI LOSYRDHONAMUGGI PUTEVERKURDI PGGSF5TP GEKELVOLGI GSYRDHONAMUGGI PUTEVERKURDI PGGSF5TP GEKELVOLGI GSYRDHONAMUGGI PUTEVERKURTERI PHOGSF5TP GEKELVOLGI GSYRDHONAMUGGI PUTEVERKURTERI PHOGSF5TP GEKELVOLGI GSYRDHONAMUGGI PUTEVERKURTERI STANDER TUTVER THE STANDER SEKENDEL SPHGGMSKFFRAMVARGINE DSDCGAPVLQYCKHLALSQAPSTQDEMGKRKFFRAMVARGINE DSDCGAPVLQYCKHLALSQAPSTQDEMGKRKFFRAMVARGINE DSDCGAPVLQYCKHLALSQAPSTQDEMGKRKFFRAMVARGINE TUT TUTVER SEKENDEL SEKENDEL SEKENDEL SEKENDEL SEKENDEL POLST LISNYCZ GROWNAGER GROUPERGARERGERK JOKAGNSTREE ERVTCVQS LIDBFLQT V (TGSLT PLST) EVVERKEDDI PQGSF5TP SEKENDEL GLRNTPKSPLDIPDIGGLLGCTL PROFEGGSFBRESIAL POLST LISNYCZ GROWNAGER GROUPERGARERGERK JOKAGNSTREE ERVTCVQS LIDBFLQT V (TGSLT PLST) EVVERKEDDI PQGSF5TP SEKENDEL GROWNAGER FOR SEKENDEL SEKENDE	5986	1806	484	
LISNYCSIGNYAQELPQSSULGMAERARERGERYAQHSQHSER BHYTCQIGSILDREIQFYQSSLILLSTREWRKLEDIPQQSFSTP SEKHLVQLIGSYQRMCMAWKGPWAYKERULTMODLSTLYK QMELDQWAWKGDUMDTVERK'LLIFSITHEWSERFY OKKTYGYDC VERHTENVOLTPERKILLIFSITHEWSERFY OKKTYGYDC VERHTENVOLTPERKILLIFSITHEWSERFY OKKTYGYDC VERHTENVOLTPERKILLIFSITHEWSERFY OKKTYGYDC VERHTENVOLTPERKILLIFSITHEWSERFY OKKTYGYDC VERHTENVOLTPERKILLIFSITHEWSERFY OKKTYBELCHEKI TV  5987 1806 484 DAWKSTSLTFINKLWGRIRGRERGLAHPKNHLSPQQGATPQVP SPCCREPOSPERGPPERLIGLIGALAMABCOVEGSPPVPSGPPMERD GLARYPKSPIP.DPDGLACLGTLRANGEGGSFGERERISLAPDASI LISNYCSIGDINAQELFQGBOLGMAERARRGEK(NAGHSPLERE ENTYCKYGSILDBELGYLYGSGLOGARBERRERGEK(NAGHSPLERE ENTYCKYGSILDBELGYLYGSGLOGARBERRERGEK(NAGHSPLERE ENTYCKYGSILDBELGALTUNANGEGGFGERERISLAPDASI LISNYCSIGDINAQELFQGBOLGMAERARRGERYNAGRING GMIANDOWNMYGIGHMOTYPEK (VHPPSSPPY) OKKHETTYDG VERHTKENVOLTPRELLILIPHILBSVBSLISUDVERREITTYDGG FTALBERCPHILAKTIQARAKKKORLOFTSGGWGYFFRHWARGIN BSDCGAFVLGYCKHLALSQPPSFTQQDMPKLRRQIYKBLCHCKL TV  5988 1292 410 PKYYLISFIGLIESSISRDRIHMVIMTLLATHBLWWFTCCFP LIGGYVFTUVFGIPFITTLIMPALLILIPHILBSVBSLISUDVERREITTYPNGT REGERYRAGERYGERYGERYSKRYATOLLSCAN ARNENGOGGANAVERYCH ESGEPGGSKGREFYSSKRYATOLLSCAN ARNENGOGGANAVERYCH ESGEPGGSKGREFYSSKRYATOLLSCAN ARNENGOGGANAVERYCH RYCKLILBSSISRDRIHMVIMTLLATHBLWARTLTPYNGTE ALMUHPKORSISLIPHILTYSLATTORTHYNATHLATHBLUMDHPTCEP LIGGYVFTUVFGIPFITTLIMPALLLIPHANAFTLTPYNGTE ALMUHPKORSISLIPHILTYSLATTORTHYNATHLATHBLUMDHPTCEP RYGKALBILKKHILBVTTQKTUNAALSGSCI. ALMUHPKORSISLIPHILTYSLATTORTHYNATHLATHBLUMDHDDTAE FYGKALBILKKHILBVTTQKTUNAALBGSCI. ALMUHPKORSISLIPHILTYSLATTORTHYNATHLALSLSPE RQMWYBPARKERSBRYGGGRGGGGGGGGGGANALAT REGERKABERVATSTILRBLADAGGSTCGAFANALAT REGERKABERVATSTILRBLADAGGSTCGAFANALAT REGERKABERVATSTILRBLADAGGSTCGAFANALAT REGERKABERVATSTILRBLADAGGSCI. ALBERTPSGAGGGGGGGGGGGGGGGGGAFACATAGGGGGGGAGGAFANALAT REGERKABERVATSTILRBLADAGGGGGGGGGGGGGGAFANALAT REGERKABERVATSTILRBLADAGGGGGGGGGGGGAFANALAT REGERKABERVATSTILRBLADAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1	ļ	<u> </u>	SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMBED
EHTTCUGS LLDERUGT_VESSLIPLS:TUSTWIKEDITEQUEST;  SEKSLULGLIG SEGNEMGAMMUR DEPNATKENDITATOLETT.TY  ONNICHO OWNICHO OWNICH STATE ON THE SEKSLULGLIG SEGNEM SERVEN SERVENS LISTUMENT TYPISO  WILDRICH SERVENS LLT PILLEVENS; LSTUMENT TYPISO  NETURRICH LLT PILLEVENS; LSTUMENT TYPISO  NETURRICH LLT PILLEVENS; LSTUMENT TYPISO  NETURRICH LLT PILLEVENS; LSTUMENT TYPISO  NETURRICH LLT PILLEVENS; LSTUMENT TYPISO  NETURRICH LLT PILLEVENS; LSTUMENT TYPISO  NETURRICH LLT PILLEVENS; LSTUMENT TYPISO  SPECREPSSPRIPPSPRIPPSPRICH LARLEVENS LSTUMENT PROPERTY  SPECREPSSPRIPPSPRIPPSPRICH LARLEVENS LSTUMENT PROPERTY  SPECREPSSPRIPPSPRIPPSPRICH LARLEVENS LSTUMENT PROPERTY  SPECREPSSPRIPPSPRIPPSPRICH LARLEVENS LSTUMENT PROPERTY  SREGUNDLOLG SEGNEM SEGNEM SEGNEM SERVEN AND REAL TYPISO  RETURE CHILARY LORGE PLANT REAL TYPISO  RETURN SEGNEM	1	1	Ī	GLRWTPKSPLDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASI
SREGIULALI COSTORMICIAMAVIREPRISTY NURTETISTICO QNEILINDOWAMINOLIVATURENS EN VIRENTESTICO VERNTENDO L'ANTECNILLA PUBLICA VIRENTESTY NURTETISTICO VERNTENDO L'ANTECNILLA SOPPST TO QUIMPELETISTICA PURE CONTROLLA SOPPST TO QUIMPELETISTICA SOPPST TO QUIMPELETISTICA SOPPST TO QUIMPELETISTICA SOPPST TO QUIMPELETISTICA SOPPST TO QUIMPELETISTICA SOPPST TO QUIMPELETISTICA SOPPST TO QUIMPELETISTICA SOPPST TO QUIMPELETISTICA SOPPST TO QUIMPELETISTICA SOPPST	l	1	1	LISNVCSIGDHVAQELFQGSDLGMAREAERFGEK\AGQHSPLRE
SREGIULALI COSTORMICIAMAVIREPRISTY NURTETISTICO QNEILINDOWAMINOLIVATURENS EN VIRENTESTICO VERNTENDO L'ANTECNILLA PUBLICA VIRENTESTY NURTETISTICO VERNTENDO L'ANTECNILLA SOPPST TO QUIMPELETISTICA PURE CONTROLLA SOPPST TO QUIMPELETISTICA SOPPST TO QUIMPELETISTICA SOPPST TO QUIMPELETISTICA SOPPST TO QUIMPELETISTICA SOPPST TO QUIMPELETISTICA SOPPST TO QUIMPELETISTICA SOPPST TO QUIMPELETISTICA SOPPST TO QUIMPELETISTICA SOPPST TO QUIMPELETISTICA SOPPST	i	i		EHVTCVGSILDEFLOT\YGSLIPLSTDEVVEKLEDIFOOEFSTP
QNILDIOWIMMCGULVIDITYERK VIETENSFEY\DKLETKSTIDE VEXITATION OF THE HART LAD POLITIVES IL SOURCE KEY FEMINARION DEDGAFVLOYCKHLALSOPES FTOOMPELIEVES IL TYPES RTIMRECERH LAKTLORAWIKORLDSTROCK KEY FEMINARION DEDGAFVLOYCKHLALSOPES FTOOMPELIEVES INTERCES FEMINARION DEDGAFVLOYCKHLALSOPES FTOOMPELIEVES INTERCES FEMINARION TO SPECIAL DESCRIPTION OF THE WARM OF T		l		
VERNTEND DE PRILETE PUBLICUMS DE LEGENDA DE L'AURITEME DE LA AURITEME DE L'AURITEME DE		1	1	
RTIMRICE BILARTI (ADRAVKEDELD PIGGERE DY ENNIVARIO) DSDCGAPTUGY CHILALS OPPS FTOOD MP KIRROLY KRICHCKI. TV  DAMKSTSITPHIKLIKGEHEGRIRG LAIPE RIGHT SEPOCGO TYPOYD SPECEPPOSPRIG PPP FRIGILICAL LAIRENGE POOCGO TYPOYD SPECEPPOSPRIG PPP FRIGILICAL LAIRENGE POOCGO TYPOYD SPECEPPOSPRIG PPP FRIGILICAL LAIRENGE POOCGO TYPOYD SPECEPPOSPRIG PPP FRIGILICAL LAIRENGE POOCGO TYPOYD SPECEPPOSPRIG PPP FRIGILICAL LAIRENGE POOCGO TYPOYD SERVICE STANDAY OF THE STORY WERE LAIRENGE POOCGO TYPOYD SERVICE STANDAY OF THE STORY WERE LAIRENGE POOCGO THE STANDAY OF THE STORY WERE LAIRENGE POOCGO TYPOYD SERVICE STANDAY OF THE STORY WERE LAIRENGE POOCGO THE STANDAY OF THE STANDAY WERE LAIRENGE POOCH TO SERVICE THE STANDAY OF THE STANDAY WERE LAIRENGE POOCH TO SERVICE THE STANDAY OF THE STANDAY WERE LAIRENGE POOCH TO SERVICE THE STANDAY OF THE STANDAY	Į.	i	1	I
DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQTYKELCHCKL TY  TY  1806  484  DAMKSTSLTFBIKLHGRIRGGRIRGILABEDCYRGSPPVPSGPPMEID GLKWTPKSPLDFDSGLLGCTLENDGFGGSGPSERSCLAPPDAS LISNVCSLGDRVAQELFQGSDLGMAEBSRRFGEK_AGGIFFARE EHVTCVQSLLDBRLTAT, YGSLLFLSTDEVUERELBGIFQQSFSTRS SRKGLVLQLIQSYGRMFGDRWAYRGFRVAYKRINIJMDDGTLTYG CRMLINDQVMBNYGDLWDTVPGKVQHPMSPTYJOKLGFTYG CRMLINDQVMBNYGDLWDTVPGKVQHPMSPTYJOKLGFTXYG CRMLINDQVMBNYGDLWDTVPGKVQHPMSPTYJOKLGFTXYG CRMLINDQVMBNYGDLWDTVPGKVQHPMSPTYJOKLGFTXYG CRMLINDQVMBNYGDLWDTVPGKVQHPMSPTYJOKLGFTXYG CRMLINDQVMBNYGDLWDTVJCKNYGDLGTTYG VKRWTKNYDLINRELLLIPHLEVBBSLISUDVRRFTTYTPGG RTINBCCPKHLAFVLQARAVKGDRDJAGDWFKLRRQTYRRCCKL VKRWTKNYDLINRELLLIPHLEVBBSLISUDVRRFTTYTPGG RTINBCCPKHLAFVLQARAVKGDRDJAGDWFKLRRQTYRRCCKL TY  5988  1292  410  FYXYFISFLGLLESSHSEDDRIHMLVJAFFLLATHBILVBWFFCCEPQ RLDCTYLMAGIMPNPQINIKALLPGLPS\ABGLLTYGENTAKGM PSELBPQISKKKEPYSSSKYATDLLSVALBRHAFTLATHBILVBWFFCCEPQ RLDCTYLMAGIMPNPQINIKALLPGLPS\ABGLLTYGENXNAC RGTALVNLIFYGLBPFIKTLADAFALLTYGENXDATTSYNNAT RSELBPQISKKKEPYSSSKYATDLLSVALBRHAFTLATHTYTYNNTED ALWWLFHQRPSSLBPLLKTJSTLTGGRWTIMTQKMDLDBDTAB KFKQKLLBLERHRTTQKTMCDARASTLADATLTYNNTET ALWWLFHQRPSSLBPLLKYLSTATTGGRWTIMTQKMDLDBDTAB KFKQKLLBLERHRTTQKTMCDARASTLADATLTYNNTET ALWWLFHQRPSSLBPLLKYLSTATTGGRWTIMTQKMDLDBDTAB KFKQKLLBLERHRTTQKTMCDARASTLADATLTYNNTET RGGLKRABEKWATSTLSRLBCAGGSFTY TOFSKANALSISS RQBMEVEDARRGEBGKYMGDAGGSFT TOFSKANALSISS RQBMEVEDARRGEBGKYMGDAGGSFT TOFSKANALSISS RQBMEVEDARRGEBGKYMGDAGGSFT TOFSKANAGSVIH KCEDCCKEPTHYGHFRHIR HITTGKRFFSCACSKAPSDBAACK ABEKTED PLEVYNGEBGCKSYRLISLLBLINKKRRHSGRAFYKCHG REXCQCVMCKGAFTQASSLLJAHVRQHTGKFFSKANAGSVIH KCEDCCKEPTHYGHRAGNIKARHRISGBRAFYKCHG REXCQCVMCKGAFTQASSLLJAHVRQHTGKFFSKANAGSLIS CRABHIRBHDNTPHKCSVCSKAPVMGDLSKHIT HTGREKPY LCKKGGGFFMVGNLRSHINVTHQGKAGIKHLUHTAQGTIKATHLTY REXCQCVMCKGAFTALARASTAVTOLTVVPVGGAKGIKLHTAGQLAV VKOVGERDPHTHLLACLGSGGKFYQLGKKGFFADARSTANADALSISS PROGSPPPQQRSIOGERGRWARAGDES ISSLSLEVRAMHPYCLPR MHLACPREBEKAFRABANAVAPGDES ISSLSLEVRAMHPYCLPR MHLACPREBEKAFRABANAVAPGDES ISSLSLEVRAMHPYCLPR CSKRGLLSABGEKLDAACLLKPREVPVPVPVFKERQMPPANAD CSKRGGLSABCLDA	į	ł	1	_
5987  1806  484  DAMKSTSLTFHWKLMCRHRGERRGLAHPKNHLSPQGGATPQVP SPCCRPDSPRGPPPPRLGLLGALMARDGVRGSPPVPSGPPMED GLWTYKSPLDPDSGLLGSCTLRENGFGGSGPPGGRESLAPPDASI LISNVCSIGDPWQSLFQGSDLGWARBARREPGGSGPPGGRESLAPPDASI LISNVCSIGDPWQSLFQGSDLGWARBARREPGGSGPPGGRESLAPPDASI RHVTCQSILDERLGT\YGGLIPLSTDEVUERLEDIFQGPSTP SRKGLVLGLILGSYGMPGANWARGRVAYKRUDDLGTTYK GWHANDQWAMYGDLWHOTPPEK\YHPPRSFFY\DKLMFTKGDG VKRWTKNUDI PHRELLIPIHLBVHBLSTLSVDWRRTTYPFDG RTIMRCPKHLARVIQARAVKGDRLDFJGQWKGYFKMVARGNN DSDGGAFVLQYCKHLALSQPPSFTQDDWPKLRRQIYKRGCHCKL TV  FKYYFLSFLGLLESSHSRDTIHLVJLMFILLATHLVLWFTCFFQ RLDCIYLMAGIMENNQLINITALLFGLES\ABGLLTGGBRITADG LQEVPSTDVRGHFILIRELEPILCHSINDSQLINITSGRARGNN FSLBDFQISKGKEPYGSSKYATDTLLSVALMHPNQGLISWVAC PGTALSNLIYGLIPPFWTLLMPAILLLRFPAMAFTLTFYNGTE ALVMFHQKDRSIMPLKNITTGKTRNYHRDLGDFDAS FFYQKILLSLBERHIRVTTQKTDMCDABLSGSGL ALVMFHQKDRSIMPLKNITTGKTRNYHRDLGDFDAS FFYQKILLSLBERHIRVTTQKTDMCDABLSGSGL ACSSFYRMLFYDDKOVYHLDISRADGIGQVLERWYTAKLSLPR NVDDVL\AVATPLOWDDI ITACHALKSLAEPATSPCGNARALAT GGGERVARARGKVATSTISRLGAGRSTP (FGSRDLKERRGGGD, SAASGARGTFERDADRRBPPVELIKDDPTSGWARARARALAT GGGERVARARGKRBSKQKGBSGRESGAGARALAT GGGERVEPARKGRBSKQKGSGREGGRESGAGARALAT RGGERVARARGKRBSKQKGRESGREGGAGARAKALAT RGGERVARARGKRBSKQKGRESGREGGAGARAKALAT RGGERVEPARKGRBSKQKGRESGREGGAGARAKALAT RGGERVEPARKGRBSKQKGRESGREGGAGARAKALAT RGGERVEPARKGRBSKQKGRESGREGGAGARAKALAT RGGERVEPARKGRBSKQKGGGERRGGREGGAGARAKALAT RGGERVEPARKGRBSKQKGRESGREGGAGARAKALAT RCGCKRFTHFORNYKHIR HITMGRKPFYCCRECKARSDPAACK AHRKTISPLKPYGCEGCKSYRLISLIALKKRRISGRAFQCHAR RCGCKFFTHFORNYKHIR HITMGRKFPYCCRECKARSDPAACK AHRKTISPLKPYGCEGCKSYRLISLALKKRRISGRAFQCHAR RCGCKFFTHANDYNLARIHLTHALAGCFLKCBCGCGAGAA RCKRTRRHITHALAGCFLCCHCHCORQPARAVERGSGCULHGERGF CGKLFTTSGRLGRHURHGRSCTCHCHCHCROPARAVERGSGCULHGERGF CGKLFTTSGRLGRHURHGRSCTCHCHCHCROPARAVERGSGCULHGREFG CGKLFTTSGRLGRHURHGRSCTCHCHCHCROPARAVERGRSCTCHC CGKLFTTSGRLGRHURHGRSCTCHCHCHCROPARAVERGRSCTCHC CGKLFTTSGRLGRHURHGRSCTCHCHCHCROPARAVERGRSCTLAGREFT LCCKGGGFBYCGCKGKFTANARAVARARAFTSKAT VKQVGEDPBTHTLLACHGCGCKGKFTANARAVARARAFTSKAT VKQVGEDPBTHTLLACHGCGCCHCHCORGCFLUKGATHARAATARANSP	i	ì	1	
S987   1806   A84   DAMKSTSLTPHWKLMCHRIGERRGIALIGRHUS-POQGGATPQVP   SPCCRFDS-PRGP-PPRIGLIGALIMARDCVRGS-PPVSG-PPMED   GLKWTPKS-PLEP-PS-LLIGALIMARDCVRGS-PPVSG-PPMED   GLKWTPKS-PLEP-PS-LLIGALIMARDCVRGS-PP-SGRESLA-PDAS-I LISNVCS-IGDHVAQSLI-PGGSDLGWARERAR-PGGK-LAGGIS-LISNVCS-IGDHVAQSLI-PGGSDLGWARERAR-PGGK-LAGGIS-LISNVCS-IGDHVAQSLI-PGGSDLGWARERAR-PGGK-LAGGIS-LISNVCS-IN-COMMINGD-WIND-PROMINGD-WIND-PGGS-PPGGRESLA-PDAS-I SRKGLI-VGLA-LISN-LISN-LISNVC-RETTI-PTDG-PT-SRKGLI-VGLA-LISN-LISN-LISN-LISNVC-RETTI-PTDG-PT-SRKGLI-VGLA-LISN-LISN-LISN-LISNVC-RETTI-PTDG-PT-SRKGLI-VGLA-LISN-LISN-LISN-LISN-LISN-LISN-LISN-LISN	1	1	!	· · · · · · · · · · · · · · · · · · ·
SPCCRPDSPENGPPPRIGLICALIAMABCOURGSPEVPSGPPMERD GLARPTHSEPLOPDSGLIGGCTLINGPGGGGSPESCLAPPDASI LISNVCSIGDHVAQKLPQGSDLGMAEBAERPGEK\AGQHISPLRE EHVTCVQSLLDBFLQT\YGGLIPLSTIDEVUERLBDIPQGGFSTP SRRGUVQLILQSYGMMGANWAMGFWAVAKRUIMDDLGTLYG CRMLBDQMMNYGDLWHOTVPEK\VHPPRSFFY\DKLRFKKODG VKRWTKNVDI INRELLLIPLHLEUPBGLISUVDWRRFTTYFDSG RTINBRCPKHIANYLQABAVKNDRLDFJQGWRGYFKNWARQNN DSDCGAFVLQYGHLALSQPPSFTQDDWRLRGTYKNWARQNN DSDCGAFVLQYGHLALSQPPSFTQDDWRLRGTYKNWARQNN DSDCGAFVLQYGHLALSQPPSFTQDDWRLRGTYKNWARQNN DSDCGAFVLQYGHLALSQPPSFTQDDWRLRGTYKNWARQNN DSDCGAFVLQYGHLALSQPPSFTQDDWRLRGTYKNWARQNN DSDCGAFVLQYGHLALSQPPSFTQDDWRLRGTYKNWARQNN DSDCGAFVLQYGHLALSQPPSFTQDDWRLRGTYNWTCHPQ RLDCTYLMAGIMPNPOINIXALLPGLPS\ABGLLTYGDKITADG LQRVPFTDVRGHFTLLREEPLLCHSINDPGQLIVSUVAGC PGTALSNLTYGLIAPPTTLIREEPLLCHSINDPGQLIVSUVAGC PGTALSNLTYGLIAPPTTLIREEPLLCHSINDPGQLIVSUVAGC PGTALSNLTYGLIAPPTTLIREEPLLCHSINDPGQLIVSUVAGC PGTALSNLTYGLIAPPTTLIREEPLLCHSINDPGQCLIVSUVAGC ALMWEHQNESSINDLIKVILSATTTGGRWRI HYTQKMDLOBDTAB KFYQKLLBLEKHIRVTTQKTDMQARLSGSGL  AGSFYRMALFVQDGKDVYHLDI SNAAGIGQVLEKWYTAKLSLSPR NUDDVI\AVATYLQMQDLITAVHARAKSLARPSGOMARALAT BGGERRAKEERVATSTLSQLEQAGGSTYGDWFRANKAKALAA ACSSYYRMALFVQDKDVYHLDI SNAAGIGQVLEKWYTAKLSLSPR NUDDVI\AVATYLQMQDLITAVHALKSLARPSGOMARALAT BGGERRAKEERVATSTLSPLEQAGRSTY IGPSRDLKEERGQQA SAASGARGTEKADARREPPVBLLKUDTSTRAMARREAALESS EQGMRVBARKEERSQKGSGERERGAGDABVKBEGGGLENGRAA BGGERSSAAGERSGKGERSGKGGBRGGAGABVKBEGGGLENGRAA BGCGCKPFTHYNDRYRHI HITTGGRPFSCRESCKAFSDPAACK ABBKTEPSLKPWGCBGGKSYKLISLLIARKRRISGARARREAGEN GGKWYBARKGRKCHCHONKYNOVGHI KABLKTHLADGEPLKCEEGGK PTTSGNLERHELINGBKEPVCUTHCORQAPAGARBARARETSKA VKQCGEPPTHILTAGCSGCKYYLLIADRGAPATHAGREY LCDKGGGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	i		1	TV
GLR#TPKSPLDPDSGILSCTT_PNOPGGQSGPEGRSLAP PDBS I LISNVCS IGDIVAQKLPQSGDLGMAREAERPERSK \ AGGBYSPLRE EHTYCQG ILDBFLGT\ \ \text{Tysslipistdevickledifqgefsyt} SRIGIJVLQLIQSSQRMEGNARVRGFRVAY KRHUTMDDLGTING CRMINDQWMNYGGLWDDTVSK\ \text{Tysspiry \text{Type}} SRIGIJVLQLIQSSQRMEGNARVRGFRVAY KRHUTMDDLGTING CRMINDQWMNYGGLWDDTVSK\ \text{Type} \text{Type} \text{Type} \text{Type} RTINBECPKHIAYLQARAVKENDLD-FJGWGFYRWAYARGN DSDGGAFVLQYCKHLALSQPFSTQQDMFKLRRQIYKBLCHCKL TV  5988  1292  410  FRRYFISFIGLLESSISRDRIHNLVIMFILLATHINJWWFTCFPQ RIDCITLANGIMENPQLAITRALLEGLFS\ \text{ABGLITGSRITADG} LQEVPSTOVFGHFILIRKLEBLLCHSDBDSQLIWTSSRNARKSN PSLBDPQHSKGKEPYSSSKYATDLLSVALBNENMQGU/SSNVAC PGTALFNLITYGLIPPFIWITLIMPAILLIAPANFILTFYNSTE ALWILPHQKPSSLBFLKYLSATTGGGRNYIMTGKHDLDEDTAE KFYQKLLBLEBHRIVTIGKDTNOARLISGEN FYGKLEBLEHRIVTIGKTNOARLISGEN FYGKLEBLEHRIVTIGLEGUNGGRGLGLCDCTFVVDGVHFYAHKAVLA ACSSFFRMIFTDGKOVVHLDISRRAGLGQVLERMYTTAKLSLSFP NVDDVI\ANVTFLQMDDIITAGAHASGLGQVLERMYTTAKLSLSFP NVDDVI\ANVTFLQMDDIITAGAHASGLAGQVLERMYTTAKLSLSFP NVDDVI\ANVTFLQMDDIITAGAHASGLAGQVLERMGGGQLENGEA BGGBRARKERKVATSTLSRLEQAGRSTPTGSSBARABAALEBSS EQBMEVEPARRGBERQKSGERGBEGAGPASVKEBGSQLENGEA PERNREESSATTSLGGRIGSBRGRLSGFTGSWBARABKAALEBSS EQBMEVEPARRGBERQKSGERGBEGAGPASVKEBGSQLENGEA PERNREESSATTSLGGRIGSBRGRLSGFTGSWBARABKAALEBSS EQBMEVEPARRGBERQKSGERGBEGAGPASVKEBGSQLENGEA PERNREESSATTSLGGRIGSBRGRLSGFTGSWBARABKAALEBSS EQBMEVEPARRGBERQKSGERGGBEGAGPASVKEBGSQLENGEN PERNREESSATTSLGGRIGSBRGRUSGFTGFTESKAYGSVI I KCEDCCKFFTTYTONFRIHIRIHTSHERFSCRGCXABFSDPAACK AIBEKTLPPLKPYGCEECGKSYFLISILANIKKRISGBRRYRCED CGKLFTTSGNLKRHGLVINSGEKFYQCOTYGGRSPSDPTSKMRHL KCEDCCKFFTTYTONFRIHIRIHTSHERFSCRGCXABFSDPAACK AIBEKTLPPLKBERCHCHOKKFNOVENIKABLKI HILDGERGGR FTTSGNLKRHIRIHSGERFYQCOTYGGRSPSDPTSKMRHL KCEDCCKGFFTHYNDINLSIVKTVHOGRAGIKI KILBPEGSSRVSVVT VDDWYTLARFALAATAVTQLIVVPYGGAGIKI KILBPEGSSRVSVVT VDDWYTLARFALAATAVTQLIVVPYGGAGIKALKHERPATSSEVSEN PKGSSPPPQGGGGGRGSGGGGRGSRGGFTGAPYGTLAGFUNGTHAGT CSRKEGLSIANSERGLDSACLALKPREVETVYFKENGPPARAP CSRKEGLSIANSERGLDSACLALKPREVETVYFKENGPPARAP GGGRARKGRHAKKSERDPAACACGFARARRANAAALBE	5987	1806	484	, — — ···
LISNYCSIGDRYAQKIFQGSDLGMAREARREGEK\AGGISPLARE EHYTCVQSILDERLQT\YGSLIPLSTDEVUEKLEDIPQQEPSTP SRRGIJVLLIQSTQRNEGRARVAGFRAYAYRHVLTNDDLGTLYK QNMINDQWNNYGGLWMDTVDEK\UBERNSFY\DKLRTKSYDQ VKRNTKTGVDINKELLLIPLISTUPWRRTTTYFDSQ WKRNTKGVDIPKRELLIPLISTUPWRRTTTYFDSQ ETIMBRCPRHIAKYLQARAVKKORLDFHQGWKGYFKNWARQIN DSDGGAFVLQVCKHLALSQPFSPTQQDMPKLRRQIYKBLCHCKL TV  5988  1292  410  FKRYFISFIGLLESSISRDRIHNLVIMFILATHNLVWWFTCRFQ RLDCIYLANGIMNNQGIAN KALLFGLFS\ABGLLTGGKTADG LQEVPFTDVFGHFILIRELEPLL-GBMPSQLIWTSSRARKSN PSLEDPQGISKKERYSSSKATATDLLSVAHRYQGGUSVNAC GGTAL*NLITYGLLPPFIWTLIMPAILLRPRANAFILTFYNDTE ALMWLENGDRSINPLIKULATTGGGRATUTGWOLDEDTAE KFYQKLLBLEKHIRVTIQKTDDQARLGGSCL  AMSFPQBSGHVIBQINQQGGIGLLCCT*FVVDGVHFKAHKAVLA ACSSYFMHEVDQKDVVHLDISMAGLGGVLEMYTAKLSISPP NVDDVL\AVATFI-QMQDIITACHALKSLARPATSPGGNARLAST BGGDKRAKKERVATSTISLERLGAGRSTFYGDKTESKAYGSV HKCEDCGKEFTHTUNFKRHIRIHTGREPFSCRECSKAFSDPAACK ABERTISPLERVOTSCRESKYLISLILAHOPENDLKERGGGAQ SAASGAROTEKDADPREPPDVELKDDTGGPAAARRAALSESS EQEMBVEPARKGBEKVATSTISLERLAGAGSTFYGDKTESKAYGSV HH KCEDCGKEFTHTUNFKRHIRIHTGREPFSCRECSKAFSDPAACK ABERTISPLERPYGCEDCKSFTILISLINALDEPLKCERGGGAQ SAASGAROTEKDADPREPPDVELKURGGGAG LENGEA ABERTISPLERPYGCEDCKSFTILISLINALDEPLKCERGGGAQ SAASGAROTEKDADPREPPDVELKURGGGAG KINGERGSKYNT KCEDCGKEFTHTUNFKRHIRIHTGREPFSCRECSKAFSDPAACK ABERTISPLERPYGCEDCKSFTILISLINALDEPLKCERGGGAQ FTSGGLKHRHRHEGSKYVCIHCORQPADDGALGRWRIHTIC BKPCQCUMCGKAPTQASSLIAHVRQHTGEKFYVCERCGKRFVQS SQ:ANHIRHHONIRPHKCSVCSKAFVNVODISKHILIHTAQALKW PQTDADFYQQGGGGGTPAASGARGSGGGAGGARGSGRUNLHEEAGD SQ:ANHIRHHONIRPHKCSVCSKAFVNVODISKHILIHTAQALKW PQTDADFYQQGGGGGTHPAAGATLAGHLONCYSI PDPP MHIACPERBOKATAABMAVPAAGDES ISSLSELVRAMHPYCLPN VVRQVSPGFPRVIDILSSILTATGRAGGEGQVLAHEEAGD SQCAAKIGHGLGSLADPRUTLAGGECVULETURQAATABDLAITSK VKVQGEDPNTHILIACDSCOBKFILDSKDLAGGEGQVLAHEEAGD SQCAAKIGHGLGSLADPRUTLAGGECVULETURQAATABDLAITSK VKVQGSPGGRAGGSGRGSRGGSRGGSRGSRGGSTVOTHEREAGD TSPTAPECPPPBA  GGGRAKKGKERDPRVIDILSETSSALLLARDRYTLESTENAVPRVIT CSRKEGLISIANSEKLDSACLLARPREVVERVYPKEPONPANAAP GGGRAKKGKERDPAALDTTONTPITHISTSGLUDSAQAS PMYDSVERRDFLANGERDLDIYPHLAGGTVUNDERU	i	1	l	SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED
LISNYCSIGDRYAQKIFQGSDLGMAREARREGEK\AGGISPLARE EHYTCVQSILDERLQT\YGSLIPLSTDEVUEKLEDIPQQEPSTP SRRGIJVLLIQSTQRNEGRARVAGFRAYAYRHVLTNDDLGTLYK QNMINDQWNNYGGLWMDTVDEK\UBERNSFY\DKLRTKSYDQ VKRNTKTGVDINKELLLIPLISTUPWRRTTTYFDSQ WKRNTKGVDIPKRELLIPLISTUPWRRTTTYFDSQ ETIMBRCPRHIAKYLQARAVKKORLDFHQGWKGYFKNWARQIN DSDGGAFVLQVCKHLALSQPFSPTQQDMPKLRRQIYKBLCHCKL TV  5988  1292  410  FKRYFISFIGLLESSISRDRIHNLVIMFILATHNLVWWFTCRFQ RLDCIYLANGIMNNQGIAN KALLFGLFS\ABGLLTGGKTADG LQEVPFTDVFGHFILIRELEPLL-GBMPSQLIWTSSRARKSN PSLEDPQGISKKERYSSSKATATDLLSVAHRYQGGUSVNAC GGTAL*NLITYGLLPPFIWTLIMPAILLRPRANAFILTFYNDTE ALMWLENGDRSINPLIKULATTGGGRATUTGWOLDEDTAE KFYQKLLBLEKHIRVTIQKTDDQARLGGSCL  AMSFPQBSGHVIBQINQQGGIGLLCCT*FVVDGVHFKAHKAVLA ACSSYFMHEVDQKDVVHLDISMAGLGGVLEMYTAKLSISPP NVDDVL\AVATFI-QMQDIITACHALKSLARPATSPGGNARLAST BGGDKRAKKERVATSTISLERLGAGRSTFYGDKTESKAYGSV HKCEDCGKEFTHTUNFKRHIRIHTGREPFSCRECSKAFSDPAACK ABERTISPLERVOTSCRESKYLISLILAHOPENDLKERGGGAQ SAASGAROTEKDADPREPPDVELKDDTGGPAAARRAALSESS EQEMBVEPARKGBEKVATSTISLERLAGAGSTFYGDKTESKAYGSV HH KCEDCGKEFTHTUNFKRHIRIHTGREPFSCRECSKAFSDPAACK ABERTISPLERPYGCEDCKSFTILISLINALDEPLKCERGGGAQ SAASGAROTEKDADPREPPDVELKURGGGAG LENGEA ABERTISPLERPYGCEDCKSFTILISLINALDEPLKCERGGGAQ SAASGAROTEKDADPREPPDVELKURGGGAG KINGERGSKYNT KCEDCGKEFTHTUNFKRHIRIHTGREPFSCRECSKAFSDPAACK ABERTISPLERPYGCEDCKSFTILISLINALDEPLKCERGGGAQ FTSGGLKHRHRHEGSKYVCIHCORQPADDGALGRWRIHTIC BKPCQCUMCGKAPTQASSLIAHVRQHTGEKFYVCERCGKRFVQS SQ:ANHIRHHONIRPHKCSVCSKAFVNVODISKHILIHTAQALKW PQTDADFYQQGGGGGTPAASGARGSGGGAGGARGSGRUNLHEEAGD SQ:ANHIRHHONIRPHKCSVCSKAFVNVODISKHILIHTAQALKW PQTDADFYQQGGGGGTHPAAGATLAGHLONCYSI PDPP MHIACPERBOKATAABMAVPAAGDES ISSLSELVRAMHPYCLPN VVRQVSPGFPRVIDILSSILTATGRAGGEGQVLAHEEAGD SQCAAKIGHGLGSLADPRUTLAGGECVULETURQAATABDLAITSK VKVQGEDPNTHILIACDSCOBKFILDSKDLAGGEGQVLAHEEAGD SQCAAKIGHGLGSLADPRUTLAGGECVULETURQAATABDLAITSK VKVQGSPGGRAGGSGRGSRGGSRGGSRGSRGGSTVOTHEREAGD TSPTAPECPPPBA  GGGRAKKGKERDPRVIDILSETSSALLLARDRYTLESTENAVPRVIT CSRKEGLISIANSEKLDSACLLARPREVVERVYPKEPONPANAAP GGGRAKKGKERDPAALDTTONTPITHISTSGLUDSAQAS PMYDSVERRDFLANGERDLDIYPHLAGGTVUNDERU	1	ļ	!	GLRWTPKSPLDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASI
HHTTCVQSILDREQTATASTEDEVVEKLEDIFQOERSTE SRKGLVLQLIQSYQRHQRAMVRGPRAYAYKRVATHODDETLYC QNHANQOWRNYCDLWIDTVPEK VHEPRASFFY DIKLTKSYDC VRINTGVDI INNKLLLIP IHLEVHRSLIS VDVRRTTTYFDEG RTIMRCCPKHLAYLQARSYKORDLIFASGYKGRYFMAYNARQNN DSDCGAFVLQVCKHLALSQPFSFYQQMPKKRRQIYKERCHEKK TV  5988  1292  410  FKXYPLSFIGLESSISRDRIBNIVIMFILATIBNIVMPTCEPQ RLDCTYLANGIMPRQLAI KALLFGLEYA MGGLITTGKKITHAC LQEVPETDVFGHP ILITELRPLLCHSDMPSQLIWTSSINDARKSN PSLEDPQHSKKKEPYSSSKYATDLLSVALNINNFRQGLYSVNAC PGTALFNLIVTGLIPPPI HUTLIMPAILLIALFPRANFTLTPYNGTE ALWILPHQXPSIS.HPLIKYLSATTGGGRNYLMTQKRDLDEDTDAE KFYQKLLELBEHRIVTVIGKTHOARBISGS-BWYTAKKSLSP PKYQKLLELBEHRIVVIGKTHOARBISGS-BWYTAKKSLSP NVDDVL\AVATFLQMQDI ITACHALKSLAEPATSPGGNARALAT BGGBRARKBRVATSTLERLBQAGRSTF1 GPSRDLERRGCQAQ SAASGAGUTERDAPREPPVELKDPTSGMARABEAALSESS BQMRVEPARRGBERQKSQEEQEBEGAGPASVKBEGSQLENGRA PERNREBSASTTSGGGI SESRRGLBSGTFTSGMARABEAALSESS BQMRVEPARRGBERQKSQEEQEBEGAGPASVKBEGSQLENGRA PRENRESSASTTSGGGI SESRRGLBSGTFTSGMARABEAALSESS BQMRVEPARRGBERQKSQEEQEBEGAGPASVKBEGSQLENGRA AHBRTISPJARFVGCEPCKSFVILISLIALRERSGCAPAG KCECCKFFTHTVINFFRIHTRIHTPGRFSCRCCSKAFSDPACK AHBRTISPJARFVGCEPCKSFVILISLIALRERSGCAPAG COKLFTTSGNLKRHQLVHSGEKPYQCDVCGRSFSDPTSKMRHLE THIDTOKBIKCPHCDKKFMQVCINI.KGABLKI HAGDETKREGCQAA HERRITESPJARFVGCEPCKSFVILISLIALRERSGCAPAGRAFIRITE BFCQCVMCGRAFTQASSLIAHVQRTGGRFVYCERCGRRFVQS SGCANHI RHIMINTPRIKCSVCSKAFVINGDETEULKRETSKA VKQVQEEDPNTHILYACDSCDKFFLORRFYLTSTRALTSKA VKQVQEEDPNTHILYACDSCGKFFLORREVYCERCGRRFVQS SGCANHIRMINTPRIKCSCRSKAFVYCERCGRRFYQS SGCANHIRMINTPRIKCSCRSKAFVYCERCGRAFTIALTHQSHDASLIS LIEDFGSLGRVENSLDDFSMBERM_QDFTEULKRETSKA VKQVQEEDPNTHILYACDSCGKFFLORREVYLERCGGPALAR FYGDSSGGGRRSGGGGSGGRGSRGAPYGTLGRAVSGGGVLIHEBAGD SFYSISKILGFSLRDRUBMBELMALQDFTLIATHQSTMABLSLIS LIEDFGSLGRVENSLDDFSMBELMALQDFTLIATHQSTMBASLIS LIEDFGSLGRVENSLDFDSMBELMALQDFTLIATHQSTMBASLIS LIEDFGSLGRVENSLDFDSMBELMALQDFTLIATHQSTMBASLIS LIEDFGSLGRVENSLDFSSALLLARPERVFFLANGFFRANDFALR CSRKEGLSLANBERKLDSACLLKPREVVETVYPKEPCNPPANAAP GSQRAKKGRRFAXAFRYLSSALLLARPERVFFTVYFKEPCNPPANAAP GSQRAKKGRRFAXAFRYLSSALLLARPERVFTCHVLARTSSELVBELPA PMYD	I	1	j .	LISNVCSIGDHVAQKLFQGSDLGMAEEAKRPGEK\AGOHSPLRE
SRKGLVILQLIGSTORMEGRAMVGERVAYKRHULTMDDLGTLYG CRMILNDQVMMYGDLVMDTVPKKVUPFNSPY\DKLRTKGYDC VRIMTKNVDI PNRSLLLIPIHLBVHMSLLSVDVRRTTLTYPDGG KTIMERCPKHLAKVLQARAVKURLDZJQGWKGYFKMWARQNN DSDCGAPVQYCKHLALSQPSPTQQDWKLRRQTYKRELGCKL TV  5988  1292  410  FKXYFISPIGILESSHSRDRIHNLVMMFLARTENIJWMPTCRPQ RIDCIYLNAGIMPNPQLNIKALLPGLPS\ABGLLTQDKITADG LQBVPSTUVPGEHPILLRELEPLICHSDNPSQLIWTSENNARKSN PSEDPQHSKKREPYSSSKYATDLLSVALKNMPNQGLISVSNVAC PGTALSNLTYGLIPPFWTLLMPAILLLRPRAMPTLTPYNGTE ALVMLFNGLPSPSIAMPLKVISJNTORGNNYMTQKMDLDEDTAR KFYQKILLBLEKHIRVTTQKTDNQARLGGSCL  AMDFPQHSQHVLEQINQQRQLGLLCDCTYVDGVHFKAHKAVLA ACSSYFKMLFVDQRDVVHLDISNARGLGQVLBVMTTAKLSLSPR NVUDVI\AVATFLOWDIITACHALKSLARBATSPGGRARALAT BGGGLRRAKBRAVATSTLISLEQAGRSTGSSBLUKDERGGQAQ SAASGARQTEKADAPREPPVELKEPDTSGRAARBRAALSESS EQMEWEVPARKHERGORGPGERGERGAPVWEGSGLRNGRA PHENRESSAGTDGGQLGSRARGLRSGTVGDRTESKAYGSVIH KCEDCCKEPTHTNMFRHHRIHTGEKPFSCRESSKAFDDPAACK ARBRITSPJRAFYGGERGGSRGSRGBGREBERGAQA AGRATISPJRAFYGGERGGKFLANGRAFWKERGGAQA SAASGARGTEKADAPREPPVULKEDTSGRAARBRAALSESS EQMEWEVPARKHERGGREGERGERGAPVWEGGSGLRNGRA PHENRESSAGTDGGQLGSRARGLRSGTVGDRTESKAYGSVIH KCEDCCKEPTHTNMFRHHRIHTGEKPFSCRESSKAFDDPAACK ARBRITSPJRAFYGGERGGREGERGERGVENVERGALQRHVRHTE EXCECUMGRAPPOASSILAHVRGHTSKAFUNGGRAAGRHVRHTHT EXCECCKREPTHTNDFRHHRIHTITACHGRAPTERERYVCTRCGRRPQS SQLANHIRHIDNIRPHKCSVCSKAFVNVGGLSRHII IHTGEKFY LCDKCSRGFNRVDRILBSINKTVHQGKAGIILLEREGSSKVSVVT VDDMVLLARTALALATAVTQLTVVFVGRAAVTADETBULAGELSKA VKQVQKEDPNTHILITACDSCGKFLDANSLAQHURHTTACALUM PQTDADFYOQNTGGTHAPAGVVLQARGELVFRPDCAGRGQPALAE TSPTAPECPPAB  5990  2 4700 FGREDSGGGRAGGGRGSRGSRGSRGDAPYGTLGAVSGEGVLLHERAGD MHLACPBEBCKATAARMAVPAAGDES ISSLSELVRAMHPYCLPN LTHLASLEDBLQGOPDLILPEGCVUETUGGAAATGDDLEITV VVRQVSPEGPRPVLLIDSLETSSALQLLMPTLESBTRAAVPRVTL CSRKEGLSIABERKLDSACLLKPREVVEPUVPKERPNPANAAP GSRGAKRGKKSKSRGPAAACVSGVARRIRSSSRGGSTVGTVTSVTS QVDNLGKQPQBELQKRGSGPLQGKGRPRARRANAAALENSSPRN LBRBAQGSPAKGREKKSRGPLDLTRGFUCHVETUTGTVTFTTHLIJSUDGARQA FMYDOSVSRDPTANGEULAGPVVLDGELVLAGSTSSELVEPLPA	ł	Į.	i	
CIMILIDOUNININGOLUMDITUREK\UHIPENSEPY\DELETIKGYDG VRIWTKNYOLI PIKUSUMSKITJUVARRITITYFDG RTILINEKCPEHTAKYLQARAVKKORLDZIQGWKGYPKIMVARQINI DSDCGAFVUQYCKHLALSQPESPTQQDMPKIRRQIYKELGICKI, TV  5988 1292 410 FXXYPISPIGLESSHERDRI HILLVIMPLATHILIVWMPTCREP RIDCIYLNAGIMPINQILI KALLEGIBNDESQLUWTSSINARKSIN LQEVPSTOVPGHPTLIREEEPILGISDNPSQLUWTSSINARKSIN PSLEDDYGHSKKKEPYSSSKYATOLLSVALINININOGGLYSIVAC PGTALSTILIYGILDPPTUTLIMPALTILIPRAMPTLTPYNGTE ALWWLPHORPSSIAPLIKYLSATTOFGRINYIMTQRDLDEDTAE KPYOKLILBERHIRVITYINTOLDPATESCI.  5989 194 2610 ANDFPQHSQHVILEQINQQRQLGILCDCTFVVDGVHFKAHKAVLA ACSSYFKMEFVDQROVHULDI SINARGIAQVULEWTYTAKLSISPS NYDDVI\AVATFLQMDJ ITTACHAKSLARPATSPGGRAKALS EGGEKRAKESKVATSTISHLEQAGETYTOGFSDALEERRAGOQAQ SANGGRAQTEKDADPREPPVELKDOFGMARREARALGES EQEMEVEPARKGEBEQKEQBEQEBEGGPAEVKEBGGQLENGE GEKEPTSGOKRAKESKVATSTISHLEQAGETYTOGFSDAPACK AHKKTISPLKPYGCEBCGKSYRLI SILIMLKKKRHSGGRAYKGED CGKLPTTSGNILKRIGULMSGERPYCCHGCSRSSPDTESKMYGSVIH KCEDCKERFTIYMOFKHAIR IHTTGEKPPSCRECSKAFSDAPACK AHKKTISPLKPYGCEBCGKSYRLI SILIMLKKKRHSGERAYKGED CGKLPTTSGNILKRIGULMSGERPYCCHGCSRSSPDTESKMHLE THDTDKEHKCPHCDKKFNOVGNIJKAHLKI HIADGPLKCRECGKQ PTTSGNILKRIGULMSGERPYCHCRESSPDTESKMHLE THDTDKEHKCPHCDKKFNOVGNIJKAHLKI HIADGPLKCRECGKQ FTTSGNILKRIGULMSGERPYCHCRESSPDTESKMYDL SGJANHIRHINNIPPIKCSVCSKAFVNYGGLSSKHI IHTGGKPY LCKCKGRGFTONGDALSSILIAHVRGTIGERPYVCTRCCKRRYQS SGJANHIRHINNIPPIRCSVCSKAFVNYGGLSKHI IHTGGKPY LCKCKGRGFTONGDALSSILIAHVRGTERPYVCTRCCKRRYQS SGJANHIRHINNIPPIRCSVCSKAFVNYGGLSKHI IHTGGKPY LCKCKGRGFTONGDALSSILIAHVRGTERPYVCTRCCKRRYQS SGSPANGGRFTONGDALSSILIAHVRGTERPYVCTRCCKRRYQS SGSPANGGFPPOQUSGGRGREENVASTRAGOTHALTHITACALVM PQTDADPYTGQGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ł	1	I	
VKRWTKNUDI PNIKKILLI IPIHLEVBIRSLI SUDVRRTITTYPDSG RTINBRCPKHIAKUJQARAVKKORLDJ-HGGGKGYFKMVARQNN DSDCGAFVLQVCKHIALISQPFSFTQQDMPKLRRQI YKRICCICKI TV  FKXYPIS-PLGILLESSHSRDRI HINLVIMFLLATHINLVWWFTCRPQ RIDCI YLNAG IMPNPQLNI KALL PGLPS\ABGLITQDK ITADG LQBVPSTUVPGIEPFI HLIRELEPILCHISDNPSQLI WTSIKNARKEN PSIEDPQHSKKEPYSSSKYATDLL SVA JAKNINPNQGILYSWYAC PGTAL-TILTYGI LPPF WTILLWPA ILLLRPPRAM-PTLTP YNGTE ALMWLEVGRYBSLAPPL KIVISATTOFGRIN YMTOKHDLOBDTAE KFYQKILLBLEKHIRVTIQKTDNQARLSGSCI  5989  194  2610  AMDFPQBSGHVILBOLANQARLSGSCI  SWYDONIA, AVATPLONGDI ITACHALKSLARPATSPGGNARALAT EGGIKRAR AREKVATSTI.SILBOAGRST PIGSRDLKEBRGGOAQ SAASGABQTEKADAPREPPPVELKEDPTSGWAABEARALSBSP ROGENEVAR AREKVATSTI.SILBOAGRST PIGSRDLKEBRGGOAQ SAASGABQTEKADAPREPPPVELKEDPTSGWAABEARALSBSS EQDMVEPARKSBEKQKEOEDGBEGAGPARVKBEGSGLENGER PERNRESSEAGTDSGGULGSBARGILAGSTYODETESKAYGSVIH KCEDCCKEPTHYGHFKHIR II HTGEKPPSCHECSKAFSDPAACK AHEKTISPLKPYGCEECGKSYRLISLINLIKKRHSGSGARYRCED CGKLPTTSGNLKRRGUMSGERPYCCDYCGRSPSPTSKWHILE TEDTDKEHKCPHCDKKPNOVGRI KAHLKI HI HGGELP KCREGGKQ FTTSGLIKRHIRI HISGERPYCL HCOAPAGAGAI KILEPEEGSKVSVVY VDDWYTLARTEALAATAVTQLTVVPVGAAG I KILEPEEGSKVSVVY VDDWYTLARTEALAATAVTQLTVVPVGAAG I KILEPEEGSKVSVVY VDDWYTLARTEALAATAVTQLTVVPVGAAG I KILEPEEGSKVSVVY VDDWYTLARTEALAATAVTQLTVVPVGAAG I KILEPEEGSKVSVVY VDDWYTLARTEALAATAVTQLTVVPVGAAG I KILEPEEGSKVSVVY VDDWYTLARTEALAATAVTQLTVVPVGAAG I KILEPEEGSKVSVVY VDDWYTLARTEALAATAVTQLTVVPVGAAG I KILEPEEGSKVSVVY VDDWYTLARTEALAATAVTQLTVVPVGAAG I KILEPEEGSKVSVVY VDDWYTLARTEALAATAVTQLTVVPVGAAG I KILEPEEGSKVSVVY VDDWYTLARTEALAATAVTQLTVVPVGAAG I KILEPEEGSKVSVVY VDDWYTLARTEALAATAVTQLTVVPVGAAG I KILEPEEGSKVSVVY VDDWYTLARTEALAATAVTQLTVVPVGAAG I KILEPEEGSKVSVVY VDDWYTLARTEALAATAVTQLTVVPVGAAG I KILEPEEGSKVSVVY VDDWATAATARTAATAVTQLTVVPVGAAG I KILEPEEGSKVSVVY VDDWATAATARTAATAVTATTUPPHCAGGG KAHLAATAGATAGATAG FGCPDFSGGGARGSGGGGRGSRSGABSCRGAPYGTLAGREDDALLE VV VROVSEGGRARGSGAGSRSGARGACGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	1	ļ	· · · · · · · · · · · · · · · · · · ·
PTIMBECPHILAKTIQARAVKURILDZEIGUKGYPKMYNARQINI DSDCGAFVLQYCKHIALSQPFSPTQQDMPKLRRQIYKBLCHCKL TV  PKYYPISPIGLESSISRDRIHILVIMFLLATHINIVMWFTCRPQ RLDCITLANGIMPRPQINITKALIFELSP\ABGLITGGKITADG LQBVPETDVPGIPTLIRELEPILCISINDPSQLIWTSIRNARKSN PSLEDPQHSKGKEPPYSSKYATDLLSVALINNIPNQQGLYSNVAC PGTAL"NLITYGTLEPPTWTLLMPATLLLYPTAMAFTLTPYNGTE ALVWLPHQKPSSIAPPLIKYLSATTGFGRNYUMTQRWDLDEDTAB KFYQKILBELBKHIRVTIQKTDMQARLESSGLI  5989  194  2610  ANDPPOBSOHVLBGINQQRQLGIALCDCT*VVDGVHFKAHKAVLA ACSSYPKMLIFVDQKDVVHLDISNARGLGQVULFMYTAKLSLSPE NVDDVI\ANATPICMQDIITTACHALKSLARBATSPGGRARALAT BGGBRAKBEKVATSTLSILBQAGESTPIGPSBALKEBRGGQAQ SANGGRQTFERADAPREPPVEIKLEPTGGARABRARALSESS EQBMEVEPARKSBEQKBGERQEBEGACPARVEEBGGOLENGRA PHENRIESSATTDSQELSSRARGLRSGTYGDRTESKAYGSVIH KCEDGSKEFTHTOMFKHHIR IHTGEKPFSCRECSKAFSDPAACK AHBRITESPLKPYGCERCGKSYRLISLLINLKRKHHSGRAYNCHB CGKLFTTSGNLKRRGLWHSSERPYCGRESSPSDFTSKMHLE THDTDKEHKCPHCDKKRNOVGRIKAHLKIHTADGPLKCREGGGA PTTSGNLKRRILVHSGEKPYVCIHCQROFADPGALQRHVRITTG BKPCQCVMGGRAFQASSLIAHVRQHTGERPYVCRECKERCVGS SG:ANHIRBHINIPAHKCSVCSKAFVNYGDLSRHIITHTGEKPY LCDKCGRGRRYDNIALSSUKVTHQGKAGIKILEPEGSSVSVVT VDDMYTLATEALAATAVTQLTVVPYGAAVTADETEFULGABTSKA VKQVQEEDPNTHILYACDSCGDKFLDANSLGHVRIHTGALVM FQTDADPYQQTSGGGTNPAGGQULAGGELVFRPRDGAREGQPALAE TSFTAPECPPPAB  5990  2 4700  FGCPDFSGGGARGSGWGSRSQAPYGTLGAVSGEGVILLHERAGD SGFVSLSRLGPSLRPDRSMPPSRR PROQSPPPQQRSJGGERESEVASFSGDTLAGELDRUCSSI IDDP MHLACPERBDKATAARMAVPAAGDES ISSLSELVRAMHPYCLDR LTHLALSLEDBLQEQDPDDLTLPEGCVULGQAATAGDDLEIPV VVROVSPGPRFVLLDBLSLETSSALQLLMPTLESBTRANVPXVII CSRKRGLSIANBERKLDSACLLKPREVVEPVPVERCNPANNAP GSGRARRGRKKKSKRGAACVGVGVARRINSBSBRGGGTVGTVTSVTS QVUNLQKDPOERICKESGPLQKGRPRAMARABAALKNSSPRN LERSAGQSSPAKEGRLQLDLTYPKLADTTIGTNPTTHLSLVDSAQAS PMYDDSVSRADPTANGEVPLAGRPVPDOFLAVLASTSSELVSPLPA	ſ	Į		1
DSDGGAFVLQYCKHLALSQPPSTTQQDMPKLRRQIYKBLCHCKL TV  TV  S988  1292  410  PKKYPISPIGLLESSHSRDRIHNIVIMFLLATHNIVWFTCRPQ RLDCITINAGINPNPQLNI KALLPGLPS \ABGILTQGBKITADG LQBVPBTDVPGIP ILITRELEPLLATHNIVWFTCRPQ RLDCITINAGINPNPQLNI KALLPGLPS \ABGILTQGBKITADG LQBVPBTDVPGIP ILITRELEPLLATHNIVWFTCRPQ REDCITINAGINPNPQLAI KALLPGLPS \ABGILTQGBKITADG LQBVPBTDVPGIP ILITRELEPLATGGRANY INTORMDLBETTAE ALVMLPHQRPSSLHPLIKYLSATTGGRANY INTORMDLBETTAE KFYQKILIBLEKHIRVTIQKTDNQRQLGLLCDCTPVVDGVHFKAHKAVLA ACSEYFKMLFVDQKDVVHLDI SHRAGLGQVLBFWTTAKLSLSPR NVDDVL\AVATFLOMQDI ITALALKSLARPATSPGGMARALAT BEGERKRAKERKVATSTLSFLEQAGRSTPT GPSRDLKERGGQAQ SAASGARQTRKADAPREPPVELKPDPTSGWAABRAALSES EQDMEVEPARKGEBEQKEQEEQEEGGACPAEVKEEGGQLENGBA PBENRREESAGTDGGQELGSEARGLESGTYGDRTESKAYGSVIH KCEDCKRFTHYGNFKHH IR HTTGEKPFSCRECSKAPSDPAACK AHERITISPLKPYGGCECKSYRLIKJHKKRKHSGRAYTKGD CGKLPTTSGNLKRHQLVHSGBKPYQCDYCGRSFSDPTSKMRHLE THDTDKEHKCPHCDKKRNQUSNLKAHLKHLADGFLKCREGKQ FTTSGALKHHLEHISGEFLYVCHCQQPADDGALQREVRIHTG EKPCQCVMCGKAPTQASSLIAHVQQHTGRKPYVCRCGKRFVQS SC.ANHIRHDDNIRPHCSVCSKAPTWADGLKRHL IHTGEKPY LCDKCGRGFNRVDNLRSHVKTVHQGKGGIKILBPEEGSBVSVVT VDDMVILATEALAATAVTQLTVPVGAAVTADSTEVLKAETSKA VKQVQBEDNTHILIJKADSGCDKFURTAQASTLAHRAGRHFYKLRETSKA VKQVQBEDNTHILIJKADSGCDKFURTAQASTLAHRAGRHFYKLRETSKA VKQVGBEDNTHILIJKADSGCDKFURTAQASTLAHRAGRHFYKRAETSKA VKQVGBEDNTHILIJKADSGCDKFURTAGASTLAHRAGRHFYKRAETSKA VKQVGBEDNTHILIJKADSGCDKFURTAGASTLAHRAGRHFYKRAETSKA VKQVGBEDNTHILIJKADSGCDKFURTAGASTLAHRAGRHFYKRAETSKA VKQVGBEDNTHILIJKADSGCDKFURTAGASTLAHRAGRHFYKRAETSKA VKQVGBEDNTHILIJKADSGCDKFURTAGASTLAHRAGRHFYKRAETSKA VKQVGBEDNTHILIJKADSGCDKFURTAGASTLAHRAGRHFYKRAETSKA VKQVGBEDNTHILIJKADSGCDKFURTAGASTLAHRAGRHFYKRAETSKA VKQVGBEDNTHILIJKATCHGGRAGLIKHTMGSTMABTSKLURSH ERGCITARGANTAGRAGATSCAARGATAGASTLAHRAGRAFTAGASTLAHRAGRAFTAGASTLAHRAGASTLAGSTLAHRAGASTLAGGTAGATAGATAGATAGATAGATAGATAGATAGATAG	1	1		
5988 1292 410 FRYSTISFIGILESSHSRDRIHNLVIMTILATHNLVWFTCRPQ RIDCITIANGIMPNEQUNIKALLFGLFS\ABGLLTQGDKITADG LQBVFBTDVFGIFILIRELBPLLCHSDNPSQLIWTSSRNARKSN FSLBDPQHSKGKEPYSSSKYATDLLSVALINNPNQGLYSNVAC PGTALSINLTYGLIDPFFWILLIMARILLLRFRANFTLTPYNGTE ALVWLFHQRDSSLHPLIKYLSATTGGGRNY HTTQKMDLDBDTAE KFYCKLIBLEKHIRVTTQKTDNQARIGSGIL  5989 194 2610 AMDFPQHSQHVLBQLNQQRQLGLLCDCTYVVDGVHFKAHKAVLA ACSEYFKMLFVDQKDVVHLBQLNQQRQLGLLCDCTYVVDGVHFKAHKAVLA ACSEYFKMLFVDQKDVVHLDISRAAGLGQVLBFMTTAKLSLSPE NVDDVI,AVATFLQMQDIITACHASLAEPATSSFGGNBKALAT EGGDKRAKEEKVATSTLSRLBQAGRSTPJGPSRDLKEERGGQAQ SAASGAGYTEKADAPREPPPVELKPDPTSGMAABABAALSESS EQMEVEPARKGEEGQKBGREGEGGFABVKEERGGGAA SAASGAGYTEKADAPREPPPVELKPDFTSGMAABABALSESS EQMEVEPARKGEEGGKFABVKEERGGGAA CGKLFTTHGORFKRHILLTHREPSGCRECKSVHIGE RERTTSPLKPYGCEECGKSYRLISILNILRKKRHSGBARYRCKD CGKLFTTHGORFKRHILLTHREPSGCRECKSYRLIS THOTDERHCPHOKKFRNOVENIKABLKHTHADGLKCERGKGK FTTSGALKHRLRIHSGBKPYVCLHCQRQPADEGALQRIVRITHTG EKPCQCVMCGKAPTQASSLIAHVRQHTGEKPYVCERCGKRFVQS SCLANHIRHINNIPPHKCSVCSKAFVNVODLSKHILIHTGEKPYV LCDKCSRGFINVDALRSILVATVQHTGGKAGIKILBPEGGSEVSVVT VDDMYTLATEALAATAVTQLITVPVFGAAVTADETEVLKABISKA VKQVGEEDPNTHILIYACDSGGDKFLDANSLGHVRIHTAGALVM FQTDADFYQQYGFGGTHPAGQVLQAGKLVFRPRICABEGGPALAE TSPTAPECPPPAR  5990 2 4700 FGPGPDSGGARGSGWGSRGQAPYGTLGAVSGGEQVLLHEERGD SGFVSI.SRLGPSLADKDLEWBELMLQDETLLGTMGSTMDASLIS LIEDGSGLGVENDLIPPSHDDSFPJFENTSPKLESPKLPSWRPFRS PRWGQSPPPQQRSDGBREEVASFSGQTLAGELDNCVSSIPDPP MHLACPEBEDKATAARMAVPAAGDESISSLSLVRAMHPYCLDN LITHAALSLEDELGQBDDLTTLPECCVVLET UGQAATAGDLEIPV VVROVSGCPRPVILDDSLETSSALQLLMFTLESTFRAAVPKYTL CSEKEGLSLNSEKLDSACLLKPREVEPVVPFVPREPONPPANAAP GSGRARKGRKKKSKQQPAACVECTVJRET UGGAATGADLEIPV VVROVSGCPRPVILDDSLATTSSALQLLMFTLESTFRAAVPKYTL CSEKEGLSLNSEKLDSACLLKPRAVRAWARAMARALENGSSPK GSGRARKGRKKKSKQQPAACVECTYARRIKSSSRGGSTUGTEVTS QVDNLQKQPGERVLLADFTLAGKTVARABARARARAARAARAARAALENGSSPK LERSAGQSSPAKEGPLLLYPKLADTIQTNPIPTHLSLVDSAQAS PMYDSVRADPTAAGPVLAGFGVUDGLGULASTSSELVEPAR		ŀ	1	
1998  1292  410  FKKYFISFIGLLESSHSRDRIHNLVIMFILATHNLVWFTCRPQ RLDCITIANG IMPNEQINI KALLFGLFS ASBOLLTQGENTTADG LQBVPBTUVPGIFF ILIRRLEPLICHGNDRSQLIVGESRIARKEN FSLEDPQHSKGREPYSSKYATDLLGVALINRHPNQGLYSNVAC PGTAL'NLTYGILPPFIWTLIMPAILLLRPFANAFTLTPYNGTE ALWILFHQRESHPLIKVISATTGGRRYVIMTQMIDLEDTAE KFYQKILBLEKHIRVTQKTDNQARLSGSCI  AMPEPGBGOHUGRUGQGGGGLOCTFVVDGVBFKAHKAVLA ACSEYFMLFVQQKUVVHLDI SNAAGLGQVLEFMYTAKLSLS PR NVIDVI\AVATFLOMQDI TTACALKSLARPATSGGENRAKAN BGGERRAKERVANTSTLSRLEQAGRSTPJ GGSRDLKEERGGQAQ SAASGAGOTEKADAPREPPVELKPDPTSGWAAABARALSESS EQMEVEPARKGEBEDKSQEEQESGAPTGLABUKGERGGGAQ SAASGAGOTEKADAPREPPVELKIPDPTSGWAAABARALSESS EQMEVEPARKGEBEDKSQEEQESGAPTGLABUKGERGGGAQ SAASGAGOTEKADAPREPPVELKIPDPTSGWAAABARALSESS EQMEVEPARKGEBEDKSQEEQESGAPTGLABUKGERGGAP KCEDCKEFTHYGHFRHIR IHTGEKPFSCRECSKAFSDPAACK AHERTISPLKPYGGEGECGSYBLILINLRKKRRHSGRAPVEGS CGKLFTTSGNLKRHCLHISGEKPYCCTUCGORFADPACK AHERTISPLKPYGGEGECGSYBLILINLRKKRRHSGRAPVEGS CGKLFTTSGNLKRHCLHISGEKPYCCTUCGORFADPACREGRYGG SCANNITRHHONITRHPHCSVCSKAFVIVGDLSKHI IHTGEKPY LCDKCGRGFNRVDNLRSHVKTVHQGKGGI KILEPEGSEVSVVT VDDWYLATEALAATAVTQLIVATORGCDRFTUCTRABTEVLKAELSKA VKVQVGEDPNTHILI YACDSGCDRFLDANSLAGHUK HTTAQALVM FQTDADPYQQYGFGGTWBAGQVLQAGELVFRPRGAEGQPALAE TSPTAPECPPPAB  5990  2 4700  FGGEDDSGGGRUSGSWGSRGQAPYGTLGAVSGGGVULHERAGD SGFVSISRILGPSLGPBVDLBWBRIMLQDFTLLGTMGDLEIPV VVRQVSFGFRPVLDDSLOFTSSALQLLMPTLESTFAAVPRVTL CSKKGLISINSERKLDSACLLKPREVEEVVYKFGPQBPANAAP GSGRARKGRKKSKSQRPACVEGTARRABSSRGGSTYGTEVTS QVDNLQKQPGETLQRESLINSERKBSSRGGSTYGTEVTS QVDNLQKQPGETLQRESLINSERKBSSRGGSTYGTEVTS QVDNLQKQPGETLQRESLINSERKBSSRGGSTYGTEVTS QVDNLQKQPGETLQRESLINSERSBRSSRGSPROTTERSTRICATERAAPRAPKEPLAGDLEIPV VVRQVSFGFRPVLLDDSLETSSALQLLMPTLESTERAAVPRVTL CSKRGLISINSERKLDSACLLKPREVEEVVYKFGPQBPPANAAP GSGRARKGRKKSKSQRPAACVEGTARRABSSRGGSTYGTEVTS QVDNLQKQPGETLQRESLGRAGKFSRARRABAALRINSSFRN LERSAGQSSPAKEGPLLLYPKLATGTYGPLTSSLLVSPLPA		Į.		
RIDCIYLNAGIMPNPQLNIKALLFGLPS\ABGLITQGDKITADO LQBVPBTDVPGHY ILITRILBPLLCHISDMPSQLIMTSGRNAKSN FSLBDPQHSKGKEPYSSKYATDLLSVALNNINPOQGLYSNVAC PGTALCHLTYGILPPPIWTLMPATLLILPPANAFTLTPYNGTE ALVWLPPQKPBSLNPLIKYLSATTGGRNYIMTQKMDLDBDTAB KFYQKLLBLEKHIRVTIQKTDNQARLSGSCL  5989 194 2610 AMDPPQBBQHVLBQLNQQRQLGLLCCCT-YVUGVHFKAHKAVLA ACSEYFKMLFVDQKDVVHLDISNAAGLGQVLBPWTTAKLSLSPB NVDDVL\AVATFLQMQDIITACHALKSLARPATSPGGNARALAT BGGDKRAKBEKVATSTLSRLBQAGRSTPIGPSRDLKBERGGQAQ SAASGAOTEKADAPREPPPVELDPTSGWAAARKAALSBSS EQEMEVEPARKGEBQKBQBQEBBAGGPABVKBBGSQLENGBA PBENRINBESAGTDSGQBLGSBRAGLRSGTYGBRTESKRYGSVIH KCEDCGREPTHANDFRENHIRITADEPLKGPTSGWAAARKAALSBSS CQKLFTTSGNLKRHQLVHSGBKPYQCDYCGRSFSDPTSKMHLB TEDTDKEHCPH-CDKKFNOVGHIKAHLKIHLDGFLKCRECGKQ FTTSGNLKRHLRHSGBKPYVCLUHCQRQPADGALQRHVRIHTG BKPQCCVMGKAAPTQASSLLJAHVRQHTGBKPYVCERGCKRFVQS SQLANHIRHIDNIRPHKCSVCSKAPVNGDLSKHIITHTGEKPY LCDKCGRGFPRVDNLRSIIVKTVHQQKGAGIKILBEBEGSKVSVVT VDDWYLATFELAATATVQLTVPGAVTADBETVLKABISKA VKQVQBBDPNTHILYACDSCGDKFLDANSLAHQHVRIHTQALVM FQTDADFYQQYGFGGTWPAGQULQAGBLVFRPRGABGQPALAB TSFTAFPCCPPPBG SGFVSISRLGPBLRNDLBMBELMLQDSTLLGTMQSYMDASLIS LIEDFSGLGKVBHLPBSWDFSPFLETSSFLDFSWRPPRSR PRWGQSPPPQQRSDGBBREBVASFGGOTLAGBLDNCVSIPDPBP MHLACPBEBGKATAARMAVPAGGDES ISSLEDLVRAMHPYCLPN VVRQVSFGPRPVLLDDSLBTSSALQLLMPTLESETRAAVPKVTL CSRKEGLSILNSBEKKDSACLLKPREVVEPVVPKEPQNPPANAAP GSQBARKGRKKKSKSQPAACVEG YARKLRSSSRGGSTVGTEVTS QVDNLGKQPQEBIQKESGPLQKSGPLQKFRARRANAAAARNAALKNSPRK LERSAGQSSPAKEGPLDLYPKDATIQTNPIPTHLSLVDSAQAS PMFVDSVBADPTAVGPVLDGGLGKGKFRAMRANAAAARABSLBLAS	!	L		
LQBVPETDVPGHPILIRELBPLLCHSDMPSQLIFTSSRNARKSN PSLEDPQHSKGKEPYSSSKYATDLLSVALNINFNQQELYSNVAC PGTALCMLTYGILPPPIWTLIMPAILLIRPPRANAFTLTPYNGTE ALVWLERIGRPSLINPLIKYLSATTGFGRNYIMTQKMDLDEDTAE KFYQKLLBLEKHIRVTIQKTDNQARLGGSCL  5989 194 2610 AMDFPQBSGHVLEQUNQQRQIGLGCTT:VVUDGVHFKAHKAVLA ACSSYFKMLFVDQKDVVHLDISNAAGLGQVLEHWTTAKLSLSPE NVDDVL\AVATPLQWQDIITACHALKSLAEPATSPGGNARALAT BGGEKRAKBEKVATSTLSRLEQAGRSTPIGPSRDLKBERGGQAQ SAASGAROTEKADAPREPPPVBLKEDPTSGWAARABARALSESS EQEMEVEPARKGEBEQKBQEQEBEGAGPAEVKEBGSQLENGBA PEENIRWEESASTDSGQELGSBARGLRSGTYGBRTESKAYGSVLH KCEDCGKEPTHYNDFKRHIRIHTGEKPPSCECSKAPSDPAACK AHBKTISPLKPYGCDECGKSYRLISLINLRKRRHSGERGYLENGKA AHBKTISPLKPYGCDECGKSYRLISLINLRKRRHSGERGYCERG CGKLFTTSGNLKRHGLVHSGERFYGCDYGCRBSFSDPTSKMRHLE THDTDKBHKCPHCDKEFNOVGRIKABLKIHTADGPLKCREGGK PTTSGNLKRHGLVHSGBKPYCCDYGCRBSFSDPTSKMRHLE THDTDKBHKCPHCDKEFNOVGRIKABLKIHTADGPLKCREGGK PTSGNLKRHLRHSGSRPYVCHQQKAGIKKLBEEGGSVLF EKPCQCVMCGKAFTQASSLIAHVRQHTGEKPYVCERCGKRPVQS SG.ANHIRHIDNIRPHKCSVCSKAFVNYGDLSKHIIITHGEKPY LCDKCSRGPMYNDINLRSIUKYVHQGKAGIKKLBEEGSBUSVVT VDDMYTLATEALAATAVTQLTVVPVGARATADETEVLKAEISKA VKQVQEEDENTHLLYACDSCDKFLDANSLAQHVWIHTAQALVM PQTDADPYQQYGFGGTWPAGQVLQAGGLVFRPRDCABGQPALAE TSPTAPECPPPAB  5990 2 4700 FGFGPPSGGGARGSWGSRSQAPYGTLGAVSGEGVULHERAGD SGFVSISRIC-PSGLINKDLEMBELMLQDETLLGTMQSYMDASLIS LIEDFGSLGEVEMSLPDPSWDFSPPSFLETSSPKLPSWPPPBRR PRWGQSPPPQQRSDGEBEBELMADDETLIGTMQSYMDASLIS LIEDFGSLGEVEMSLPDPSWDFSPPSFLETSSPKLPSWPPBRR PRWGQSPPPQQRSDGEBEBELMADDETLIGTMQSYMDASLIS LIEDFGSLGEVEMSLPDPSWDFSPPSFLETSSPKLPSWPPPBRR PRWGQSPPPQARGBERGKARSANAPABADES ISSLSELVRAMHPYCLEN VVRQVSPGRPFVLIDDSLETSSALQLLWPTLESTRAAVPKVTIL CSEKEGLSLNSREKLDSACLLKPREVVEPVVPKEPERPNPANAP GSQRARKGRKKKSKRQPAACVEGYARRIRGSSRGGSTVGTEVTS QVDNLQKQPQETIQKSGFLQCKGKPRAWARAMAANALKNSSPRN LERSAGQSSPAKEGPLDLYPKLADTIQTNPTPTHLISUVDSAQAS PMYVDSVBADPTAVGPVULAGFVPUDPGLVULGTVDLAGTSSELVEPLPA	5988	1292	410	
FSLEDPGHSKGKEPYSSSKYATDLLSVALNRNPNOGGLYSNVAC PGTALTNITYGILPPFINTLIRPFANAFITIPYNGTE ALVWLEPIGKEPSLINPLIKYLSATGGGRNYIMTOKMDLOEDTAE KFYCKLLBLEKHIRVTIOKTDNOARLSGSCL AMDFPQHSQHVLEOLNOQROLGILLCCTTYVDGVHFKAHKAVLA ACSSYFKMLFVDCKDVHLDI SNAAGLGQVLERMYTAKLSLSPE NVDDVL\AVATFLOMQDITTACHALKSLARPATSPGSNARALAT EGGEKRAREKKVATSTISRJOAGRSTPT 10FSRDLKEERGGQAQ SAASGARQTEKADAPREPPPVELKEPDTSGMAARARALSESS EQEMEVEPARKGEERGKBOREQEERGGAPAEVKEEGGGLENGBA PERNRESSATDSGGELGSRGLKSGTTGORTESRAVGSVH KCEDCGKEPTHTONFKRHIRIHTGEKPFSCRECSKAFSDPAACK AHEKTISPLAPVGCEEGGKSYRLISLINLRKKHESGERYRCED CKIKJFTTSGRLKRHQLWHSGEREPVCDYCGRESPDFYSKMHLE THDTDKEHKCPHCDKKFNQVGNI.KAHLKIHIADGPLKCRECGKQ FTTSGRLKRHLRHISGEKEPVCLHCQRQADBGAACREVRIHTG EKPCQCVMCKAFTQASSLIAHVQUHGERPYVCERGGKRIPVGS SQ:ANHIRHIDNIRPHKCSVCSKAFVANGDLSHHI IHTGEKPY LCDKCGRGFNRVDNLRSIVKTVHQGKAGIKILBPEEGSEVVVT VDDMVTLATEALAATAVTQLTVVYVGAAVTADETEVLKAEISKA VKQVOBEDPNTHLIAACDSGOKFLDANSLAGHVRHTHAQALVM FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRDGABEGABA TSPTAPECPPPAB  5990 2 4700 FGPGPDSGGGRRSGGGSRSQAPYGTLGAVSGGBQVLLHERAGD SGFVSLSRLGPEIRDKDLEMBEHLQDETLLGTMQSYMDASLIS LIEBFGSLGEVENSLPDPSWDFSPFSFLETSSKLESMRPPRSR PRWGQSPPQQGTBGRBEEEVASFSGGILAGELDNCVSSIPDFP MHLACPEEBDKATAARMAVPAAGDES ISLSELVRAMHPYCLDN LTHLASLEDBLQSDPPDLTLDPECVVLETVGQAATAGDDLETUV VVRQVSBGPRPVLIDDSLETSSALQLLMPTLESETRAVPKVTL CSRKEGLSLNSERKLDSACLLKMPREVPEVPEVPRPVRPPNPANAP GSQRARGRKKKSKRQPAACVEGYARRLRSSBRGGSTVGTEVTS QVDNLGKQPQEELQKESGFLOGGKBPRAWARAARABAALENSSPRN LERSAGQSSPAKERFLDSACLVEGYARRLRSSBRGGSTVGTEVTS QVDNLGKQPQEELQKESGFLOGGKBPRAWARAARABAALENSSPRN LERSAGQSSPAKERFLDSACVEGYARRLRSSSBRGSTVGTEVTS		1	Ì	The state of the s
PGTALEMLITGLIPPETWILLMPAILLLREPRANAPTLTPYNGTE ALVWLPHQKPRSLNPLIKYLSATTGFGRNYIMTQRMDLDEDTAE KFYQKLLBLEKHTRUTTQRTDQARLSGSCL  5989 194 2610 AMDFPQBSQHVLEQLNQQRQLGLLCDCTZVVDGVHFKAHKAVLA ACSEYFKMLFVDQKDVVHLDISRAAGLGQVLERMYTAKLSLSP NVDDVL\AVATFLQMQDI ITACHALKSLARPATSPGRNARALAT EGGEKRAKEKVATSTLSRLEQAGRSTP1GFSRDLKSERGGQAQ SAASGARQTEKADAPREPPVELLKARSLARPATSPGRNARALAT EGGEKRAKEKVATSTLSRLEQAGRSTP1GFSRDLKSERGGQAQ SAASGARQTEKADAPREPPVELKARSTGARARAALSESS EQEMEVEPARKGEBEQKBOREQEEBGAGPAEVKEGGQLENGER PERNRESESAGTDSGQELGSBARGLRSGTYGDRTESKAYGSVIH KCEDCGKEFTHYGNFKRHIRIHTGEKPYSCRECSKAFSDPAAK KAHKRITSPLAPPYGCEBCGKSYRLISLINLRKKRHSGERAYRCBD CGKLFTTSGNLKRRILRIHSGEKPYCDYCGRSFSDPTSKMRHLE THDTDKEHKCPHCDKKFNOVGNIKAHLKIHLAGPEKKRECGKQ FTTTSGNLKRRILRIHSGEKPYVCHCQRQPADPGALQRHVRIHTG EKPCQCVMCGKAPPQASSLLAHVRQHTGERPYVCERGGKRPVGS SQLANHIRHIDNIRPHKCSVCSKAFVNVGDLSKHI I IHTGEKPY LCCKCGRGFMRVDNLRSIUVKTVHQGKAGI KILEPERGSKVSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA VKQVQEEDPMTHILIACDSCGBKFLDANSLAGHVRIHTAQALVM FQTDADFYQQYGFGGTWPAGQVLQAGKLVFPRDGABGQPALAE TSPTAPECPPPAB  5990 2 4700 FGFGPDSGGGRRSGSGRSGQAPYGTLGAVSGGEQVLLHERAGD SGFVSI-SRLGPSLINDKDLERBELMLQDETLLGTMQSYMDASLIS LIEDFGSLGEVEMSLPDPSWDPSPSFLETSSPKLPSWRPPRSR PRWGGSPPQGGSGRBRESVASFSGGLAGELDNCWSI IPDFP MHLACPERBOKATAARMAYPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDELQEQPDLITLPEGCVVLEIVGQAATAGDDLEIPV VVRQVSSGPRPVLIDDSLETSSALQLLMPTLESETRAAVPKVTL CSKREGLISLNSERKIDSACLLLMPTLESETRAAVPKVTL CSKREGLISLNSERKIDSACLLLMPTLESETRAAVPKVTL CSKREGLISLNSERKIDSACLLLMPTLESETRAAVPKVTL CSKREGLISLNSERKIDSACLLLMPTLESETRAAVPKVTL CSKREGLISLNSERKIDSACLLLMPTLESETRAAVPKVTL CSKREGLISLNSERKIDSACLLLMPTLESETRAAVPKVTL CSKREGLISLNSERKIDSACLLLMPTLESETRAAVPKVTL CSKREGLISLNSERKIDSACLLLMPTLESETRAAVPKVTL CSKREGLISLNSERKIDSACLLLMPTLESETRAAVFKVTL CSKREGLISLNSERKIDSACLLLMPTLESETRAAVFKVTL CSKREGLISLNSERKIDSACLALLARPEVVEPVVPVDREDQNPANAPA GSQRARKGRKKKSRQPACVEGYARRLRSSSRGSTVGTEVTS QVDNLQKGPQEELQKEGSGPLAGEGKPRAWARAMAAALBRNSSPRN LERSAGQSSPAKEGPLDLYPKLDADTLOTPHLSILVDSAQAS PMYDSVBADPTAVGEPULGGPVPVDDGLUDLASTSSELUPDL	1			LQEVFETDVFGHFILIRELEPLLCHSDNPSQLIWTSSRNARKSN
ALWWLPHQKPRSLMPLIKYLSATTGFGRNYIMTQKMDLDEDTAE KFYQKILBLEKHIRVTIQKTDNQARISGSCL  AMPPPQHSGNIVE, SQLAGGGGGLCCCT YVDGVHFKAHKAVLA ACSEYPKMLFVQQKDVVHLDI SNAAGLGQVLBFMYTAKLSLSPE NVDDVI, AVATTPLQMQDI TTACHALKSLARPATSPGGNARALAT EGEDKRAKBEKVATSTISHLOAGRSTP 106FSDLKEERGQAQ SAASGARQTEKADAPREPPPVELKPDPTSGMAARAEAALSESS EQEMEVEPARKGBERGKBQREQEEBGAGPAEVKBEGGOLENGRA PERNINESSATTDSQQELGSBARGLRSGTYGDRTESKAYGSVIH KCEDCCKEPTHTONFKHLIKITHGEKPFSCRECSKAFSDPAACK AHRKTIEPPLKPYGCEBCGKSYRLISLINLRKRRHSGRAYNCED CGKLFTTSGNLKRHQLVHSGEKPYQCDYCGRSFDPTSKMRHLE THDTDKEHKCPHCDKKFNOVGNIKARLIKIHJADGPLKCEBCGKQ FTTSGNLKRHLRIHSGKPYVCLHCQRQPADPGALQRHVRIFTG EKPCQCVMCGKAPTQASSLIAHVQNHTGEKPYVCERCCKRFVQS SQLANHIRHIDNIRPHKCSVCSKAFVNVGDLSKHIIHTUGEKPY LCDKCGRGPMRVDNLRSINVKTVHQGKAGIKILEPEEGSEVSVVT VDDMVILATEALAATAVTQLTVVFVGAAVTABETEVLKAEISKA VKQVGEDDMTHLIYACDSGODKFLDANSLAGHVRIHTAQALVM FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRDGABGQPALAE TSFTAPECPPPAB SGFVSLSRLGPSLRDKDLEMBELMLQDETILGTMQSYMDASLIS LIEDFGSLGRUENSLEPPSNDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGBEBEKASFSGQILAGELDNCVSSIPDPP MHLACPEEDKATAARMAVPAACDESISSLSELVRAMHPYCLPN LTHLASLADELQROPDDLTLPEGCVULETUGQAATAGDDLEIPV VVROVSPGPRFVILLDDLETSSRLQLLIMPTLESTERAVPKVTL CSKREGLSLNSEKKLDSACTLLKPREVVEPVVPKEPQNPANAAPA GSQRARKGRKKKSRQPAACVEGYARRLRSSSEGGSTVGTEVTS QVDNLQKQPQETLQKESGFLQGKGRFRAMARAMAALBRSSFRN LERSAGGSSPARKERLDLATTQFVPVDDGLVDLASTSSELUFPLPA		İ		FSLEDFQHSKGKEPYSSSKYATDLLSVALNRNFNQQGLYSNVAC
### PORTUBEL HEND TO A TO A MORPO PORTUBE CONTROL OF THE PROPERTY OF THE PROPERTY	ļ	1		PGTALTNLTYGILPPFIWTLLMPAILLLRFFANAFTLTPYNGTB
5989  194  2610  AMDPPQHSQHVLEQLINQQRQLIGLLCDCTYVVDGVHFKAHKAVLA ACSSYFMILFVDQRUVVHLDISINABGLGQULERMYTAKLSLSPR NVDDVL,\AVATPLOMQDI LITACHALKSLARPATSPGGNRALAT EGGEKRAKEEKVATSTLSRLEQAGRSTPIGPSRDLKEERGGQAQ SAASGARQTEKADAPREPPPVELKEPDFTSGMAABARALISESS EQEMEVEPARKGEERQKBOREQEEGGAPEVKEEGSQLENGEA PERNKREESAGTDSGQELGSBARGLRSTYGORTESKAYGSVIH KCEDCGKEFTHYGRFKRHIRIHTGKEPFSCRECSKAFSDPAACK AHEKTE'SPLKPYGCEECGKSYRLISLLNLRKKRHSGEARYRCED CGKLFTTSGNLKRRQLVHSGEKPYCCDYCGRSFSDPTSKMRHLE THDTMSEHKCPHCDKKFNOVGNIKAHLKIHIAGPLKCRECGKQ FTTSGNLKRHLRIHAGEKPYVCIHCORQPADDEBAQRHVRIHTG EKPCCVWGGKAFYQASSLIAHVVQHTGEKPYVCERCGKRFVGS SQLANHIRHIDNIRPHKCSVCSKAFVNVGDLSKHII IHTGEKPY LCDKCSRGFPRVDNILSIIVKTVHQCKAGIKILEPEGSSKVSVVT VDDMVTLATRALAATAVTQLTVPVVGAAVTADETEVLKARISKA VKQVGEDPNTHILIYACDSCGDKFLDANSLAQHVRIHTAQALVM FQTDADPYQOYGFGGTWPAGQVLQAGELVFRPDGABGQPALAE TSPTAPECPPPAB  5990  2 4700 FGFGPDSGGGRRGSGWGSRSQAPYGTLGAVSGGEQVLLHERAGD SGFVSLSRLGPSLRDKDLEMBELMLQDETLIGTMQSYMDASLIS LIEDFGSLGRVEMSILPDPSWDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGBEBEBVASFSGQTLAGELDNCVSI PDPP MHIACPEEBDKATAARWAVPAAGDES ISSLSELVRAMHPYCLEN LTHIASLEDBLQBCQPDDLTLPEGCVVLETUGQAATAGDDLETPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETRAAVPKVTL CSRKEGLSLNSERKLDSACLLKPREVVEFVVVPKEPQNPPANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLGRQPGEIQKESGPPLQGKGRPRAWARAWAAALKRSSFRN LERSAGGSSPAKEGPLDLYPKLADTJQTVNPIFTHISLYDNSAOAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	1		ĺ	ALVWLFHQKPESLNPLIKYLSATTGFGRNYIMTQKMDLDEDTAE
ACSEYFKMLFVDQKDVVHLDISNAAGIGQVLEPMYTAKLSLSPE NVDDVL\AVATFLOMDIITACHALKSLARPATSPGGNARALAT BGGEKRAKBEKVATSTLSRIEQAGRSTPIGPSRDLKERGGQAQ SAASGASCTEKRADAPREPPPVELKPDPTSGMAARABAALSESS EQEMEVEPARKGBEEQKBQEEQEBGGAPAEVKEEGSQLENGBA PERNRESSAGTDGQELGSBARGLRSGTYGDRTESKAYGSVLH KCEDCGKGPTHYGNYRHIRIHTGEKPPSCRECSKAFSDPAACK AHERTISPLKPYGCEECGKSYRLISLLNLRKKRHSGEARYRCED CGKLFTTSGNLKRHGLVHSGERPYQCDYCGRSFSDPTSKMRHLE THDTDKBHKCPHCDKKFNOVGNIKAHLKIHTAGEPLKCRECGKQ FTTSGNLKRHLRIHSGERPYVCLHCQRQPADPGALQRHVRIHTG BKPCQCVMCGKAPTQASSLIAHVRQHTGEKPYVCERCGKRPVQS SCIANHIRHIDNIRPHKCSVCSKAPVMVGDLSKHILIHTGERPY LCDKCGRGPRNVDNLRSIUKTVHQGKAGIKILEPEGGSKSVVT VDDMVTLATEALAATAVTQLTVVPVGRAVTADBTEVLKAEISKA VKQVQBBDPNTHILVACDSGDKFLDANSLAQHVRIHTAQALVM FQTDADPYQQYGPGGTWPAGQVLQAGELVFRPRDGABGQPALAE TSPTAPECPPPAB  5990 2 4700 FGPGPDSCGGARGSGWGSRSQAPYGTLGAVSGGEQVLHEERGD SGFVSLSRLGPSLADKDLEMBELMLQDBTLLGTMQSYMDASLIS LIEDFGSLGEVEMSLPDPSDPSPPSFLETSSPKLDSWRPPRSR PRWGQSPPPQQRSDGBEEBEVASFSGQTLAGELDNCVSSIPDPP MHLACPEBBCKATAABMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDBLQGQPDDLTLPBCCVVLEIVGQAATAGDDLEIPV VVROVSPGPPFVLDDSLETSSALQLLMPTLESRTAAVPKVTL CSKEGLSLNSEKKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARGSRKKKSKRQPAACVEGYARALRSSRGQSTVGTEVTS QVDNLUKQPQPELQKESGPLQKGKRPRAWARAMAALKNSSPRN LKRSAGGSSPAKEGFLDLYPKLADTIQTNPTPTHLSLVDSAQAS PMFVDSVEADPTAVGPVVDRGLVGLASTSSELVEPLPA	1	<b>,</b>		KFYQKLLELEKHIRVTIQKTDNQARLSGSCL
ACSBYFKMLFVDQKDVVHLDISNAAGIGQVLBFMYTAKLSLSPE NVDDVL\AVATPLOMQDIITACHALKSLARPATSPGSMARALAT BGGDKRARBERVATSTBIGEDGAGSTPIGPSRDLKERGGQAQ SAASGABQTEKADAPREPPPVELKEPDTSGMAABABAALSESS EQEMBVEPARKSBEBQKBQBEQEBEGGAPABVKEBGSQLENGBA PEBNRDESAGTDSGQELGSBARGLRSGTYGDRTESKAYGSVLH KCEDCGGFTHTGNPFKRHIRIHTGSRPFSCRECSKAFSDPAACK AHBKTESPLKPYGCEECGKSYRLISLLNLRKKRHSGKARYRCED CGKLPTTSGNLKRHQLVHSGSBEPYQCDYCGRSFSDPTSKMRHLB THDTDKBHKCPHCDKKFNOVGNIKAHLKIHLADGPLKCRECGKQ FTTSGNLKRHLRIHSGBKPYVCLHCQROPADPGALQRHVRIHTG BKPCQCVWCGKAPTQASSLIAHVQHTGSERPYVCRCGRFFVQS SQLANHIRHIDNIRPHKCSVCSKAFVNVGDLSKHIIIHTGBKPY LCDKCGRGPNRVDNLRSIUKTVHQGKAGIKILEPEGSSKVSVT VDDMVTLATBALAATAVTQLTVVPVGAAVTADETEVLKAEISKA VKQVQBBDPNTHILVACDSCGDKFLDANSLAGHVRIHTAQALVM FQTDADFYQQYGFGGTWPAGQVLQAGELVFRPRDGABGQPALAE TSPTAPECPPPAB  5990 2 4700 FGPGPDSCGGARGSGWGSRSQAPYGTLGAVSGGEQVLHERAGD SGFVSILSRLGPSLADKDLEMBELMLQDETLLGTMGSYMDASLIS LIEDFGSLGEVEMSLPDPBDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSIDGBEBEVASFSGQTLAGELDNCVSSIPDPP MHLACPEBBCKATAABMAVPAAGDESISSLSBLVRAMHPYCLPN LTHLASLEDBLQGCPDDLTLPBCCVVLEIVGQAATAGDDLEIPV VVRQVSPGPPPQTBLDDSLETSSALQLLMPTLESETRAAVPKVTL CSKKEGLSLNSEKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARGGRKKKSRQPAACVEGYARALRSSSRGGSTVGTEVTS QVDNLKQPQPELQRESGPLQGKGKPRAWARAMAALENSSPRM LKRSAGGSSPAREGELDLYPKLADTIQTNPTPTHLSLVDSAQAS PMFVDSVEADPTAVGPVDAGEVPVDDGLVDLASTSSBLVEPLPA	5989	194	2610	AMDFPQHSQHVLEQLNQQRQLGLLCDCT?VVDGVHFKAHKAVLA
NVDDVI.\AVATPI.QMQDIITACHALKSLAEPATS PGGNARALAT BGGDKRAKBKVATSTLSHLEQAGRSTP IGFSRDLKEERGQAQ SAASGAEQTEKADAPREPPVELKEPDPTSGMAABEARALSESS EQEMEVEPARKGEBEQKBQEEQEEGAGPAEVKEEGSQLENGEA PERNRESSAGTDGGQELGSRARGLRGGTYGDRTESKAYGSVIH KCEDCGKBFTHTGDFKRHIR IHTGEKPFSCRECSKAFSDPAACK AHEKTISPLKPYGCEECGKSYRLISLINLRKKRISGBARYRCED CGKLFTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE THDTDKEHKCPHCDKKFNQVGBNLKAHLKIHLADGFLKCRECKQ FTTSGNLKRHLRIHSGERPYVCIHCQRGPADDGALGRHVRIHTG EKPCQCVMCGKAFTQASSLIAHVRQHTGEKPYVCERCGKRFVQS SQLANHIRHHDNIRPHKCSVCSKAFVMVGDLSKHIIIHTGEKPY LCDKCGRGFNRVDNLRSHVKTVHQGKAGIKILEPEEGSEVSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA VKQVQBEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM FQTDADFYQQYGFGGTMPAGQVLQAGELVFRPRCGAEGQPALAE TSFTAPECPPPAR  5990 2 4700 FGFGPDSCGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHERAGD SGFVSLSRLGPSLADKDLEMBELMLQDETLLGTMGSYMDASLIS LIEDFGSLGBVEMSLDPDSMDPSPPSFLETSSPKLPSWRPPRSR PRRGQSPPPQQRSDGBEREKVASFSGQTLAGELDNCVSSIPDFP MHLACPEEBKATAABMAVPAAGDESISSLSLVRAMHPYCLPN LTHLASLEDBLQBQPDDLTLPEGCVVLEIVGQAATAGDDLEIFV VVRQVSPGPRFVLLDDSLETSSALQLLMPTLESETRAAVPKVTL CSKEGLSLNSERKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARGSRKKKSKBQPAACVEGYARRLRSSRGQSTVGTEVTS QVDNLUKQPQEELQRESGFLQGKGKFRAWARAWAALKRSSFRN LKRSAGGSSPARGGELQKESGFLQGKGKFRAWARAWAALKRSSFRN LKRSAGGSSPARGGELDLYPKLADTI QTDPIPTHLISLVDSAQAS PMFVDSVEADPTAVGPVVDRGLVDLASTSSELVEPLPA		Ì	<b>'</b>	, — ··· ·
EGGERRAKEEKVATSTLSRLEQAGRSTPIGPSRDLKEERGGQAQ SAASGAECTEKADAPREPPPVELKEDPTSGMAAAEARALSESS EQEMEVEPARKGEEQKEGERGACPABVKEEGSQLENGHA PERNRESSAGTDSGQEIGSEARGLRSGTYGDRTESKAYGSVIH KCEDCGKEFTHYGNFKHIRIHTGEKPFSCRECSKAFSDPAACK AHEKTESPLKPYGCEEGGKSYRLISLLNLRKKRHSGKRAYRCED CGKLFTTSGNLKRHGLVHSGEKPYQCDYCGRSFSDPTSKMRHLB THDTDKEHKCPHCDKKFNOVGNI-KAHLKIHLADGPLKCRECGKQ FTTSGNLKRHLRIHSGEKPYVCIHCQRQPADPGALQRIVRIHTG EKPCQCVMCGKAFTQASLAVRQHTGEKPYVCERCGKRFVQS SQ-LANHIRHHDNIRPHKCSVCSKAFVNVGDLSKHIIHTGEKPY LCDKCGRGFNRVDNLRSHVKTVHQGKAGIKILBPEEGSEVSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETBVLKAEISKA VKQVQBEDPNTHLLYACDSGCBKFLDANSLAQHVRIHTAQALVM FQTDADPYQQYGFGGTWPAGQVLQAGELVFRPDGAEGQPALAE TSPTAPECPPPAE TSPTAPECPPPAE SGFVSLSRLGPSLRDKDLBMERLMLQDETLLGTMQSYMDASLIS LIEBFGSLGBVEMSLPPDSNDFSPSFLETSSPKLPSWRPRSR PRWGQSPPPQQRSDGEEBEBVASFSGQTLAGELDNCVSSIPDFP MHLACPEEBGKATAARMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEBELQEQPDDLTLPEGCVVLBIVGQAATAGDDLEIPV VVRQVSPGPRFVLLDDSLETSSALQLLMPTLESETRAAVPKVTL CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSBRGOSTVGTEVTS QVDNLQKQPQEELQKESGPLOLYPRABARAALKNSSPRN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSBLVEPLPA		· ·	·	
SAASGAEQTEKADAPREPPVEIKPDPTSGMAAEAEAALSESS EQEMEVEPARKGEBEQKEDEBGAGPABVKEBEGGLENGEA PEBRIREESASTDSGQEGEBGAGPABVKEBEGGLENGEA KCEDCGKEFTHTGONFKRHIRIHTGEKPFSCRECSKAFSDPAACK AHEKTESPLKPYGCEECGKSYRLISLLNLRKKRHSGEARYRCED CGKLFTTSGNLRRHQLVHSGERPYQCDYCGRSFSDPTSKMRHLB THDTDKEHKCPHCDKKFNQVGNLKAHLKIHIADGPLKCRECGKQ FTTSGNLRHHLRHISGERPYVCTHCQRQFADPGALQRRVRIHTG EKPCQCVMCGKAPTQASSLIAHVRQHTGEKPYVCERCGKRPVQS SQLANHIRHHDNIRPHKCSVCSKAFVNVGDLSKHIIHTGBKPY LCDKCGRGFNRVDNLRSHIVKTVHQGKAGIKILBEGSBVSVTT VDDMVTLATEALAATAVTQLTVVYGAAVTADBTEVLKAEISKA VKQVQBEDPNTHLLYACDSCGDKFLDANSLAGHVRIHTAQALVM FQTDADFYQQYGFGGTWPAGQVLQAGELVFRPDGAEGQPALAE TSPTAPECPPPAB  5990 2 4700 FGPGPDSGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHERAGD SGFVSLSRLGPSLRDKDLEMBELMLQDETLLGTMQSTMDASLIS LIEDFGSLGBVEMSLPDPSWDPSPPSPLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGBBREVASFSGQTLAGELDNCVSSIPDPP MHLACPEBEDKATAARMAVPAAGDESISSLSELVRANHPYCLEN LTHLASLEDBLQEQPDDLTLPEGCVVLBIVGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETERAVPKVTL CSEKEGLSLNSERKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKRQPAACVGGYARRLRSSSEGGSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAMAALENSSPKN LERSAGQSSPAKRGRKKSKRQPAACVGGYARRLRSSSEGGSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAMAALENSSPKN LERSAGGSSPAKRGRKKSKRQPAACVGGYARRLRSSSRGSTVGTSVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAMAALENSSPKN LERSAGGSSPAKGRKKSKRQPAACVGGYARRLRSSSRGSSTVGTSVTS	1 .			
EQEMBUE PARKGEBEQKEQEEGAGPABUKKEGSQLENGEA PREMERESAGTDSGQEI.GSBARGLRSGTYGDRTESKAYGSVIH KCEDCGKEFTHYCMYRCHER IHTGEKPFSCRECSKAFSDPAACK AHEKTESPILKPYGCEEGCKSYKI.ISLLMI,RKKRHSGEARYRCEB CGKLFTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE THDTDKBERCPHCDKKPMQVGRI,KAHLKI HIADGPLKCRECGKQ FTTSGNLKRHLRIHSGEKPYVCLHCQRQPADPGALQRHVRIHTG BKPCQCVWGCKAFPQASSLIAHVRQHTGEKPYVCERCGKRFVQS SQLANHI RHHDNIRPHKCSVCSKAFVNVGDLSKHI I IHTGEKPY LCDKCGRGFMRVDNLRSIIVKTVHQGKAGIKILEPEGSBVSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA VKQVQBEDPNTHILYACDSCGDKFLDANSLAGHVRIHTAQALVM FQTDADFYQQYGFGGTWPAGQVLQAGELVFRPRDGAEGQPALAE TSPTAPECPPAB  5990 2 4700 FGFGPDSGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHERAGD SGFVSLSRIGPSLRDKDLEMBELMLQDETLLGTMQSYMDASLIS LIEDFGSLGBVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGRBEEVASFSGQTLAGELDNCVSSIPDFP MHLACPEBEBKATAARMAVPAAGDESISSLSLIVRAMHPYCLPN LTHLASLEDBLQEQPDDLTLPEGCVVLBIVGQAATAGDDLEIFV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETRAAVPKVTL CSBKEGLSLNSERKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRAKGRKKKSKRQPAACVGGYARRLRSSSRGGSTVGTKVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAMAALENSSPKN LERSAGQSSPAKGRKKKSKRQPAACVGGYARRLRSSSRGGSTVGTKVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAMAAALENSSPKN LERSAGQSSPAKGRKKSKRDPADTAUGPVVDGLVDLASTSSELVEPLPA		l .	į.	
PEENRNEESAGTDSQELGSBARGLRSGTYGDRTESKAYGSVIH  KCEDCGKRFTHTGMFKRHIRIHTGEKPFSCRECSKAFSDPAACK AHEKTESPLKPYGCEDCGKSYRLISLINLRKKRHSGERAPYRCED CGKLFTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDFTSKMRHLB THDTDKEHKCPHCDKKFNQVGNLKAHLKIHLADGPLKCRECGKQ FTTSGNLKRHLRIHSGEKPYVCIHCQRQPADPGALQRHVRIHTG EKPCQCVMCGKAFTQASSLIAHVRQHTGERPYVCRRCGKRFVQS SQLANHIRHDNIRPHKCSVCSKAFVNVGDLSKHIIIHTGEKPY LCDKCGRGFRRVDNLRSILWKVVHQGKAGIKILBPEEGSBVSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADBTEVLKAEISKA VKQVQBEDPNTHILYACDSGDKFLDANSLAQHVRIHTAQALVM FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRDGABGQPALAE TSPTAPECPPPAB  5990 2 4700 FGFGPDSGGARGSGWGSRSQAPYGTLGAVSGGBQVLLHEERAGD SGFVSLSRLGPSLRDKDLEMBELMLQDETILGTMQSYMDASLIS LIEDFGSLGBVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGBBEEVASFSGQILAGELDNCVSSIPDFP MHLACPEBEBKATAABMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDBLQBQDDLTLPEGCVVLEIVGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSKKGLSINSERKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKQPQAACVEGYARRLRSSRGGSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAMAALENSSPKN LKRSJAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSSAQAS FMPVDSVBADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	i		1	
KCEDCGKEFTHTGNFKRHIRIHTGEKPFSCRECSKAFSDPAACK AHEKTPS PLKPYGCEECGKSYRLISLLINLRKKRHSGEARYRCED CGKLFTTSGNLKRHQLVHSGEBCPYQCDYCGRSFSDPTSKMEHLE THDTDKEHKCPHCDKKFNQVGNLKAHLKIHIADGPLKCRECGKQ FTTSGNLKRHLRIHSGEKPYVCTHCQRQPADPGALQRHVRIHTG EKPCQCVMCGKAFTQASSLIAHVRQHTGEKPYVCERCGKRPVQS SQLANHIRHHDNIRPHKCSVCSKAFVNVGDLSKHII IHTGEKPY LCDKCGRGFMRVDNLRSIVKTVHQGKAGIKILEPEEGSEVSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA VKQVQEEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRCGAEGQPALAE TSPTAPECPPPAB  5990 2 4700 FGPGPDSGGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHERAGD SGFVSLSRLGPSLRNDLEMBELMLQDETILGTMQSYMDASLIS LIEDFGSLGEVEMSLPPDSWDFSPPSFLETSSPKLPSWRPPRSR PRWGSPPPQQRSDGBEBEEVASFSQTLAGELDNCVSSIPDFP MHLACPEEBDKATAARMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDELQEQPDDLTLPEGCVVLETVGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSEKRGLSINSERKLDSACLLKPREVVEPVVPKEPQNPANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALBNSSPKN LKRSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEDLPA	ļ	ł		
AHERTESPLKPYGCEECGKSYRLISLLNIRKKRHSGEARYRCED CGKLFTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE THDTDKBHKCPHCDKKFNQVGNLKAHLKIHLADGPLKCRECGKQ FTTSGNLKRHLRIHSGEKPYVCIHCQRQPADPGALQRHVRIHTG EKPCQCVMCGKAPTQASSLIAHVRQHTGEKPYVCERCGKRPYQS SQLANHIRHHDNIRPHKCSVCSKAPVNVGDLSKHILIHTGEKPY LCDKCGRGPNRVDNLRSHVKTVHQGKAGIKILEPEEGSEVSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA VKQVQEEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRGABGQPALAE TSPTAPECPPPAR  5990 2 4700 FGPGPDSGGARGSGWGSRSQAPYGTLGAVSGEQVLLHERAGD SGFVSLSRLGPSLRDKDLEMBELMLQDETLLGTMQSYMDASLIS LIEDFGSLGEVEMSLPDPSWDFSPSFIETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGBEBEEVASFSGQILAGELDNCVSSIPDPP MHLACPEEBDKATAARMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDELQEQPDDLTLPEGCVVLEIVGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSKREGLSINSEEKLDSACLLKPREVVEPVVPKEPQNPANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGRPRAWARAWAALENSSPKN LKRSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	ł .	1	!	
CGKLFTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE THDTDKEHKCPHCDKKFNQVGNIKAHLKI HIADGPLKCRECGKQ FTTSGNLKRHLRIHSGEKPYVCIHCQRQADGGALQRHVRIHTG EKPCQCVMCKAFTQASSLIAHVRQHTGEKPYVCERCGKRFVQS SQ:ANHIRHIDNIRPHKCSVCSKAFVNVGDLSKHII IHTGEKPY LCDKCGRGFNRVDNLRSHVKTVHQGKAGIKILBPEEGSEVSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADBTEVLKAEISKA VKQVQBBPDNTHLLYACDSCGDKFLDANSLAQHVRIHTAQALVM FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRDGAEGQPALAE TSPTAPECPPPAB  5990 2 4700 FGPGPDSGGARGSGWGSRSQAPYGTLGAVSGGGVLLHERAGD SGPVSLSRLGPSLRDKDLEMBELMLQDETLLGTMQSYMDASLIS LIEDFGSLGEVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGEBEBEVASFSGQILAGELDNCVSSIPDPP MHLACPEEBBKATAARMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDELQEQPDDLTLPEGCVVLETUGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSKREGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPANAAP GSQRAKKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVUDNLQKQPQELQKESGPLQGKGKPRAWARAMAALENSSPKN LKRSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA		İ		
THDTDKEHKCPHCDKKFNQVGNIKAHLKIHIADGPLKCRECGKQ FTTSGNLKRHLRIHSGEKPYVCIHCQRQPADPGALQRHVRIHTG BKPCQCVMCGKAPTQASSLIAHVRQHTGEKPYVCERCGKRPVQS SQLANHIRHHDNIRPHKCSVCSKAPVNVGDL9KHIIIHTGEKPY LCDKCGRGPRVDNLRSHVKTVHQGKAGIKILBPEEGSEVSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADBTEVLKABISKA VKQVQBEDPNTHLLYACDSCGDKFLDANSLAQHVRIHTAQALVM FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRDGAEGQPALAE TSPTAPECPPPAB  5990 2 4700 FGPGPDSGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHEEAGD SGPVSLSRLGPSLRDKDLEMBELMLQDETLLGTMQSYMDASLIS LIEBFGSLGBVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGEBEBEVASFSGQTLAGELDNCVSSIPDFP MHLACPEEBDKATAAEMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDBLQEQPDDLTLPEGCVVLEIVGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETRAAVPKVTL CSBKEGLSLNSERKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKRSGPLQGKGKPRAWARAWAAALBKBSSPKN LERSAGQSSPAKGGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	I	1		
FTTSGNLKRHLRIHSGEKPYVCIHCQRQFADPGALQRHVRIHTG  BKPCQCVMCGKAPTQASSLIAHVRQHTGEKPYVCBRCGKRFVQS  SQ:ANHIRHIDNIRPHKCSVCSKAFVNVGDLSKHII IHTGEKPY  LCDKCGRGFNRVDNLRSIIVKTVHQGKAGIKILBPEEGSBVSVVT  VDDMVTLATEALAATAVTQLTVVPVGAAVTADBTEVLKAEISKA  VKQVQBEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM  FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRDGABGQPALAE  TSPTAPECPPPAB  5990 2 4700 FGEGPDSGGARGSGWGSRSQAPYGTLGAVSGGBQVLLHERAGD  SGPVSLSRLGPSLRDADLEMBELMLQDETLLGTMQSYMDASLIS  LIEDFGSLGBVEMSLPPPSWDFSPPSFLETSSPKLPSWRPPRSR  PRWGQSPPPQQRSDGBEBEBEVASFSGQTLAGELDNCVSSIPDFP  MHLACPEBEDKATAAEMAVPAAGDESISSLSELVRAMHPYCLPN  LTHLASLEDBLQEQPDDLTLPEGCVVLEIVGQAATAGDDLEIPV  VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESSTRAAVPKVTL  CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP  GSQRARKGRKKKSRQPAACVEGYARRLRSSSRGQSTVGTEVTS  QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALBNSSPKN  LERSAGQSSPAKGGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS  PMPVDSVBADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	1	I		CGKLFTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE
BKPCQCVMCGKAPTQASSLIAHVRQHTGEKPYVCERCGKRFVQS SQLANHIRHHONIRPHKCSVCSKAPVNVGDLSKHII IHTGEKPY LCDKCGRGFMRVDNLRSIIVKTVHQGKAGIKILBEEGSBVSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA VKQVQEBEDRTHILVACDSCGDKFIDANSLAQHVRIHTAQALVM FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRDGAEGQPALAE TSPTAPECPPPAB  5990 2 4700 FGFGPDSGGARGSGWGSRSQAPYGTLGAVSGGBQVLLHEERAGD SGFVSLSRLGPSLRDDLEMBELMLQDETILGTMQSYMDASLIS LIEDFGSLGEVEMSLPPDSWDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGBEBEEVASFSGQILAGELDNCVSSIPDFP MHLACPEBEDKATAARMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDELQEQPDDLTLPEGCVVLEIVGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSEKRGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPRANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAALKNSSPKN LERSAGQSSPAKGGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	1	į.	1	THDTDKEHKCPHCDKKFNQVGNI.KAHLKIHIADGPLKCRECGKQ
BKPCQCVMCGKAPTQASSLIAHVRQHTGEKPYVCERCGKRFVQS SQLANHIRHHONIRPHKCSVCSKAPVNVGDLSKHII IHTGEKPY LCDKCGRGFMRVDNLRSIIVKTVHQGKAGIKILBEEGSBVSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA VKQVQEBEDRTHILVACDSCGDKFIDANSLAQHVRIHTAQALVM FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRDGAEGQPALAE TSPTAPECPPPAB  5990 2 4700 FGFGPDSGGARGSGWGSRSQAPYGTLGAVSGGBQVLLHEERAGD SGFVSLSRLGPSLRDDLEMBELMLQDETILGTMQSYMDASLIS LIEDFGSLGEVEMSLPPDSWDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGBEBEEVASFSGQILAGELDNCVSSIPDFP MHLACPEBEDKATAARMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDELQEQPDDLTLPEGCVVLEIVGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSEKRGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPRANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAALKNSSPKN LERSAGQSSPAKGGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	1	1		FTTSGNLKRHLRIHSGEKPYVCIHCQRQFADPGALQRHVRIHTG
SQLANHIRHHDNIRPHKCSVCSKAFVNVGDLSKHILIHTGEKPY LCDKCGRGPNRVDNLRSHVKTVHQGKAGIKILEPEEGSEVSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAETISKA VKQVQEEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM FQTDADFYQQVGFGGTWPAGQVLQAGELVFRPRDGAEGQPALAE TSPTAPECPPPAB  5990 2 4700 FGPGPDSGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHERAGD SGFVSLSRLGPSLRDKDLEMBELMLQDETLLGTMQSYMDASLIS LIEDFGSLGEVEMSLPDPSWDPSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGBEBEEVASFSGQTLAGELDNCVSSIPDPP MHLACPEEBDKATAARMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDELQEQPDDLTLPEGCVVLETVGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSKRGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAALENSSPKN LKRSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	.]	J	j	EKPCQCVMCGKAFTQASSLIAHVROHTGEKPYVCBRCGKRFVOS
LCDKCGRGFNRVDNLRSIIVKTVHQGKAGIKILEPEEGSEVSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA VKQVQEEDPNTHILLYACDSCGKFLDANSLAGHVNRIHTAQALVM FQTDADFYQQYGFGGTWPAGQVLQAGELVFRPRDGAEGQPALAE TSPTAPECPPPAB  5990 2 4700 FGPGPDSGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHERAGD SGPVSLSRLGPSLRDKDLEMBELMLQDETLLGTMQSYMDASLIS LIEDFGSLGEVEMSLPDPSWDFSPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQSDGEBEBEVASFSGQILAGELDNCVSSIPDFP MHLACPEEBBKATAARMAVPAAGDES ISSLSELVRAMHPYCLPN LTHLASLEDELQEQPDDLTLPEGCVVLETUGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSKREGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQELQKESGPLQGKGKPRAWARAMAALENSSPKN LKRSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA		<b>,</b>	1	
VDDMVTLATEALAATAVTQLTVVPVGAAVTADBTEVLKAEISKA VKQVQBEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRDGABGQPALAE TSPTAPECPPPAB  5990 2 4700 FGPGPDSGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHEEAGD SGPVSLSRLGPSLRDKDLEMBELMLQDBTLLGTMQSYMDASLIS LIEBFGSLGBVEMSLPPSWDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGBEBEBVASFSGQTLAGELDNCVSSIPDFP MHLACPEBEDKATAABMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDBLQBQPDDLTLPEGCVVLETVGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLBTSSALQLLMPTLESBTRAAVPKVTL CSBKEGLSLNSERKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKBSGPLQGKGBPRAWARAWAALKNSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVBADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	1	]·	1	1
VKQVQBEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRDGAEGQPALAE TSPTAPECPPPAB  5990 2 4700 FGPGPDSGGARGSGWGSRSQAPYGTLGAVSGGGQVLLHEEAGD SGPVSLSRLGPSLRDKDLEMBELMLQDETLLGTMQSYMDASLIS LIEBFGSLGBVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGBEBEBVASFSGQTLAGELDNCVSSIPDFP MHLACPEBBDKATAAEMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDBLQEQPDDLTLPEGCVVLETVGQAATAGDDLEIPV VVRQVSPGFRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSBKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAALKNSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVBADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	I	ì		
FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRDGABGQPALAE TSPTAPECPPPAR  5990 2 4700 FGPGPDSGGGARGSGWGSRSQAPYGTLGAVSGGBQVLLHERAGD SGPVSLSRLGPSLRBADLEMBELMLQDETLLGTMQSYMDASLIS LIEDFGSLGBVEMSLPPPSWDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGBEBEBVASFSGQTLAGELDNCVSSIPDFP MHLACPEBBDKATAARMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDBLQEQPDDLTLPEGCVVLEIVGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESSTRAAVPKVTL CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAALKNSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVBADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	]	•	1	
TSPTAPECPPPAB  5990 2 4700 FGPGPDSGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHERAGD SGFVSLSRLGPSLRDKDLEMBELMLQDETILGTMQSYMDASLIS LIEDFGSLGBVEMSLPPBVBTSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGBBEBEVASFSGQTLAGELDNCVSSIPDFP MHLACPBEBDKATAARMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDELQEQPDDLTLPEGCVVLEIVGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETRAAVPKVTL CSKKRGLSINSERKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSRQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQELQKESGPLQGKGKPRAWARAWAAALMNSSPKN LKRSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVBADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	l	I	1	1 " = = =
5990 2 4700 FGPGPDSGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHERAGD SGPVSLSRLGPSLRDKDLEMBELMLQDETLLGTMQSYMDASLIS LIEDFGSLGEVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGEBEBEVASFSGQTLAGELDNCVSSIPDFP MHLACPEEBBKATAARMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDELQEQPDDLITLPEGCVVLETUGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSKKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRAKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQELQKESGPLQGKGKPRAWARAMAALENSSPKN LKRSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	I	1	}	
SGFVSLSRLGPSLRDKDLEMEKLMLQDETLLGTMQSYMDASLIS LIEDFGSLGEVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGBBEEEVASFSGQTLAGELDNCVSSIPDFP MHLACPEBEDKATAARMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDELQEQPDDLITLPEGCVVLETVGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETRAAVPKVTL CSEKEGLSLNSEEKLDSACTLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQCKGKPRAWARAMAALKNSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVBADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	F655	<del> </del>		1
LIEDFGSLGBVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGBBBEBVASFSGQTLAGBLDNCVSSIPDFP MHLACPEBBDKATAAEMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDBLQBQPPDDLTLPEGCVVLETVGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESBTRAAVPKVTL CSBKRGLSLNSBEKLDSACLLKPREVVBFVVPKEPQNPPANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKRSGPLQGKGKPRAWARAWAAALKNSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVBADPTAVGPVLAGPVPVDPGLVDLASTSSELVBPLPA	5990	2	4700	
PRWGQSPPPQQRSDGBBEBEVASFSGQTLAGBLDNCVSSIPDPP MHLACPEBEDKATAAKMAVPAAGDESISSLSBLVRAMHPYCLPN LTHLASLEDBLQBQPDDLTLPEGCVVLETVGQAATAGDDLBIPV VVRQVSPGPRPVLLDDSLBTSSALQLLMPTLESBTBAAVPKVTL CSBKEGLSLNSEBKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKBSGPLQGKGKPRAWARAWAAALKRSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVBADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	1	1		-
MHLACPEEBDKATAAEMAVPAAGDES ISSLSELVRAMHPYCLPN LTHLASLEDBLQEQPDDLTLPEGCVVLETVGQAATAGDDLETPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETERAVPKVTL CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGEPRAWARAWAALKRSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	1		İ	
MHLACPEEBDKATAAEMAVPAAGDES ISSLSELVRAMHPYCLPN LTHLASLEDBLQEQPDDLTLPEGCVVLETVGQAATAGDDLETPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETERAVPKVTL CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGEPRAWARAWAALKRSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	Į.	1	1	PRWGQSPPPQQRSDGEBEEEVASFSGQTLAGELDNCVSSIPDFP
LTHLASLEDELQEQPDDLTLPEGCVVLEIVGQAATAGDDLEIPV VVEQVSPGPRPVILDDSLETSSALQLLMPTLESETEAAVPKVTL CSKKEGLSINSEKKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKBQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQSKGKPRAWARAWAAALKINSSPKN LKRSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	I	į.	1	
VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETRAAVPKVTL CSEKEGLSLNSEEKLDSACILKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKEQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALENSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	ſ	1	}	i e e e e e e e e e e e e e e e e e e e
CSEKEGLSLNSEEKLDSACILIKPREVVEPVVPKEPQNPPANAAP GSQRAKKGRKKKSKBQPAACVEGYARRIKSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALENSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	ſ	ĺ	1	
GSQRARKGRKKKSKBQPAACVEGYARALKSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALKNSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVBADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	ł	l	l	
QVDNLQKQPQRELQKESGPLQGKGKPRAWARAWAAALKNSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVKADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	j			
Lersagosspakegplolypkladtiqtnpipthlslvdsaqas pmpvdsvbadptavgpvlagpvpvdpglvdlastssblvbplpa				
PMPVDSVBADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA		!		
i i	1 '	1		
EPVLINPVLADSAAVDPAVVPISDNLPPVDAVPSGPAPVDLALV	1			1
	L	<u> </u>	<u></u> _	EPVLINPVLADSAAVDPAVVPISDNLPPVDAVPSGPAPVDLALV

Mo: molcotide location   corresponding   corresponding   corresponding   corresponding   cofirst   amino acid   amino ac	CPO I	Predicted	Predicted end	1 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
Mo:   mucleotide   location   corresponding to first   mino acid   residue of amino acid   residue of amino acid   residue of amino acid   sequence   se	SEQ			Amino acid segment containing signal peptide
Cocation   Corresponding   Cofirst   amino acid   Cofirst   amino acid   Cofirst   C		_ ,		
Courcesponding to first amino acid residue of amino acid residue of amino acid residue of amino acid equence   Sectine, T-Threonine, N-Valline, amino acid equence   Sectine, T-Threonine, N-Valline, amino acid equence   Sectine, T-Threonine, N-Valline, section of amino acid equence   Sectine, T-Threonine, N-Valline, section   Sectine, T-Threonine, N-Valline, section   Sectine, N-Threonine, N-Valline, section   Section, N-Vaposible nucleotide insertion)   Section, N-Vaposible nucleotide insertion   Sectine, T-Valline, section   Section, N-Vaposible nucleotide insertion   Section, N-Vaposible nucleotide insertion   Section, N-Vaposible nucleotide insertion   Section, N-Vaposible nucleotide insertion   Section, N-Vaposible nucleotide insertion   Section, N-Vaposible nucleotide insertion   Section, N-Vaposible nucleotide   Section, N-Vaposible nuc	NO:			
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid aequence  ##################################				
amino acid residue of amino acid sequence  sequence  amino acid sequence  amino acid sequence  amino acid sequence  better the colon, the possible mucleotide deletion, the colon, the possible mucleotide deletion, the colon, the colon, the colon and the colon, the colon and the colo			ľ	
mino acid mequence  ##TVyptopham, X-Tyxosime, X-Ukknown, *-Sto Codon, /-possible nucleotide deletide deletide deletide deletide		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence    Codo.,   -possible nucleotide detection,    -possible nucleotide insertion    DPFWROTTPYDPUNKSRYTDERGAVSGRIGGSAPOLLVES   DPFWROTTPYDPUNKSRYTDERGAVSGRIGGSAPOLLVES   RQRGASTERKSPQPFTGERUSSPTYTTGLADICT.VI PPAP.     RTALGRSDFTLERGUSPTSTYTGLADICT.VI PPAP.     RTALGRSDFTLERGUSPTSTYTGLADICT.VI PPAP.     RTALGRSDFTLERGUSPTSTYTSKAPPAPASCHAPP   PSQRAPTLARSPPUNGSVARAPPTPSSAPAGLAPPASCHAPP   PSQRAPTLARSPPUNGSVARAPPTPSSAPAGLAPPASCHAPP   PSQRAPTLARSPPUNGSVARAPPTPSSAPAGLAPPASCHAPP		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence    Codox, /-possible mucleotide insertion		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence   N=possible nucleotide insertion		amino acid	semence	
DPPFINDITEPDEPUNKSRPTDPREGGNISSALGGSRPGILIVES  LDPPTITITEPSVERSTATHERAPPENSLSERTE RQROABTERESQUPPICEURSI PRETPICIADICCIVI IPPAG  KTALQRSPETPLISICUTVPUPSPASPSPEPPVSKYVASSPITE PSGSPELIARDSPUTQSVSYNVETPPSRSAALPPAGGIGNE LPPPICOPPSILISMGPVLEDPFITYAPLESDPCYPRISPEG CLPPPICOPPSILISMGPVLEDPFITYAPLESDPCYPRISPEG CLPPPICOPPSILISMGPVLEDPFITYAPLESDPCYPRISPEG CLPPPICOPPSILISMGPVLEDPFITYAPLESDPCYPRISPEG CLPPPICOPPSILISMGPVLEDPFITYAPLESDPCYPRISPEG CLPPPICOPPSILISMGPVLEDPFITYAPLESDPCYPRISPEG CLPPPICOPPSILISMGPVLEDPFITYAPLESDPCYPRISPEG CLPSCOPPOLITION CONTROL OF	· {	semience	1	
DIPPTITIPEVREVUDELKTESGTSATTHEARPRPISLSEERER RQQRABTERERSPOPPTGKYBEADEPTFTGTALTVIPPAP KTALQRSDETPELSICLUPVGSDEASEPJBEPGTSVASSPJTE PSQEMELLARDSPPTGKYSEADEPTBYBCAUCHPP PSQEMELLARDSPPTGKYSEADEPTBYBCAUCHPP PSQEMELLARDSPPTGKYSEADEPTBYBCAUCHPPBYBCAUCHPP PSQEMELLARDSPPTGKYSEADEPTBYBCAUCHPPBYBCAUCHPPBYBCAUCHPPBYBCAUCHPPBYBCAUCHPPBYBCAUCHPPBAGCAUCHPPBYBCAUCHPPBAGCAUCHPPBYBCAUCHPPBAGCAUCHPPBYBCAUCHPPBAGCAUCHPPBYBCAUCHPPBAGCAUCHPPBYBCAUCHPPBAGCAUCHPPBAGCACHPPBAGCACHPPBAGCACHPPBAGCACHPPBAGCACHPPBAGCACHPPBAGCACHPPBAGCACHPPBAGCACHPPBAGCACHPPBAGCACHPPBAGCACHPPBAGCACHPPBAGCACHPPBAGCACHPPBAGCACHPPBAGCACHPPBAGCACHPPBAGCACHPBACACHPBACACHPBACACHPBACCACHPBACA				
RQROADSTERRISQUPTGKMPSLDPETPTGLADIDCTUT POR KTALGRSDETIGLELCUPVORDSASPRIPERPSKEVALSSPITE PSQEMELLARDSDPTQSVSDAVPTPDPBMSAALPPDROGLGMP LPPPPLQDPSLPLSKOFVLDPFTHTADLPSWPCYPHVSPGC CLPPPTVTUNSGTTGATAVPTPTSVPMAPPPSSTCT GPPBRVLPLSMPPLSGGTGGAPTCTETTVCVPTASPPSSTCT GPPBRVLPLSMPPLSGGTGGAPTCTETTVCVPTASPPSSTCT GPPBRVLPLSMPPLSGGTGGAPTCTETTVCVPTASPPSSTCT GPPBRVLPLSMPPLSGGTGGAPTCTETTVCVPTASPPSSTCT GPPBRVLPLSMPPLSGGTGGAPTCTETTVCVPTASPPSSTCT GPPBRVLPLSMPPLSGGTGGAPTCTETTVCVPTASPPSSTCT KPUSAGUAPPPSGGTGAPTCTASPASELAPETCTTTT KPUSAGUAPPPSGGTGAPTCTASTCASPSTCT GPPBRVLPLSMPPLSGGTGAPTCTASTCASPSTCT KVSALVQSPQMKALACVSAGCVTVERPASERLAPETCTTTT KPUSAGUAPPPSGGTARDSGTLARGGTTAPPPDGUMEP AVSLLAKAKSPKSTAQBGTLARGGTTAPPPDGUMEP AVSLLAKAKSPKSTAQBGTLARGGTVTAPPPDGUMEP AVSLLAKAKSPKSTAQBGTLARGGTVTAPPPPDGUMEP AVSLLAKAKSPKSTAQBGTLARGGTVTAPPPPDGUMEP AVSLLAKAKSPKSTAQBGTLARGGTVTAPPPPDGUMEP AVSLLAKAKSPCVARSTCASSPSSGGNARGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS				•
KTALGRSPETPLRICLUPVGPBASPBRPVSKEPVASPPAGGLAMP   PSGRMPLLARPSPWGVGVSPAVPTPBMSAALPPPAGGLAMP   LPPPPLQPPSLPPWGVSPAVPTPBMSAALPPPAGGLAMP   LPPPPLQPPSLPPWGVSPAVPTPBMSAALPPPAGGLAMP   LPPPPLQPPSLPPWGVSPAVPTPSWARPPAGVSPYSSGTG   GPBRWLPLSMRAPPLSIGLEGGAPGTETRVEWKEVPASSGTG   GPBRWLPLSMRAPPLSIGLEGGAPGTETRVEWKEVPASSGTG   GPBRWLPLSMRAPPLSIGLEGGAPGTETRVEWKEVPASSGTG   GPBRWLPLSMRALGVSSGCTVSRFASSKLAPSTGSTPH   KPPLPATRAVPTRGSTVPKLDAVHPARLRKLSFLOTFDSTPH   KPPLPATRAVPTRGSTVPKLDAVHPARLRKLSFLOTFDSTPH   KPPLPATRAVPTRGSTVPKLDAVHPARLRKLSFLOTFTGSTPH   KPPLPATRAVPTRGSTVPKLDAVHPARLRKLSFLOTFTGSTPH   AVSLLARAMS PSSTAGGGTLAGGGTSAKHPAPRLGGGVG   AVSLLARAMS PSSTAGGGTLAGGGTSAKHPAPRLGGGVG   AVSLLARAMS PSSTAGGGTLAGGGTSAKHPAPRLGGGVG   RVIVGSGDHPCVVRSRTPPKK\MPALLIPVGSRRNVKRHQ   AVSLLARAMS PSSTAGGGTLAGGGTSAKHPAPRLGGGVG   TIKPVISLGPAAPPPPC-LAGSREPLDBRTSSGQADPSAPCT-   TIKPVISLGPAAPPPPC-LAGSREPLDBRTSSGQADPSAPCT-   SFRRRSDSRRNVSSSGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	1			
PSGEMELLARPSPOYGSVSFANDPTPENGALLPPROGGLAM LPPP2LQPDSLPLKMBVLDDPTHYAPLPSWPCYPVSPSG CLPPPTVPLWSGTTGA7ANVPPTCSVPWARPPARVSPYSSTC GPPERVLPLSMBPLSLGLEGGAPOTETETVEWRPPDSSTC GPPERVLPLSMBPLSLGLEGGAPOTETETVEWRPPDSSTC GPPERVLPLSMBPLSLGLEGGAPOTETETVEWRPPDSSTC GPPERVLPLSMBPLSLGLEGGAPOTETETVEWRPPDSSTC GPPERVLPLSMBPLSLGLEGGAPOTETETVEWRPPDSSTC HEVSALVQSPQMKALACVSAGCVTVERPDSSELAPETGGTTET KPUPLATKAVPTPGGTVPVELAPALRIKLSFLTPTPTGS DVVQAPTSELGTERASDLSSILAGPEKSERAKECOPPEAPADRUMPE KPUPLATKAVPTPGGTVPVELAPADRIKLSFLTPTPTQS DVVQAPTSELGTERASDLSSILAGPEKSERAKECOPPEAPADRUMPE AVSILAKAKSPKSTAQBGTLKPEGVTSARVIDAGVTLQBGVHG RUIVGSGIHDYCVERSETPKK\NPALLIPSVGSRNNVERC GROGGUTPGERSPDDLANDGGTPGATPOHQUMPE AVSILAKAKSPKSTAQBGTLKPEGVTSARVIDAGVTLQBGVHG RUIVGSGIHDYCVERSERDENETSSGADDESAPCLA SLLSPBASPCRNNNTSTPPEESAKGRSKRCYRSACRSASPSS GROGGRGRIGNSGSVGSGNSTERSSGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS			1	The state of the s
LPPPTQPPSLPILSMGPVLTDPFTTYPALLSWGPTQSPWSPGS CLPPPTTUPEUVSGFTQATAMPPTGSVDPADPPSSYCE CLPPPTTUPEUVSGFTQATAMPPTGSVDPADPPSSYCE GPRSWILPISSADPSLIGLEGRGADVTEEPTTVETUREVPASHE EKWSLIVJSPQMKALACVSAGVTVEERSESERLKPETQETEUP KPLPATKAVPTPRGSTVPLLPAVHPARLRKLSFLFTRTGS UVVQAFISELTIEGISADLSSJLEGPKESSERKKECPPPAPADSLE KPLPATKAVPTPRGSTVPLLPAVHPARLRKLSFLFTRTGS GNSGGDLPQEKRPLDRLQAPELANVAGLTPPATTPPHQLMKP AVSLLAKAKSPSTAGAGTLKPEGVTSAKKECPPPAPADSLE GNSGGDLPQEKRPLDRLQAPELANVAGLTPPATTPPHQLMKP AVSLLAKAKSPSTAGAGTLKPEGVTSAKKECPPPAPADSLE KRIVGSGDHDYCVRSRTPPKK,WPALLIPRVSSRRNVERIO TIKPVISLIGAPAPPPCTAASSEPLDHETSARVLGGGVTS RVIVGSGDHDYCVRSRTPFKK,WPALLIPRVSSRRNVERIO TIKPVISLIGAPAPPPCTAASSEPLDHETSARVLGGGATS SLLSPEASPCRIMNTRTPPEPSAKGRSMRCYRKACRSASPS GMGRRGNRSRVSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS				-
CLPPPTVPLUSGTFRAYAWPPTCSVPRAPPPSSYSTC  GPIGMOFEGGUAPPHSTUPPPTLPPASICRAVPQEMESRGT  GPPENVLPLSMAPPSIGLPGHAPYGTTPTVEVKPVPASHER  EKVSALVQSPQMGALACVSAEGVTVERFASERIKPFTQEVRP  KPPLPATKAVVFTRGSTVPLAPHIPALAFISFLTFRTGOS  DVVQAFISELGIBASULSGJFRKSEAKKECPPPASADSL  GNSGGUDIPGKRPLDRIJQAPELANVGALFSFLTFRTGOS  DVVQAFISELGIBASULSGJFRKSEAKKECPPPASADSL  GNSGGUDIPGKRPLDRIJQAPELANVGALFSFLTPTGOS  RVIVGSGUDIPQCVQAFISETSCAKKECPPPASADSL  GNSGGUDIPGKRPLDRIJQAPELANVGALFSFRANVGRUDIP  AVSLLAKAKSPKSTAQBGTLKPBGVTSAKHIPAAVRLQEGVIGI  RVIVGSGUDIPQCVQAFRATERSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	j		J	PSQEMPLLARPSPPVQSVSPAVPTPPSMSAALPFPAGGLGMPPS
CPLIGNOPEG-QUAPPENT UPPPLIP PASTGRAY-POPPMES RET.  GPPENVLPLSHAPPLSIGLEQHGA-POTTEPTT VEW VPVPASPH  EKVSALVQS-PQMGALACVSARGVTVERFASERLK/PETTETTGS  DVVQAFISELIGEASULS-SILEGFEKESERLK/PETTETTGG-  DVVQAFISELIGEASULS-SILEGFEKESERLK/PETTETTGG-  GNGGGUD LPQEKPLDRIQAPELANVAGLTPPATPPHQLMKP-  AVSLLAKAKSP KSTAGGET LEGENVASKEC-PPPADADSLI-  RVIVGSCDHDVC\VRSRTPPKK\MPALLIPEVGSRNNVKRHQ-  RVIVGSCDHDVC\VRSRTPPKK\MPALLIPEVGSRNNVKRHQ-  TIKPVISLIGPAAPPPETAASREPLIDHETS-SEQADPESAPCLA-  SILSPEASPCKNIMMTRTP-PEPESARGRSMCYKARCRSASPS-  GMGGRGRNRSENVSGSSRNTSRASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS				LPPPPLQPPSLPLSMGPVLPDPFTHYAPLPSWPCYPHVSPSGYP
GPERNULPLINARPELICALCHIANOTEPTRYSTUKPUNDSHE EKVSALVQS-PQMKALACVSAGGVTVERPASERILKPEQPTPTTYG RPPLPATKAVUTERQSTUPKLPAVEPASERILKPEQTETTYG UVQAFISEIGIBASDLSGLEGFEKSEAKKECPPPARADSL GNSGGUDIPGKEPLDRIQAPELANVAGITATPHOLUMEN AVSLLAKAKSPKSTAQECTIKPEGUTSAKHIPAAVRIQEGVEG RVIVGSGUDIPGKEPLDRIQAPELANVAGITATPHOLUMEN TIKPVISIGPAPPPCTAASREPLDHETSSEQAPSAPCLA SLISPEASPCENDMYTETPEPPSAKORSHANSES GWGGREGNNSRSVSGSNRTSBASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS			1	CLPPPPTVPLVSGTPGAYAVPPTCSVPWAPPPAPVSPYSSTCTY
EKVSALVOS POMKALACVSARGOVTVEREPASERIAKPETQETEP KPPLPATKAVPTPRQSTVPKLPAVHPRALKUS FLPTPTRTQG DVVQAPTGETGIRASDISSLLEQFEKSEAKRECPP PAPADSL GNSGGVDI PQEKRELDRIQAPELANVAGIJTPEATHETPHQIMKEP AVSILLAKAKSPKSTAGGETLAKSGRUTSAKIPAAVRLQGGVIG RVIVGSGDHDYC\VESETPPKK\MPALLI PBVGSKRNVKRIQ TIRVUSLGAPAPPPETCHASREPELDRITSEQADPSAPCLA SLISPEASPCRROMNTETPERSAKQRSMECYEKACRSASPS: GMGRIGKRINSESSGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS				GPLGWGPGPQHAPFWSTVPPPPLPPASIGRAVPQPKMESRGTPA
EKVSALVOS POMKALACVSARGOVTVEREPASERIAKPETQETEP KPPLPATKAVPTPRQSTVPKLPAVHPRALKUS FLPTPTRTQG DVVQAPTGETGIRASDISSLLEQFEKSEAKRECPP PAPADSL GNSGGVDI PQEKRELDRIQAPELANVAGIJTPEATHETPHQIMKEP AVSILLAKAKSPKSTAGGETLAKSGRUTSAKIPAAVRLQGGVIG RVIVGSGDHDYC\VESETPPKK\MPALLI PBVGSKRNVKRIQ TIRVUSLGAPAPPPETCHASREPELDRITSEQADPSAPCLA SLISPEASPCRROMNTETPERSAKQRSMECYEKACRSASPS: GMGRIGKRINSESSGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS			İ	GPPENVLPLSMAPPLSLGLPGHGAPOTEPTKVEVKPVPASPHPK
RPPLANTKAVPTPRQSTVPKLANVHRILSPLEPTRYCG   DVVQAFISEIGIBADLSSILEQPEKSBAKKECPPPAPADGS    GNSGVDIPQEKRPLDRIQAPELANVAGJTPRATPHQLMKP    AVSLLAKAKSPRSTAQBGTLKPEGVTSAKHPAAVKLQGVVHG    RVINVGSDDDVC\URSETPPK\MPALIBEVGSRNIVKRRQ    TIKVVLSILAPAAPPPPCTAASRRPLDHRTSSQADPSAPCLA,   SLLSPPASPCRNDMYRTPPEFSAKQRSMECYRKACRSAFS:   GMGRIGNRSBVSSGSMTSEASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS			ŀ	
DVVQAFISEIGIRASDLSSLLEGPEKSEARKECPPPADADSL GNSGVDIPQEKRPLDRLQAPELANVAGITPPATPPHQLMKEP AVSLLAKAKSPKSTAGEGTIKPEGVTSAKHIPAAVRIQEGVHS RVIVGSGDHDYC\VBSRTPPKK\MPALLIBEVGSKRNYKERIQ TIRPVISLGPAAPPPECTLAASREPLIBTESBQADPSAPCLA SLISPEASPCRNDNYRTPPERSAKQRSMECYEKACRSASPS: GMGRIGHNSRUSSGSHRTSEASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS			j	
CINSGGUTI PQEKRELDRIADAPELANVAGI. PPATPPHOLIMEP AVSILIAKAKS PRSTAQEGTI-KPEGUTSAKIIPAAVRIQEGVHEI RVIVICSGORDOTC\VESRTPPKK\MPALLI PEWGSRMNVKRHQ TI KVVISIGPAAPPPCTAAGREPIDIRTSSEQADPSAPCIA. SILISPEAG CRUMMITTPPERSAKGRKYKRKORSASPS GWGGRIGHNSRSVSGSINTTSEASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS			ł	1
AVSILAKATE PRITAQECTILIPEGUYZAKIPAAVELQEGUYEE RVHVGSGDHDYC\VRSTPPKK\MPALLIPEVGSRMNVRHOL TIKVUSLOPAAPPPCTAASREPLHRITSSEQADPSAPCLA SILSPEASPCRNDMNTRTPPESAKQRSMRCKTRKACGSASPS GWGGRGGROSSEGSSESSESSESSESSESSESSESSESSESSESSESSE			l	, = <del>-</del>
RVIVGSGDHDYC\VBSRTPPRK\MPALLIPEVGSRMNVKRHQ TIKPVLSLGPAAPPPPCTAASREPLDHRTSSEQADPSAPCLA SLLSPBASPCRNDNYTETPSEPSARCSAMCTRKACRSASPS: GWGGRGNNSRSVGSGNNTSERSSSSSSSSSSSBSBSBSLS: HKRRRSSCSSGSRSRCSSSSSSSSSSSSSSSSSSSSBSRSSSSSSSSSS			1	
TIKPVI.SIGPAAPPPPCTAASRRPLDHRTSSSQADPEAPCTA SILSPEASPCRNDMNTRTPPEPSAKQRSMRCYRKACRSASPS: GMGGRAGINSRSVSGSINTTSRASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS			1	The state of the s
SLISPEASPCRNDMITTTPPEFSAKQRSMCYTRACRSASPS: GWGGRIGHNSRSVYSGSSMSTESASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS			1	
GWQGRGRRNSRYSGSSINTISEASSSSSSSSSSSSSSSRSRSRS HKRWRSSCSSGSRRRCSSSSSSSSSSSSSSSSSSSSSSRSRS PSPRRSSDRRRYSSYRSIDHYDRQRVLQKRRATEERRVVTI IPGRWTRSHLKQRFSVYGBIEBCTTHYBLQGDNYGFVTYRYA APAAIBSGHKLRQADEQPFDLCPGGRQPCKRSYSDLDSNREI DPAPVXSKPDSLDFDTLLKQAQKMLRR  5991 334 1379 RLSSHFSQCSPSIYC\TKPDKGGNVTSFBRKKTELYQBLGIQ DRFQHVMSITVRNNRIIMRMEYLKAVITPBCLLILDYRNIN GWLFRZLPSQLGSGCGJUTYPLPFEFRATBALLQYWINTLGG SILQPLILBYLDALGDPKRSSVDBSKLHILLQNGKSLSELET KIFKESILBYLDEBELLBELCYGKWSDDQVPEKSSAGIDHRAF ELLLENYYRLADDLSNARRELRVLIDDSQSIIFINLDSHRNV REMIQLIMGTFFSLSIFGIMGNASSIASSUBDQVPEKSSAGIDHRAF ELLLENYYRLADDLSNARRELRVLIDDSQSIIFINLDSHRNV REMIQSIMPATFSLSFIGK, MARSSIASSUBGNEHAFINLTY MPMSSGLINBRILSFIGK/LANSSIASSUBGNEHAFINLTY MPMSSGLINBRILSFIGK/LANSSIASSUBGNEHAFINLTY GVFFSILGTSILLNLGGIKLRAFUTIGNLALASTCFIMSPY QLKKMFEATRILATIVMLLCFIFTLCAALAWHKKGLAVLFCII FLEMTWYSLSYIPYARDAVIKCCSSLIS  5993 1650 594 ABGIGSNAVMAGIGNAGRMERGGATGALGWGCKLPSAFCFF SVAMDMEQRVEKIGBGTYGVVYKAKMRRTGQLVALKKTRLDLI BGYPSTAIRBISLLKELKHNIVRILDVUNINBRKLYLVFEFL DLKKYMDSTPGSELPHLIKSYLPQLLQGVSFCHSHRVIHKD PQNILINBELGAIKLADGGLARAFGVPLRTYTHEVVTLWYRAP LLATRFYTTAVDINSIGCIFABMYTRKALFPGDS\EIDQ\LFF RHLGTFSBUTWGGVTQLPDVKGSFPRNTRKGLBEIVPNLEFP RDLIMQLLQYDPSQRITAKTALAHPYFSSPPEPSPARQYVLQ FRHLGTFSBUTWGGVTQLPDVKGSFPRNTRKGLBEIVPNLEFP RDLIMQLLQYDPSQRITAKTALAHPYFSSPPEPSPARQYVLQ HREIANDSKPPEVEPDLGBKVBTEGRSBFILLPSRLIBPA PQPGILGAVTGPRKGGSRRNAWGQSYABLISQAIESAPERRI HNRATGKSSWWMINPEGGKGGKRAPRRASMDSSSKLIRGRSI PKKRPSSNASSVSTRLSPLRPBSVLABEITPASVSSYAGGVP LANGLELLLDGLMITSSHSLLSRSGLSGFSLGHPGVTGPHTTYS SLFSPAGGPLSAGGGCFSSSQALRALITSDTPPPPADVLMTQ LLRGLELLLDGLMITSSHSLLSRSGLSGFSLGHPGVTGPHTTYS SLFSPAGGPLSAGGGCFSSSQALRALITSDTPPPPADVLMTQ PLISQAPTTLLLGGLPSSSKLATGVGLCPPKPLBAPGPSSLVF PLISQAPTTLLLGGLPSSSKLATGVGLCPPKPLBAPGPSSLVF PLISQAPTTLLLGGLPSSSKLATGVGLCPPKPLBAPGPSSLVF PLISQAPTTLLLGGLPSSSKLATGVGLCPPKPLBAPGPSSLVF PLISQAPTTLLLGGLPSSSKLATGVGLCPPKPLBAPGPSSLVF PLISQAPTTLLLGGLPSSSKLATGVGLCPPKPLBAPGPSSLVF PLISQAPTTLLGGLPSSSKLATGVGLCPPKPLBAPGPSSLVF	•		l	
HKRWRRSSCSSGRSRRCSSSSSSSSSSSSSSSSSSSSSSSSS	1		Ī	SLLSPEASPCRNDMNTRTPPEPSAKQRSMRCYRKACRSASPSSQ
PSPRRRSDRRRYSSYRSHDHYQRORUQKRRAIERERVUFIA  IPGRMTRSHLKQRPSVPGBIERCTIHFVQGDNYGFUTYRYA APAAIBSGHKIRQADBQPPDLCFGGRRQFCKRSYSDLDSNRE  DPAPVASKFDSLDFDTTLKQAQKNIER  FRESHFSQCSPSIYC\TKFDKGGNVTSFBRKKTELYQBLGLQ) DLRRQHYMSITVRNNRIIMMMEVIKAVITPECLLILDYRINN QWLFRZLDSQLSGGGQLVTYPLPFERFAIRALLQYWINTICGS SILQPLILERILDALGDPKHSSVORDKHLILLQBGKSLSELETT KIFKESILRILDERELLEBLCVSKWSDPQVPRKSSAGIDHABI ELLLENYYRLADDLSNAARBLRVLIDDSQSIIFINLDSHRNV RLNLQLTMGTFSLSLFGLMGVAFGMNLESSLEEDHRIFWLITV MFMSSGLIMRRLLSFLGR/LARSSIASYGMKDNVHGGIVBGL SQQDDEBQGLTAQDSQINL/SEVLDASSLSFNTTLKWFAICF UKKMFSTRILLATIVWLLCFIFTLCAALWWHKKGLAVLFCII FLSMTWYSLSYIPYARDAVLYGSSLB  5993  1650  594 ABGIGSWAVWAGIGWAGRHDEAGGATGALGVGCKLPSAFCFFX SVAMDMFQKVEKIGBGTYGVVYKAKWRTGQLVALKKIRGLDL EGVPSTAIRSISLLKZKLKHUTULDVVENBERLLYLVFEFLS DLKKYMDSTPGSELPHLIKSYLFQLQGVSFCHSHRVIHRDI PQNILINELGAIKLADPGLARAFGVLRTTHEEVUTLWYRAPI LLATFFYTTAVDLWSIGGI FAPMVTEKALFPGDS \ETD\LFFRHLGTFSEDTWPGVQLDFSGSFRKERFOSS \ETD\LFFRHLGTFSEDTWPGVQLPDYKGSFPKWTRKGLEBIVPNLEPI RDLLMQLLQVDPSQRITAKTALAHPYFSSPEPSPARQVVLQI RH  5994  394  1934 AGGVQLHVWIRGMRIQPG/KAAAITDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPEVERDLEKKVHTERGESPILLPSRLDSRLDAFSKYFILLAGISHFYFSPCGIRGSCAGGCFSSGALFSGSFRKERABMSSSKILRGRSI PRKESSINASSWSTRLSPERSEVILABSILSALISAGRSIPHTSPVGSTRLBEADFR PKKPSGLPAPPEGATFTSPVGHRAWGSGS-CSRNRESADHFR PKKPSGLPAPPEGATFTSPVGHRAWGSGS-CSRNRESADHFR PKKPSGLPAPPEGATFTSPVGHRAWGSGS-CSRNRESADHFR PKKPSGLPAPPEGATFTSPVGHRAWGSGS-CSRNRESADHFR PKKPSGLPAPPEGATFTSPVGHRAWGSGS-CSRNRESADHFR PKKPSGLPAPPEGATFTSPVGHRAWGSGS-CSRNRESADHFR PKKPSGLPAPPEGATFTSPVGHRAWGSGS-CSRNRESADHFR PKKPSGLPAPPEGATFTSPVGHRAWGSGS-CSRNRESADHFR PKKPSGLPAPPEGATFTSPVGHRAWGSGS-CSRNRESADHFR PKKPSGLPAPPEGATFTSPVGHRAWGSGS-CSRNRESADHFT SLESPAGEPLSAGEG-CFSSGALARLLISTSPTPPPADAUTHTY SLESPAGEPLSAGEG-CFSSGALARLLISTSPTPPADAUTHTY SLESPAGEPLSAGEG-CFSSGALARLLISTSPTPPADAUTHTY SLESPAGEPLSAGEG-CFSSGALARLLISTSPTPPADAUTHTY SLESPAGEPLSAGEG-CFSSGALARLLISTSPTPADAUTHTY SLESPAGEPLSAGEG-CFSSGALARLISTSPTPADAUTHTY SLESPAGEPLSAGEG-CFSSGALARLITSPTPADAUTHTY SLESPAGEPLSAGEG-CFSSGALARLITSPT-CSSTAT-CHICKTORD PLISQAPTILLLGGLBSS			ļ	GWQGRRGRNSRSVSSGSNRTSEASSSSSSSSSSSRSRSRSLSPP
IPGRMTRSHLKQRFSVFGBIEBETTHFRVQGDNYGFVTYRYA APAAIBSGHRIAQABQPPDLCFGGRRQFCKRSYSDLDSNREI DPAPVASKPDSLDFDTLLKQAQKNLER  5991 334 1379 RLSSHFSQCSPSIYC\TKFDKQGNVTSFERKKTELYQBLGLQ DLRFQHYMSITVRNNRIIMMBYLKAVITBECLLILLDYRNIAN (MLFRSLFSQLSGEGOLVTYPLPFEFRATBALLQYNINTLQS) SILQPLILBTLDALGDPKHSSVDRSKLHILLQNGKSLSELET KIFKESILRILDERELLEBLCVSKWSDPQVFEKSSAGLDHAB: ELLLENYYRLADDLSNAARBRUVLIDDSQSIFFINLGSHRNV RLNLQLTMGTFSLSIFGLMGVAFGMNLESSLEEDHRIFWLITM MPMGSGLIWRRLLSFLGR/LARSSIASYGMKONVHGGIVEGI  5992 2 609 AGPDPRIVCGVSGSFPGGGGGGGATBWRPLRFRPWNGAMBKLR SGQDDEBQGITAQDSQINL/SEVLDASSLSFNTRLKWFALCF GVFFSILGTGLLMIPGGIKLFAVFYTLGNLAALASTCFIMGP QLKKMFSATRLLATIVMLLCFITLCAALMWHKKGLAVLFCII BGVPSTALRSISLLATLKHENTITLCAALMWHKKGLAVLFCII BGVPSTALRSISLLKALKHENTURLLDVVHNKEKLLVVFBFL DLKKYMDSTGSEIPHLIKSYLFQLLGGVSFCHSHRVIHRDI PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPI LLATTFYTTAVDINSTGCIFARMYTKALFPGDS\EIDQ\LFF FRMLGTFSEDTWPSVTQLPDYKGSFPKNTRKGLBETUPNLRF RH  5994 394 1934 AGBVQLHVWIRGMELOPQ/KABATIDLDPDFFPGSRPSCTWI RH  5994 AGBVQLHVWIRGMELOPQ/KABATIDLDPDFFPGSRPSCTWI PQPGILGAVTGPKKGGSRNAMGNOSYABLISGAIESPKRIEPP PQPGILGAVTGPKKGGSRNAMGNOSYABLISGAIESPKRIEPP PQPGILGAVTGPKKGGSRNAMGNOSYABLISGAIESPKRIEPP PKKPSGLPAPPBGATTFSVPRKGGFSFLGHEGVYGPLHTMYS PKRYSSSNASSVSTRLSPLRPBSSVLABEIPASVSSYAGGVP LNBGLELLDGLNITSSHSLLSRGSLGSFLGHEGVYGPLHTMYS SLESPAGGPLSAGGGCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGGCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGGCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGGCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGGCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGGCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGGCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGGCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGCCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGCCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGCCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGCCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGCCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGCCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGCCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGCCCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGCCCSSGALARLITSDTPPPADUTMYG SLESPAGGPLSAGGCCCSSGALARLITSDTPPADUTMYG SLESPAGGPLSAGGCCTSSGALARLITS	-			HKRWRRSSCSSSGRSRRCSSSSSSSSSSSSSSSSSSRSRSRS
APAAIBSGHKIRQADBQPFDLCPGGRRQFCKRSYSDLDSNREI DPAPVKSKPDSLDFDTLLKQAQKNIER  75991 334 1379 RLSSHFSCCSPSIYCYTKPDKGGNYTSFBRKKTELYQBLGIQI DLRFQHVMSITVRNNRIIMRMEYLKAVITPBCLLILDYRNINI QMEPRILPSQLSGBSQLVTYPLPFBFRAIBALLQWHINTIQGI SILQPLILBTLDALGDPKHSSVDRSKLHILLQMKSLSELETI KIPKESILPILDERELLBELCVSKWSDPQVPEKSSAGIDHABI ELLLENYYRLADDLSNAAREREVLIDDEGSIIPINLDSHRNV RLNIQLTMGTPSLSIFFGWAFGMNLESSLEEDHRIFWIITT MFMGSGLIWRRLLSFLGR/LARSSIASYGMKDMVHGGIVEGL 5992 2 609 AGPDFRLVCGVSGSGFPGGRGQATEWRPLRFWNGAMEKLRR SGQDDEBGGLTAQDSQINI/SRULDASSISPMTRLKWFAICF GVFFSILGTGLIMLPGGIKLPAVPYTIGALAALASTCPIMGP QLKKMFEATRILATIVMLLCTIFTLCAALWHKKGLAVLFCII FLSMTWSLSIYIPARDAVIKCCSSLLS 609 AEGIGSWAVWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFP SVAMDMPQKVEKLGGGTYGVVYXKAKRATGQUALKKKIRLDL EGVPSTAIRBISLLNELKHPNIVRILDVVHNRRKLYLVFEFL DLKKYMDSTPGSELPLHLIKSYLPQLLQGVSFCHSHRVIRRD PQNILINELGAIKLADGGLARAFGUPLRTYTHEVVTLWYRAPP 1LAATRFTTAYDINSIGGIFABMVTRKALFFODS\EIDQ\LFP FRNLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLBPI RDLHMQDLQUDGYDPSGRITAKTALAHPYFSSPERFSPAARQVVLQI RH 5994 394 1934 AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWI RH 65991 AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWI PREIANQPSKPPSUPDLGEKUHTGRSEPILLDSRLDERPA PQPGILGAVTCPPRKGGSRRNAWGNGYABLISQAIERSAPKRI LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWMMINFEGGKSGKGRARRAASMDSSSKLLKGRSI PKKKPSGLPAPPBGAATFSPVGHTRAKWSGSPCSRNREBADMW FRPRSSSNASSVSTRLSPLRPBSEVLABEIPASVSSYAGGVPI LNRGLELLDGINLTSSHSLLSRSGLSGFSLQHFGVIFFHITY SLFSPASGPLAAFGSCSSKLATGVGLCPKPLBAPGPSSLVP; SLFSPASGPLAAGEGCYSSQALRALLTSDTPPPPADVIMTOQ PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLBAPGSSSLVP;				PSPRRSDRRRRYSSYRSHDHYQRQRVLQKERAIEERRVVFIGK
DPAPVKKPDSLDPDTLLKQAQKNLRR  5991  334  1379  RLSSHFSQCSPSIYC\TKFDKQGMYTSFRRKKTELYQBLGLQD DLRRQHWBITVRNRNI IMRMEYLKAVITPBCILLILDYRNINI QMLFRSLPSQLSGRGQLVTYPLPFFFRATEALLQYMINTLQS SILQPLILBTLDALGDPKHSSVDBSKLHILLQNGKSLSELBTI KIFKESILRILDERELLSBECVSKWSDPQVPKSSAGIDHAE ELLLENYYRLADDLSNAARELRVLIDDEQSIIFINLDSHRNVI RENIQLTMGTTSISIFGIMGVAFGMILESSLEBGHRIFMIITI MFMGSGLIWRRLSFIGR/LARSSIASYGMKDMYHGGIVEGL  5992  2  609  AGPDFRLVCGVSGSGFFGGRGGATEWRPLRPWNGAMEKLRR GVFFSILGTGLLWLPGGIKLPAPYFILGNLAALASTCFIMGP QLKKMFBATRILATIVMLCTFTICAALMWHKKGLAVLFCII FLSMTWYSLSTIPVARDAVIKCCSSLLS  5993  1650  594  ABGIGSWAVWAGLGWAGRHEGAGATGALGVGCKLPSAFCFF SVAMDMFQKVEKIGGGTGVYYKAKNRTGGDVALKKIRLDLL EGVPSTAIRBISLLKELKHPNIVRILDVVHNERKLYLVFEFL DLKKYMDSTFGSELPLHILKSYLFQLLGGVSFCHSHRVHRDI EGVPSTAIRBISLLKELKHPNIVRILDVVHNERKLYLVFEFL DLKKYMDSTFGSELPLHILKSYLFQLLGGVSFCHSHRVHRDI LLATRFYTTAVDIWSIGCIPAEMVTRKALFPGDS\EIDQ\LFF FRNLGTTSEDTWPGVTQLPDYKGSFPKWTRKGLEELVPALREP CDLIMQLLQYDPSQRITAKTALAHPYFSSPEFSPAARQVVLQI RH  5994  394  1934  AGBVQLHWHIRGMKIQPG/KAAATIDLDPDFEPQGRPRSCTM PRPEIANQPSKPPEVEPDLGKVWTEGRSEPILLPSRLPEPA PQPGILGAVTGPRKGSGRRNAWGNGSYABLISQAIESAPEKRI LAQIYEMMVRTVPYFKDKGDSNSSAGWKNSIRHNISHISKT HNRATGKSSWMINNFEGKSGKAPRRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATTFSPVGHFAKWSGSPCSRNREEADMW FRPRSSNASSVSTRLSPLRPESEVLABSIPASVSSYAGGVPI LNRGLELLDGINLTSSHSLLSRESIGGFSLQHFGVIFFHITT SLESPARGFIJSAGGEGGSSSQALRALLTBJTPPPPADVIMTQU FILSQAPTLLLLGGLPSSKLATGVGLCPKPLBAPGPSSLVP			ľ	IPGRMTRSELKQRFSVFGBIEECTIHFRVQGDNYGFVTYRYAEB
DPAPVKKPDSLDPDTLLKQAQKNLRR  5991  334  1379  RLSSHFSQCSPSIYC\TKFDKQGMYTSFRRKKTELYQBLGLQD DLRRQHWBITVRNRNI IMRMEYLKAVITPBCILLILDYRNINI QMLFRSLPSQLSGRGQLVTYPLPFFFRATEALLQYMINTLQS SILQPLILBTLDALGDPKHSSVDBSKLHILLQNGKSLSELBTI KIFKESILRILDERELLSBECVSKWSDPQVPKSSAGIDHAE ELLLENYYRLADDLSNAARELRVLIDDEQSIIFINLDSHRNVI RENIQLTMGTTSISIFGIMGVAFGMILESSLEBGHRIFMIITI MFMGSGLIWRRLSFIGR/LARSSIASYGMKDMYHGGIVEGL  5992  2  609  AGPDFRLVCGVSGSGFFGGRGGATEWRPLRPWNGAMEKLRR GVFFSILGTGLLWLPGGIKLPAPTYTLGNLAALASTCFIMGP QLKKMFBATRILATIVMLCTFTTLCAALMWHKKGLAVLFCII FLSMTWYSLSTIPVARDAVIKCCSSLLS  5993  1650  594  ABGIGSWAVWAGLGWAGRHEGAGATGALGVGCKLPSAFCFF SVAMDMFQKVEKIGGGTGVYYKAKNRTGGDVALKKIRLDLL EGVPSTAIRBISLLKELKHPNIVRILDVVHNERKLYLVFEFL DLKKYMDSTFGSELPLHILKSYLFQLLGGVSFCHSHRVHRDI EGVPSTAIRBISLLKELKHPNIVRILDVVHNERKLYLVFEFL DLKKYMDSTFGSELPLHILKSYLFQLLGGVSFCHSHRVHRDI LLATRFYTTAVDIWSIGCIPAEMVTRKALFPGDS\EIDQ\LFF FRNLGTTSEDTWPGVTQLPDYKGSFPKWTRKGLEELVPALREP CDLIMQLLQYDPSQRITAKTALAHPYFSSPEFSPAARQVVLQI RH  5994  394  1934  AGBVQLHWIKGMKIQPG/KAAATIDLDPDFEPQGRPSSCTM PRPEIANQPSKPPEVEPDLGKVHTEGRSEPILLPSRLPEPA PQPGILGAVTGPRKGSGRRNAWGNGSYABLISQAIESAPEKRI LAQIYEMMVRTVPYFKDKGDSNSSAGWKNSIRHILSHEKPII HNRATGKSSWMINNFEGKSGKAPRRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATTFSPVGHFAKWSGSPCSRNREEADMW FRPRSSNASSVSTRLSPLRPESEVLABSIPASVSSYAGGVPI LNRGLELLDGINLTSSHSLLSRESIGGFSLQHFGVIFFHITT SLESPARGFIJSAGGEGGSSSQALRALLTBJTPPPPADVIMTQU FILSQAPTLLLLGGLPSSKLATGVGLCPKPLBAPGPSSLVP				AFAATESGHRLROADEOPFDLCFGGRROFCKRSYSDLDSNREDF
S991   334   1379   RLSSHFSQCSPSIYC\TKFPKQGNVTSFERKKTELYQELGLQD   DLRFQHYMSITVRNNRIIMRMYLKAVITPECLILILDYRNLNN   QMLPRSLPSQLSGEGQLTYPPLPYEFRATEALLQYMINTIQG   SILQPLILBTLDALGDYRHSSVDRSKLHILLQNGKSLSELETT   KIFKESILBILDALGDYRHSSVDRSKLHILLQNGKSLSELETT   KIFKESILBILDALGDYRHSSVDRSKLHILLQNGKSLSELETT   KIFKESILBILDALGDYRHSSVDRSKLHILLQNGKSLSELETT   KIFKESILBILDALGDYRHSSVDRSKLHILLGNGKSLSELETT   KIFKESILBILDALGDYRHSSVDRSKLHILLGNGKSLSELETT   KIFKESILBILDALGDYRHSEVDLRGVBRENDYR   RLMIQLIMGTSLSILBELGHRIFWLIT   MFMGSGLIWRILLSFLGR/LARSSIASYGMKDMVHGGIVEGL   SQUDEBGLITAQDSQINI/SRVLDASSIASYMTRKMPATCF   GVFFSILGTGLLWLPGGIKLPAVPYTLGNLAALASTCFIMGP   QLKKMFERTRILATIVMLCTIFTLCAALMWHKKGLAVLPCI   FLSMTWYSLSYIPYARDAVIKCCSSLLS   GEGIGSWAVWAGLGWAGRHMERGGATGALGVGCKLPSAFCFF   SVAMDMFQKVEKIGBGTYGVVYKAKMRSTGQLVALKKIRLDLJ   BGVPSTAIRBISLLKBLKHPNITVRILDVHNBRKKLYLVFFEL   DLKKYMDSTFGSELPHILIKSYLPQLLQGVSFCHSRVIHRD   PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAP   LLATRFYTTAVDINSIGCIFAEMVTRKGLEEIVPNLBP   FRNLGTPSEDTWPGVTQLPPYKGSFPKWTRKGLEEIVPNLBP   FRNLGTPSEDTWPGVTQLPPYKGSFPKWTRKGLEEIVPNLBP   FRNLGTPSEDTWPGVTQLPPYKGSFPKWTRKGLEEIVPNLBP   FRNLGTPSEDTWPGVTQLPPYKGSFPKWTRKGLEEIVPNLBP   FRNLGTPSEDTWPGVTQLPPYKGSFPKWTRKGLEEIVPNLBP   PQPGILGAVTGPRKGGSRRNAWGNGYAELISQAIESAPEKRI   LAQIYEMMVRTVPYFKDKGGSRRNAWGNGYAELISQAIESAPEKRI   LAQIYEMMVRTVPYFKDKGGSRRAPRRRAASMDSSSKLLRGRSI   PKKKPSGLPAPPBGATETSPVGHFAKWSGSPCSRNREEADMW   FRPRSSNASSVSTRLSPLRPBSEVLAEBIPASVSSYAGGVPI   LNGLELLDGINLTSSHSLLSRESLGGFSLGHPGVTGPHITY   SLPSPAEGPLAGGEGSSSQALRALITSDTPPPPADVIMTQ   LNRGLELLDGINLTSSHSLLSRESLGGFSLGHPGVTGPHITY   SLPSPAEGPLAGGEGSSSSQALRALITEDTPPPPADVIMTQ   PILSQAPTLLLLGGLPSSKLARGVGLCPKPLEAPGPSSLVP				1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DLRFQHYMSITVRNNRIIMRMEYLKAVITPECLLILDYRNIM  QWLFRELPSQLSGEGGLVTTPLPFFFRAIRALLQWMINTLQGI SILQPLILETLDALEOPKHSSUNDRSKLHILLQNGKSLSELETH KIFKESILEILDEBELLEBLCVSKWSDPQVFEKSAGIDHAEI ELLLENYYRLADDLSMAARRELYLIDDSQSIIFINLDSHRNVI RLNLQLTMGTFSLSILFGLMGVAFGMNLESSLEEDHRIFWLITY MFMCSGLLWRRLLSTLGR/LARSSLASYGMNDWIGGIVEGL  S992 2 609 AGPPPRLVCGVSGSGFPGGRGGQATEWRPLEPWNGAMEKLRR GVFSSILGTGLLWLPGGIKLPAVPYTLGNLAALASTCPFLMGPY QLKKMFEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLFCII PLSHTWYSLSYIPYARDAVIKCCSSLLS  S993 1650 594 AEGIGSWAWAGIGWAGREWERAGGATGAGGCKLPSAFCFP SVAMDMFQXVEKIGBGTYGVVYKAKNRETGQLVALKKIRLDLI EGVPSTATREISLLKELKHENIVRILDVVHNBRKLYLIVFEFTL DLKKYMDSTPGSELPHLIKSYLFQLLQGVSFCHSHRVIHRDI PQNILINELGAIKLADPGLARAFGVPLRTYTHEVVTLWYRAP LLATTFYTTAVDIWSIGCIFADWYTKALFFGDS\BIDQLFF RRLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLRPI RDLLMQLLQYDPSQRITAKTALAHPYPSSPEPSPAARQVVLQI RH  AGBVQLHWWIRGMRIQPO/KAAAIIDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPEVEPDILGEKWHTEGRSEPILLPSRLPEPA PQPGILGAVTGPRKGGSRRNAWGNGSYABLISQAIESAPEKRI LAQIYEMWYRTVPYFKDKGDSNSAGKWNSIRHNISLIHSKFII HNRATGKSSWWMLNPEGGRSGKAPRRAASMDSSSKLLRGRSI PKKRPSGLPAPPEGATPTSPVGHFAKWSGSFCSRRREADMW FRPRSSNASSVSTRLSPLRPBSBVLABEIPASVSSYAGGVPI LNGLIELLDGLNITSSHSLLSRSGLGGFSLQHPGVTGPLHTYS SLPSPREGFPLSAGEGGFSQALRALITSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSQALRALITSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSQALRALITSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSCALRALITSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSCALRALITSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSCALRALITSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSCALRALITSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSCALRALITSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSCALRALITSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSCALRALITSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSCALRALITSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSCALRALITSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSCALRALITSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSCAGARLATSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSSQALRALITSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSSQALRALITSDTPPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSCAGRATATSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSCAGARTATSDTPPPPPADVLMTQU SLPSPREGFPLSAGEGGFSCAGARTATSDTPPPPADVLMTQU SLPSPREGFPLSAGEG	5991	334	1379	
QMLPR3LPSQLSGEGQLVTYPLPFEFRATEALLQYWINTLQGS SILQPLILBTLDALGDPKHSSVDRSKLHILLQMGKSLSSLETT KIFKESILBILDBELLBELCVEKWSDPQVFEKSSAGIDHAE ELLLENYYRLADDLSNAARELRVLIDDSQSIIFINLDSHRNV RIMLQLTMGTFSLSLFGIMGVARGMNLESSLEEDHRIFHIIT MFMGSGLIWRRLLSFIGR/LARSSIASYGMKDMVHGGIVEGL AGPDFRLVCGVGSGSGFPGGRQGATEWRPLRPWNGAMEKLRR SGQDDEBQGLTAQDSQINL/SEVLDASSLSFNTRLKWFAICF GVFFSILGTGLLMLPGGIRLFAVYTTLGNLAALASTCFFMGP QLKKMFEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLPCII PLSMTWYSLSYIPYARDAVIKCCSSLLS SPHAENTYSLSYIPYARDAVIKCCSSLLS SUMMMPCQXVEKIGBGTYGVVYXKAWRETGGLVALKKIRLDLI EGVPSTATREISLLKELKHEPINTURLDVYMBERKLYLVFFFLY DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDI FRMLGTFSEDTWPGVTQLFAEWTRKALFPGDS\BIDQ\LFF RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQI RH  SPHEIANQPSKPPEVEPDLGEKKVHTEGRSEPILLPSRLPEPAA PQPGILGAVTGPRKGGSRRNAWCNQSYAELISQAIESAPEKRI LAGIYEMWVRTVPYFKDKGDSNSAGWKNSIRHNISLHISKFII HNRATGSSSWMMINPEGGRSGRAPRRAASMDSSSKLLRGRSI PKKRPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNRERADMF FRRRSSSNASSVSTRLSPLRPBSEVLARETEASVSSYAGGVPI LNGGLELLDGLNITSSHSLLRRSGLSGFSLQHPGVTGPLHTYS SLPSPRESBYLSAGEGCFSSSQALRALITSDTPPPPPADVIMTQ PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPPGSSLVP			1	
SILQPLILETLDALGDPKHSSVDRSKLHILLQNGKSLSELETT KIFKESILETLDERELLEBLCVSKMSDPQVFEKSAAGIDHAE ELLLENYYRLADDLSNAARELRVLIDDSQSIIFINLDSHRNVI RINLQLTMGTFSLSIFGIMGVAFGMNLESSLEBEHRIFWILIT MFMGSGLIWRRLLSFLGR/LARSSIASYGMKDNVHGGIVEGL S992 2 609 AGPDFRLVCGVSGSGFPGGGGGGGATEWRPLRPWMGAMEKIRR GVFFSILGTGLLWLPGGIKLFAVFYTIGNLAALASTCFLMGP QLKKMFEATRLLATIVMLLCFIFTLCAALWHKKGLAVIPCII FLSMTWYSLSYIPYARDAVIKCCSSLLS S993 1650 594 AEGLGSWAVWAGIGWAGTHAEAGGATGALGVGCKLPSAFCFP SVAMDMPQKVEKIGEGTYGVYYKAKMRETGQLVALKKIRLDLI EGVPSTAIRBISLLKELKHPNIVRILDVVHNERKLYLVFEPLS DLKKYMDSTPGSELPHHIKSYLPQLLQGVSFCHSHRVHRDI PQNILINELGAIKLADFGLARAPGVPLRTYTHEVVTLWYRAPI LLATTFYTTAVDIWSIGCIFAEMUTRKALFPGDS\EIDQ\LFF FRNLGTPSEDTWPGVTQLPDYKGSPPKWTRKGLEBIVPNLEPH RDLLMQLLQVDPSQRTTAKTALAHPYFSSEPSPAARQVVLQI RH AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPSSCTWI PRPEIANQPSKPPEVEPDLGKKVHTEGRSEPILLPSRLPEPAG PQOGILGAVTGPKGGGSRRNAWGNGYABLISQAIBSAPEKRI LAQIYEMWVRTVPYFKDKGGSRKNASGWKNSIRHNLSLHSKFII HNRATGKSSWWHINPEGGKSGKRRASMGSSSGKLKSLERSPI PKKKPSGLPAPPEGATPTSPVGHPAKWSGSPCSRNREEADMWT FRPRSSSNASSVSTRLSPLRPESKVLABEIPASVSYAGGVPI LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLESPAGGFLSAGGGCCSSSQALRAILITSSTPPPPADVIMTQU PILSQAPTLLLLGGLPSSSKLARTGVGLCPKPLBAPGPSSLVP			1	II
KIPKESILRILDEBELLEBLCVSKWSDPQVPEKSSAGIDHAE  ELLLENYYRLADDLSNARRERVILIDBGGSIIFINLDSHRNVI  RINLQLTMGTFSLSIFGLMGVAFGMNLESSLERDHRIFWLITT  MFMGSGLIMRRLLSFIGR/LARSSIASYGMKONVHGGTVEGL  5992 2 609 AGPDFRLVCGVSGSGPFGGRQGATEWRPLRPWNGAMEKLRR  GUFFSILGTGLIMLPGGIKLPAVPYTLGNLAALASTCFIMGP  QLKKMFEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLPCII  FLSMTWYSLSYIPVARDAVIKCGSSLES  5993 1650 594 ABGIGSWAVWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFF  SVAMMPGDAVEKIGETYGVVYKAKNRTGQLVALKKIRLDLI  EGVPSTAIRBISLLXELKHPNIVRLLDVHNBERKLYLVFEFL  DLKKYMDSTPGSELPLHIKSYLPQLLQGVSFCHSHRVIHRDL  EGVPSTAIRBISLLXELKHPNIVRLLDGVSFCHSHRVIHRDL  PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPI  LLATTFYTTAVDINSIGCIFAEWVTRKALFEGDS\EIDQ\LFF  RDLLMQLLQJVDPSQRITAKTALAHPYPSSPEPSPAARQYVLQI  RH  5994 394 1934 AGEVQLHVWIRGMKLOPO/KABAIIDLDPDFEPQSRPRSCTWI  PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAG  PQPGILGAVTGPRKGGSRRNAWGNQSYABLISQAIESAPEKRI  LAQIYEMMVRTVPYFKDGSNSSAGWKNSIRHNLSLHSKFI  HNRATGSSWWMILNPEGGKSGKAPRRAASMBSSKLLRGRSI  PKKRPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWT  FRPRSSSNASSVSTRLSPLRPBSEVLABEIPASVSYARGVVPI  LINGLELLDGLNLTSSHSLLSRGGLGSFSLQHPGVTGPLHTYS  SLPSPAGGHLSAGEGCFSSSQALBALLTSDTPPPPADVILMTQ  PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP			· .	1 .
ELLLENYYRLADDLSNAARELRVLIDDSQSIFFINLDSHRNVI RENIQLTMGTFSLSIFGUMGVAFGMNLESSLEEDHRIFWILTT MFMGSGLIWRRLLSFIGMCVAFGMNLESSLEEDHRIFWILTT MFMGSGLIWRRLLSFIGMCVAFGGOATEWRPLRPWMGAMEKIRR SGQDDEEQGLTAQDSQINL/SRVLDASSLSFNTRLKWFAICF GVFFSILGTRGLLNURGGIKLFAVPYTLGNLAALASTCFIMGP QLKKMFEATRLLATIVMLLCFIFTLCAALWMHKKGLAVLPCI FLSWTWYSLSYIPVARDAVIKCGSSLES 5993 1650 594 AEGLGSWAVWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFFX SVAMDMFQXVEKIGBGTYGVVYKAKNRETGQLVALKKIRLDLI EGVPSTAIRRISLLKELKHPNIVRILDVVHNEKRLYLLVFEFL DLKKYMDSTPGSELPHLIKSYLFQLLQGVSFCHSHRVIHRDI PQNILLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFF RRLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLRFI RDLLMQLLQYDPSQRITAKTALAHPYPSSPEPSPAARQYVLQI RH  5994 394 1934 AGBVQLHVWIRGMRIQPQ/KAAATIDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPSVEPDLGEKVHTEGRSEPILLPSRLPEPA PQPGILIGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRI LAQIYEWMVRTVYYFKDKGDSNSSAGWKNSIRNISLHSKFII HNRATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWT FRRSSSNASSVSTRLSFLRPSESVLAREIPASVSSYAGGVPI LNBGLELLDGLNITSSHSLLSREGLSGFSLQHPGVTGPLHTYS SLFSPAEGFLSAGEGCFSSSQALRALLTSDTPPPPADVILMTQI PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP				
RINIQLTMGTFSLSIFGLMGVAFGMNLESSLEEDHRIFWLTTG MFMGSGLIWRRILSFIGR/LARSS LASYGMKDMVHGGTVEGL  5992 2 609 AGPDFRLVCGVSGSGFPGRGGATEWRPLRPWNGAMEKLRN GQDBEQGLTAQDSQINL/SRVLDASSLSPMTRLKWFAICF GVFFSILGTGLLWLEGGIKLPAVFTTIGNLAALASTCFIMGPY QLKKMFEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLPCII FLSWTWYSLSYIPYARDAVIKCCSSLIS  5993 1650 594 AEGLGSWAWAGIGWAGRHEAGGATGALGVGCKLPSAFCFPX SVAMDMFQKVEKIGBGTYGVVYKAKMRETGQLVALKKIRLDLII BGVPSTAIRRISLLKELKHENIVRILDVYNBERKLYLVFEFLS DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDI PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPI LLATRFYTTAVDIWSIGCIPAEMVTRKALFPGDS\EIDQ\LFF RRLGTPSEDTWPGVFQLPDYKGSFPKWTRKGLEEIVPNLEPI RDLLMQLLQVDPSQRITAKTALAHPYFSSPEPSPAARQYVLQI RH  5994 394 1934 AGEVQLHVWIRGMRIQPQ/KAAAITDLDPDFEPQSRPRSCTWI PQPGILGAVTGPRKGGSRRNAWGNQSYABLISQAIESAAPEKRI LAQTYEWMVRTVPYFKDKGDSNSAGWKNSIRHNLSLHSKFII HNEATGKSSWWMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATPTSFVGHFAKWSGSPCSRNREEADMW FRPRSSSNASSVSTRLSPLRPESKVLABEIPASVSSYAGVPI LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLFSPAEGPLSAGECCFSSSQALRALLITSDTPPPPPADVIMTQ PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP			1 .	1
MFMGSGLIWRRILSFIGR/LARSSIASYGMKDMVHGGIVEGI  5992 2 609 AGPDERLYCGYGSGSFFGGRGGATBWRPLRPWNGAMBKIRR: GUFFSILGTGLLWLPGGIKLPAVPYTLGNLAALASTCFIMGPY QLKKMFEATRILATTVMLLCFIFTLCAALWWHKKGLAVLFCII FLSMTWYSLSYIPYARDAVIKCCSSLLG  5993 1650 594 ABGIGSWAVWAGIGWAGRHWEAGGTGALGVGCKLPSAFCFW SVAMDMFQKVEKIGGTYGVVYKAKMRETGQLVALKKIRLDLJ EGVPSTAIRRISLLKELKHPNIVRILDDVHNBRKLYLVFBFLS DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDI PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPI LLATTFYTTAVDINSIGCIFAEMVTRKALFFGDS\EIDQ\LFF FRNLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLRPI RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQI RH  5994 394 1934 AGEVQLHVWIRGMRIQPQ/KAAAITDLDPDFEPQSRPRSCTWI PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIRSAPKRI LQTYEMWVETVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNBATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATPTSFVGHFAKWSGSPCSRNRERADMW FRPRSSNASSVSTRLSPLBFESEVLAEEIPASVSSYAGGVPI LNBGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLFSPAEGFLSAGBCCFSSSQALRALLITSDTPPPPADVILMTQ PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLBAPGPSSLVP			1	· · · · · · · · · · · · · · · · · · ·
5992 2 609 AGPDFRLVCGVSGSGFPGGRQGATEWRPLRPWNGAMEKLRRY SGQDDBBQGLTAQDSQINL/SEVLDASSLSPNTRLKWFAICF GVFF5ILGTGLLWLPGGIKLFAVPYTLGNLAALASTCFIMGP QLKKMFEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLPCII FLSMTWYSLSYIPYARDAVIKCCSSLL6  5993 1650 594 AEGLGSWAVWAGIGWAGRHMEAGGATGALGVGCKLPSAFCFFX SVAMDMFQKVEKIGEGTYGVVYKAKBRETGQLVALKKIRLDLI EGVPSTAIREISLLXBLKHPNIVRILDDVVINERKLYLLVFEFLS DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDI PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPI LLATTFYTTAVDINSIGGIFAEMVTRKALFFEGDS\EILQ\LFF FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPI RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQI RH  5994 394 1934 AGEVQLHVWIRGMRIQPQ/KAAATIDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPA PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRI LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWWMLNPEGGKSGKRRARGSSPCSRNREEADMW FRPRSSSNASSVSTRLSPLRPESEVLAESIPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRGSLSGFSLQHPGVTGPLHTYS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVIMTQU PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP				• · · · · · · · · · · · · · · · · · · ·
SGQDDEEQGLTAQDSQINL/SEVIDASSLSFNTRLKWFAICE GVFFSILGTGLLWLPGGIKLFAVPYTIGNLAALASTCFLMGPM QLKKMFSATRILATIVWLLCFIFTLCAALWHKKGLAVLPCII PLSMTWYSLSYIPYARDAVIKCCSSLLE  5993 1650 594 AEGLGSWAVWAGIGWAGEHMEAGGATGALGVGCKLPSAFCFP SVAMMMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLI EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEFLS DLKKYMDSTPGSELPLHLIKSYLPQLLQGVSFCHSHRVIHRDI PQNLLINELGAIKLADPGLARAFGVPLRTYTHEVVTLWYRAPI LLATRFYTTAVDINSIGGIFAEMVTRKALFPGDS\EIDQ\LFI FRMLGTPSEDTWPGVYQLPDYKGSFPKNYTKGLEETVPNLRFI RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQI RH  5994 394 1934 AGEVQLHVWIRGMRIQPQ/KAAATIDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAA PQPGILGAVTGPRKGGSRNAWGNQSYAELISQAIBSAPEKRI LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWWMLNPEGGKSGKRAPRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATTTSPVGHFAKWSGSPCSRNREEADMW FRPRSSSNASSVSTRSLSPLRPESEVLABEIPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLPSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQI PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP				
GVFFSILGTGLLWLPGGIKLPAVPYTLGNLAALASTCFLMGPM QLKRWPSATRLLATIVMLLCFIFTLCAALWWHKKGLAVLPCIJ FLSMTWYSLSYIPYARDAVIKCCSSLLS 5993 1650 594 AEGLGSWAVMGLGWAGRHMEAGGATGALGVGCKLPSAFCFPM SVAMMMFQKVEKIGEGTYGVVYKAKNRETGGLVALKKIRLDLJ EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEFLS DLKKYMDSTPGSELPLHILKSYLPQLLQGVSFCHSHRVIHRDI PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTHEVRAPPI LLATTFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFI FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLRPI RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQI RH  5994 394 1934 AGEVQLHVWIRGMRIQPQ/KAAATIDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPEVRPDLGEKVHTEGRSEPILLPSRLDEPAG PQPGILGAVTGPRKGGSRNAWGNQSYABLISQAIESAPEKRI LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATTTSPVGHFAKWSGSPCSRNREEADMW FRPRSSSNASSVSTRLSPLRPESEVLABEIPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLPSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQU PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP	5992	2	609	
QLKKMFEATRILATIVMILCFIFTLCAALWWHKKGLAVLFCII FLSMTWYSLSYIPYARDAVIKCCSSLLG  5993  1650  594  ABGIGSWAVWAGIGWAGRHMEAGGATGAIGVGCKLPSAFCFR SVAMDMFQKVEKIGGGTYGVVYKAKMRETGQLVALKKIRLDLI BGVPSTAIRBISLLKBLKHPNIVRLLDVVHNBRKLYLVFBFLS DLKKYMDSTPGSELPLHI, IKSYLFQLLQGVSFCHSHRVIHRDI PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFI FRNLGTPSEDTWPGVTQLPDYKGSFPKWTTKGLEEIVPNLBPI RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQI RH AGBVQLHVWIRGMRIQPO/KABAIIDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPEVBPDLGBKKWHTEGRSEPILLPSRLPEPAA PQPGILGAVTGPRKGGSRNAWGNQSYABLISQAIBSAPEKRI LAQIYEMMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWWMINPEGGKSGKRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNEREDDMWT FRPRSSSNASSVSTRLSPLRPBSBVLABEIPASVSSYAGGVPI LNGGLEILDGGNITSSHSLLSRGGLSGFFSLQHPGVTGPLHTYS SLFSPAEGPLSAGEGCPSSSQALBALLTSDTPPPPADVIMTQN PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLBAPGPSSLVP			]	SGQDDEEQGLTAQDSQINL/SEVLDASSLSFNTRLKWFAICFVC
FLSMTWYSLSYIPYARDAVIKCCSSLLS  5993  1650  594  ABGIGSWAVWAGIGWAGRHMEAGGATGALGVGCKLPSAFCFR SVAMMMFQKVEKIGBGTYGVYYKAKNRETGGLVALKKIRLDLI BGVPSTAIREISLLKEKHPNIVRILDUVHNERKLYLVFEFL DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDI PQNILINELGAIKLADDGLARAPGVPLRTYTHEVVTLWYRAPI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\BIDQ\LFI FRNLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLRPI RDLLMQLLQVDPSQRITAKTALAHPYFSSPEPSPAARQVVLQI RH  5994  394  1934  AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWI PRPETANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPA PQPGILGAVTGPRKGGSRRNAWGNQSYABLISQAIRSAPEKRI LAQIYEMMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWMINPEGGKSGKRAPRRAASMDSSSKLLRGRSI PKKRPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWI FRPRSSSNASSVSTRLSPLRPESEVLABEIPASVSSYAGGVPI LNGGLELLDGLNLTSSHSLLSRGGLSGFFSLQHPGVTGPLHTYS SLFSPAEGPLSAGEGCFSSQALRALLTSDTPPPPADVIMTQU PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP	ĺ			GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGPVK
5993  1650  594  ABGLGSWAVWAGLGWACRHMEAGGATGALGVGCKLPSAFCFR SVAMDMFQKVEKIGBGTYGVVYKAKNRETGQLVALKKIRLDLI BGVPSTAIREISLLXBLKHPNIVRILDDVVINERKLYLIVFEPLS DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSPCHSHRVIHRDI PQNILLINELGAIKLADRGLARAFGUPLRTTHEVVTLWYRAPI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFF RNLGTPSEDTWPGVTQLPDYKGSPPKWTRKGLEEIVPNLEPI RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQI RH  5994  394  1934  AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPEVEPDLGEKWHTEGRSEPILLPSRLPEPA PQPGILGAVTQPRKGGSRNAWGNQSYAELISQAIESAPEKRI LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWWMLNPEGGKSGKRARARRAASMDSSSKLLRGRSI PKKRPSGLPAPPEGATTTSPVGHFAKWSGSPCSRNREEADMWI FRPRSSSNASSVSTRLSPLRPESEVLAESIPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRGSLSGFSLQHPGVTGPLHTYS SLPSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQU PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP				QLKKMFEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLFCILQ
SVAMDMFQXVEKIGRGTYGVVYKAKNRETGQLVALKKIRLDLI BGVPSTAIRBISLLKBLKHPNIVRLLDVVHNBRKLYLVFBFLS DLKKYMDSTPGSELPLHLIKSYLFQLLQGGVSFCHSHRVIHRDI PQNLLINELGAIKLADPGLARAFGVPLRTYTHEVVTLWYRAPI LLATRFYTTAVDINSIGGIFAEMVTRKALFPGDS\EITQ\LF FRMLGTPSEDTWPGVTQLPDYKGSFPKNTRKGLBEIVPNLRFI RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQI RH SEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPEVBPDLGEKVHTEGRSEPILLPSRLPEPAK PQPGILGAVTGPRKGGSRNAWGNQSYABLISQAIBSAPEKRI LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWWMLNPEGGKSGKRAPRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATTTSPVGHFAKWSGSPCSRNREEADMWI FRPRSSSNASSVSTRLSPLRPESEVLABBIPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRGLSGFFSLQHPGVTGPLHTYS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQI PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP	- 1			FLSMTWYSLSYIPYARDAVIKCCSSLLS
SVAMDMFQKVEKIGRGTYGVVYKAKNRETGQLVALKKIRLDLI BGVPSTAIREISLLNELKHPNIVRLLDVVHNERKLYLVFEFLS DLKKYMDSTPGSELPLHLIKSYLPQLLQGGVSFCHSHRVIHRDI PQNLLINELGAIKLADPGLARAFGVPLRTYTHEVVTLWYRAPI LLATTFYTTAVDINSIGGIFAEMVTRKALFPGDS\EITQ\LF FRNLGTPSEDTWPGVTQLPDYKGSFPKNTRKGLEEIVPNLRFI RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQI RH  5994 394 1934 AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAA PQPGILGAVTGPRKGGSRNAWGNQSYAELISQAIBSAPEKRI LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWWMLNPEGGKSGRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATTTSPVGHFAKWSGSPCSRNREEADMWI FRPRSSSNASSVSTRLSPLRPESEVLABEIPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRGLSGFFSLQHPGVTGPLHTYS SLFSPAEGPLSAGEGCFSSQALEALITSDTPPPPADVIMTQI PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP	5993	1650	594	ABGLGSWAVWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFPGS
EGVPSTAIREISLLKELKHPNIVRILDVVHNERKLYLVFEPLS DLKKYMDSTPGSELPLHILKSYLPQLLQGGSPCHSHRVIHRDI PQNILINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFI FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLRPI RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQI RH  5994 394 1934 AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAG PQPGILGAVTGPRKGGSRNAWGNQSYABLISQAIBSAPEKRI LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATTTSPVGHFAKWSGSPCSRNREEADMW FRPRSSSNASSVSTRLSPLRPESEVLABEIPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQI PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP			l	SVAMDMFOKVEKIGEGTYGVVYKAKNRETGOLVALKKIRLDLEM
DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDI PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPI LLATTRFYTTAVDINSIGGIFAEMVTRKALFPGDS\EIDQ\LFF FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPI RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQI RH  5994 394 1934 AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAG PQPGILGAVTGPRKGGSRRNAWGNQSYABLISQAIESAPEKRI LAQIYEMMVRTVPYFKDKGDSNSSAGWKNSIRHNILSLHSKFII HNKATGKSSWWMLNPEGGKSGKRARARARAMDSSSKLLRGRST PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWT FRPRSSSNASSVSTRLSPLRPESBVLABEIPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLFSPAEGPLSAGEGCPSSSQALRALLTSDTPPPPADVLMTQN PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP			ļ	
PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPI LLATRFYTTAVDINSIGCIFAEMVTRKALFPGDS\EIDQ\LFI FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLRFI RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPARQYVLQI RH SEVENT AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAG PQPGILGAVTGPRKGGSRRNAWGNQSYABLISQAIESAPEKRI LAQIYEMMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWWMINPEGGKSGKRRARASMDSSSKLLRGRSI PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRRREADMWT FRPRSSSNASSVSTRLSPLRPESEVLABEIPASVSSYAGGVPI LNGGLELLDGLNLTSSHSLLSRGLSGFFSLQHPGVTGPLHTYS SLFSPAEGPLSAGEGCPSSSQALRALLTSDTPPPPADVLMTQN PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP	j		1	· ·
LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\BIDQ\LFI FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLRPI RDLLMQLLQYDPSQRTTAKTALAHPYFSSPEPSPAARQYVLQI RH S994 394 1934 AGEVQLHVWIRGMRIQPQ/KABATIDLDPDFEPQSRPRSCTWI PRPETANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPA PQPGILGAVTGPRKGGSRRNAWGNQSYABLISQAIBSAPEKRI LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWWMLNPEGGKSGRRPARAGMDSSSKLLRGRSI PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNRERADMVF FRPRSSSNASSVSTRLSPLRPESEVLABEIPASVSSYAGGVPI LNGGLELLDGLNLTSSHSLLSRGGLSGFSLQHPGVTGPLHTYS SLFSPAEGPLSAGEGCFSSQALBALLTSDTPPPPADVLMTQU PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP				
FRILGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPI RDLIMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQI RH  5994 394 1934 AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLDEPAA PQPGILGAVTGPRKGGSRNAWGNQSYAELISQAIBSAPEKRI LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWWMLNPEGGKSGKRAPRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATTTSPVGHFAKWSGSPCSRNREEADMW FRPRSSSNASSVSTRLSPLRPESEVLAESIPASVSSYAGGVPI LNEGLELLDGUNLTSSHSLLSRGLSGFSLQHPGVTGPLHTYS SLPSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVIMTQU PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP			1	<del>-</del>
RDLLMQLIQYDPSQRTTAKTALAHPYFSSPEPSPAARQYVIQI RH  5994 394 1934 AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAG PQPGILGAVTGPRKGGSRNAWGNQSYABLISQAIBSAPEKRI LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATTTSPVGHFAKWSGSPCSRNREEADMWI FRPRSSSNASSVSTRLSPLRPESEVLABEIPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQI PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP				1
RH  5994  394  1934  AGEVQLHVWIRGMRIQPQ/KARATIDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLDEPAG PQPGILGAVTGPRKGGSRRNAWGNQSYARELISQAIESAPEKRI LAQIYEMVRTVPYFKDKGDSSAGWKNSIRHNLSLHSKFII HNEATGKSSWWMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWT FRPRSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTTS SLFSPAEGPLSAGEGCFSSQALRALLTSDTPPPPADVLMTQU PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPT	1		l	<del></del>
5994 394 1934 AGEVQLHVWIRGMRIQPO/KAAAIIDLDPDFEPQSRPRSCTWI PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRI LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNILSLHSKFII HNRATGKSSWWMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWT FRPRSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLFSPAEGPLSAGEGCFSSQALRALLTSDTPPPPADVLMTQN PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPT				
PRPETANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAG PQPGILGAVTGPRKGGSRRNAWGNQSYABLISQAIBSAPEKRI LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWWMINPBGGKSGKAPRRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNRERADMV FRPRSSSNSSVSTRLSPLRPESEVLABEIPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLFSPAEGPLSAGEGCPSSQALRALLTSDTPPPPADVLMTQN PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP				
PQPGILGAVTGPRKGGSRRNAWGNQSYABLISQAIBSAPEKRI LAQIYEMMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWWMLNPBGGKSGKAPRRRAASMDSSSKLLRGRSI PKKKPSGLPAPPBGATPTSPVGHFAKWSGSPCSRNRERADMVF FRPRSSSNASSVSTRLSPLRPBSBVLABBIPASVSSYAGGVPI LNEGLBLLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLFSPAEGPLSAGEGCFSSQALRALLTSDTPPPPADVLMTQN PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPT	5994	394	1934	AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL
LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWWMLNPEGGKSGRAPRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATTTSPVGHFAKWSGSPCSRNREEADMWI FRPRSSSNASSVSTRLSPLRPESEVLABEITPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQI PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP	ł			PRPEIANOPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG
LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFII HNRATGKSSWWMLNPEGGKSGRAPRRAASMDSSSKLLRGRSI PKKKPSGLPAPPEGATTTSPVGHFAKWSGSPCSRNREEADMWI FRPRSSSNASSVSTRLSPLRPESEVLABEITPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQI PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP				PQPGILGAVTGPRKGGSRRNAWGNQSYABLISQAIBSAPEKRLT
HNRATGKSSWWILNPEGGKSGKAPRRAASMDSSSKILRGRSI PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLPSPAEGPLSAGEGCFSSQALRALLTSDTPPPPADVLMTQV PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPT				LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV
PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLPSPAEGPLSAGEGCFSSQALRALLTSDTPPPPADVLMTQV PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPT				<del></del>
FRPRSSNASSVSTRLSPLRPESEVLAEZIPASVSSYAGGVPI LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLPSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQV PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPT	l	İ	<u> </u> .	
LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYS SLFSPAEGPLSAGEGCFSSQALRALLTSDTPPPPADVLMTQV PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPT				
SLFSPAEGPLSAGEGCFSSSQALRALLTSDTPPPPADVIMTQ PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVP	l			
PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLRAPGPSSLVP				
	•			
[ CMT A DODGE A TO TO THE TOTAL OF THE PARTY		•		
	Į			SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY
MENLECDMONIISDLMDEGEGLDFNFEPDP	[			MENLECDMDNIISDLMDEGEGLDFNFEPDP
5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPG	5995	2	2437	RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR
				GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1				AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNQSL
1 1 1	į.			CSVGSLSDKEVETPRKKONDORNRKRKABPYETSQGKGTPRGHK
CONDUCTOR DELICATION OF THE PROPERTY OF THE PR			ī	1

PCT/US00/34263

WO 01/53312

		14.1	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		Bequence	
<u></u>	sequence		\=possible nucleotide insertion)
1	1	1	ISDYFERRVEQPLYGLDGSAAKEATEEQSALPTIMSVMLAKPRL
Į.	i	1	DTEQLAQRGAGLCFTFVSAQQNSPSSTGSGNTEHSCSSQKQISI
ì		[	QHRQT\QSDLTIEKISALENSKNSDLEKKEGRIDDLLRANCDLR
	1	1	ROI\DEOOKMLEKYK\ERLNRCFDNEPRNFLIEKSKOEKMACRD
1	ŀ	į.	KSMODRLRLGHFTTVRHGASFTEOWTDGYAFONLIKOOERINSO
i			RERIERORKMLAKRKPPAMGQAPPATNEQKORKSKTNGAENETL
	į.		TLAEYHEQERIFKLRIGHLKKEKABIQAELERLERVRNIHIREL
	İ		
ł	l .		KRIHNEDNSQFKDHPTLNDRYLLLHLLGRGGFSEVYKAFDLTEQ
ì		į.	RYVAVKIHQLNKNWRDEKKENYHKHACREYRIHKELDHPRIVKL
1	1	1	YDYFSLDTDSFCTVLBYCEGNDLDFYLKQHKLMSEKEARSIIMQ
1		1	IVNALKYLNEIKPPIIHYDLKPGNILLVNGTACGEIKITDFGLS
i		I	KIMDDDSYNSVDGMBLTSQGAGTYWYLPPECFVVGKBPPKISNK
I.	1	1	VDVWSVGVIFYQCLYGRKPFGHNQSQQDILQENTILKATEVQFP
1		1	PKPVVTPRAKAFIRRCLAYRKBDRIDVQQLACDPYLLPHIRKSV
Į.	ł	1	STSSPAGAALASTEGASNNSSSN
5996	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB
33,50	1012	301	
		1	LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPOISSVKDRKK\AVLSGHPVVSGEPHPAA
ł			
ļ	1	1	FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
ļ			FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5997	1612	981	DQQACLIGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
l		j	LPSIVVPGSIVNEGYLNSASEGEBPCIYNRNPNACSYGVAVGVL
ľ	1		AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGRPHPAA
ł		1	FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
Į			FFS1FTWSLTAALAVRRPKDLSFQEEYSTLPP\ASAQP
5998	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWIQR/SWVSWRSRPGCE
		1	LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
i .		1	AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
į .			FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNRGTDASPGRPSPFS
1	!	i	PFSIFTWSLTAALAVRRPKDLSFQEEYSTLPP\ASAQP
5999	<u> </u>		Froitimoniamumvkktkhrototototute/mombe
5999		1000	L
L .	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP
į.	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGHDSHTLPBEWKYLPFLALPDGAHNYQBDTVFFHLPPRNGNG
İ	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPBEWKYLPFLALPDGAHNYQEDTVFPHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG
	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGHDSHTLPBEWKYLPFLALPDGAHNYQBDTVFFHLPPRNGNG
	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPBEWKYLPFLALPDGAHNYQEDTVFPHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG
	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFREKDFSQISILKRLYKHMNSSLGGASLEGS
	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFREKDPSQISILKBLYRHMNSSLGGASLEGS QVYLGLSPRDLVLHPRHKGLILFKLILLEKKVLFYYSPVNKLVG ALMTVLSLPPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD
	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQLSILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHPRHKGLILPKLILLEKKVLFYISPVNKLVG
	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGHDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVRGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEKDFSQISILKELYKHMYSSLGGASLEGS QVYLGLSPRDLVLHPRHKGLILPKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIRHGLSDCSQYRPRKSMSRDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLPQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE
	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGHDSHTLPBEWKYLPFLALPDGAHNYQEDTVFPHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMYSSLGGASLEGS QVYLGLSPRDLVLHPRHKGLILLPKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMACNHGEDAAMKTEEPLPQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE
	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGHDSHTLPBEWKYLPFLALPDGAHNYQEDTVFPHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHPRHKGLILLPKLILLEKVLFYISPVNKLVG ALMTVLSLPFGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMACNHGEDAAMKTEEPLFQVEDSS KGQEPNDTMQYLKPPSRPSPDSSESDWBTLDPSVLEDPNIKKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI
	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFREKDPSQLSILKBLYRHMNSSLGGASLEGS QVYLGLSPRDLVLHPRHKGLILFKLILLBKKVLFYISPVNKLVG ALMTVLSLPPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRSPDPSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSBSLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEKALIQIHDPELRKLLNPTTADLRFADYL
	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGHDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFBEKDFSQLSILKELYBHMNSSLGGASLEGS QVYLGLSPRDLVLHPRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGGEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNIKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTEQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVERALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV
-	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGHDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFBEKDFSQLSILKBLYBHMNSSLGGASLEGS QVYLGLSPRDLVLHPRHKGLILFKLILLBKKVLPYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTEQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVERALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK
			RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGHDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYBHMISSLGGASLEGS QVYLGLSPRDLVLHPRHKGLILPKLILLEKKVLFYISPVNKLVG ALMTVLSLPFGMIBHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QUGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIFGLISGLE EDQYGMPLAHTTKGYLCLPYMALQCHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVBKALIQIHDPELRKLLNPTTADLRFADYL VRHYTENRIDVFLDGTGWEGGDEWIRAQFAVYHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP
6000	101	1790 1561	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFREKDFSQLSILKELYRHMISSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYTSPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTITRKVMACSHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE DLGSDQTNLFPKDSVPSBSLPITVQPQANTGQVVLIFGLISGLE EDQYGMPLAIFTKGYLCLPYMALQOHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEKALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVIT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL
6000			RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQBDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFREKDFSQLSILKBLYRHMNSSLGGASLEGS QVYLGLSPRDLVLHPRHKGLILFKLILLBKKVLFYISPVNKLVG ALMTVLSLPPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTITKVMAGSHGBDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSESDWETLDPSVLEDPNLKERE DLGSDQTNLFPKDSVPSBSLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIF-KGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVBEALIQIHDPELRKLLNPTTADLRFADYL VRHYTENRIDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVWTT\SRNVYQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAERCTATMSENNKNSLESSLRQLKCHPTWNLMEGENSL DDPEDKVFYRTEPQNREFKATMCNLLAYLKHLKGQNEAALECLR
6000			RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFREKDFSQLSILKELYRHMISSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYTSPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTITRKVMACSHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE DLGSDQTNLFPKDSVPSBSLPITVQPQANTGQVVLIFGLISGLE EDQYGMPLAIFTKGYLCLPYMALQOHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEKALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVIT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL
6000			RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQBDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFREKDFSQLSILKBLYRHMNSSLGGASLEGS QVYLGLSPRDLVLHPRHKGLILFKLILLBKKVLFYISPVNKLVG ALMTVLSLPPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTITKVMAGSHGBDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSESDWETLDPSVLEDPNLKERE DLGSDQTNLFPKDSVPSBSLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIF-KGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVBEALIQIHDPELRKLLNPTTADLRFADYL VRHYTENRIDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVWTT\SRNVYQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAERCTATMSENNKNSLESSLRQLKCHPTWNLMEGENSL DDPEDKVFYRTEPQNREFKATMCNLLAYLKHLKGQNEAALECLR
6000			RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYRQIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDPSQLSILKELYBHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLPPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMACNHGEDAAMKTEEPLPQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLATFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHPTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNILAYLKHLKGQMEAALECLR KABELIQQEHADQASIRSLVTWGNYAWVYYHMGRLSDVQIYVDK
6000			RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFBEKDFSQLSILKELYBHMNSSLGGASLEGS QVYLGLSPRDLVLHPRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLPPGMIEHGLSDCSQYRPKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGGEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNIKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTEQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQOHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVERALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNYMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDBKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQMBAALECLR KABELIQQEHADQASIRSLVTMGNYAWYYHMGRLSDVQIYVDK VKHVCEKFSSPYRISSPELDCBEGWTRLKCGGNQNERAKVCFEK
6000			RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQBDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFREKDFSQLSILKBLYRHMISSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLBKKVLFYISPVNKLVG ALMTVLSLPPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTITRKVMACRHGEDAAMKTBEPLPQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE DQSSQTNLFPKDSVPSBSLPITVQPQANTSQVVLIFGLISGLE EDQYGMPLAIFTKGYLCLPYMALQOHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVBEALIQIHDPELRKLLNPTTADLRFADYL VRRVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVIT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDBKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFBDKVFYRTEFQNRBFKATMCNLLAYLKHLKGQMBAALECLR KABBLIQQEHADQASTRSLVTMGNYAWVYHMGRLSDVQIYVDK VKHVCEKFSSPYRISSPELDCBEGWTRLKCGGNQDBERAKVCFEK ALKKKPKNPEFTSGLATASYRLDNWPPSQMAIDPLRQAIRLNPD NQYLKVLLALKLHKMRERGEBEGGGEK\LVERALEKAPG\VTDV
6000			RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFREKDFSQLSILKELYRHMISSLGGASLEGS QVYLGLSPRDLVLHPRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLPPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTITRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSEDWETLDPSVLEDPNLKERE DQGSDQTNLFPKDSVPSBSLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIF-KGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVBEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRIDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTPTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHPTWNLMEGENSL DDPEDKVFYRTEPQNREFKATMCNILAYLKHLKGQNEAALECLR KABELIQQEHADQASTRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRISSPELDCEGEWTRLKCGSQNQNERARVCFEK ALKKKPKNPBFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMRERGEBEGGGEK\LVBERLEKARPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY
6000			RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFBEKDFSQLSILKBLYRHMISSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLBKKVLFYISPVNKLVG ALMTVLSLPPGMIEHGLSDCSQYRPKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMACNHGEDAAMKTEEPLPQVEDSS KGQEPNDTNQYLKPPSRPSPDSESDWETLDPSVLEDPNLKERE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVBEALIQIHDPELRKLLNPTTADLRFADYL VRHYTENRIDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVWYTT\SRNVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDBKP TEPCRTAEMCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL KABELIQQEHADQASIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRISSPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMRERGEBEGEGEK\LVBRALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY RAKVPQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR
6000			RPPMEKARRGGDGVPRGPVLHIVVVGFHHKRGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYRQIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDPSQLSILKBLYBHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLBKKVLFYISPVNKLVG ALMTVLSLPPGMIEHGLSDCSQYRPKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMACHIGEDAAMKTEEPLPQVEDSS KGGEPNDTMQYLKPPSRPSPDSSESDWETLDPSVLEDPNIKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLATFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVBEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\NSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHPTWNLMEGENSL DDFEDKVFYRTEPQNREFKATMCMILAYLKHLKGQMEAALECLR KABELIQQEHADQASIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRISSPELDCBEGWTRLKCGSQNDRRAKVCFEK ALEKKPKNPEFTSGLATASYRLDNWPPSQNATIPPLRQAIRLNPD NQYLKVLLALKLHKMREBGEEGGESEK\LVEBALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY RAKVPQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR
6000			RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQLSILKELYBHMNSSLGGASLEGS QVYLGLSPRDLVLHPRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLPPGMIEHGLSDCSQYRPKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLPQVEDSS KGGEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNILKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVERALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\NASWLSTFTTSTSQSLTEPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNILAYLKHLKGQNBAALECLR KABELIQQEHADQASIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRISSPELDCBEGWTRLKCGGNQNERAKVCFEK ALKKPKNPBFTSGLAIASYRIDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEKK\LVERALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY RAKVPQVMMIRBNGHYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDABYYFQKEFSKBLTPVAKQLIHLRYGN FQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRL
6000			RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGHDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQLSILKBLYBHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLBKKVLFYISPVNKLVG ALMTVLSLFPGMIRHGLSDCSQYRPKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QUGSDQTNLFPKDSVPSBSLPITVQPQANTEQVVLIFGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQXHLSDAIVEVBEALIQIHDPELRKLLNPTTADLRFADVL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDBKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFFDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNBAALECLR KABBLIQQEHADQASIRSLVTNGNYAWVYTHMGRLSDVQIYVDK VKHVCEKFSSPYRI3SPELDCBEGWTRLKCGGNQNERAKVCFEK ALKKKPKNPBFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMRERGBERGGGEK\LVBRALBARAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY RAKVPQVMNLRENGHYGKRKLLELIGHAVAHLKADEANDNLFR VCSILASLHALADQYEDARYYFQKEFSKELTPVAKQLLHLRYGN FOLYQMKCEDKAIHHFIBGVKINQKSREKEKMKDKLQKIAKMRL SKNGADSEALHVLAFLQEINBKMQQADEDSERGLESGSLIPSAS
	101	1561	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFREKDFSQLSILKELYRHMISSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLPPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTITRVWAGRHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDFSVLEGDPLKERE EDQYGMPLAIFTKGYLCLPYMALQOHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVERALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYHHALLAATLQLV LFRIVNVAKKIGNVMVIT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTPTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KABELIQQEHADQASTRSLVTMGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRISSPELDCEEGWTRLKCGGNQNERAKVCFEK ALKKKPKNPEFTSGLAIASYRLDNWPPSQMAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEGEK\LVERALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY RAKUFQVMNIRBNGHYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDABYYFQKEFSKELTPVAKQLIHLRYGN FQLYQMKCBDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRIL SKNGADSEALHVLAFLQRLNEKMQQADEDSERGLESGSLIPSAS SWNGB
6000			RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGHDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQLSILKBLYBHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLBKKVLFYISPVNKLVG ALMTVLSLFPGMIRHGLSDCSQYRPKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QUGSDQTNLFPKDSVPSBSLPITVQPQANTEQVVLIFGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQXHLSDAIVEVBEALIQIHDPELRKLLNPTTADLRFADVL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDBKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFFDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNBAALECLR KABBLIQQEHADQASIRSLVTNGNYAWVYTHMGRLSDVQIYVDK VKHVCEKFSSPYRI3SPELDCBEGWTRLKCGGNQNERAKVCFEK ALKKKPKNPBFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMRERGBERGGGEK\LVBRALBARAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY RAKVPQVMNLRENGHYGKRKLLELIGHAVAHLKADEANDNLFR VCSILASLHALADQYEDARYYFQKEFSKELTPVAKQLLHLRYGN FOLYQMKCEDKAIHHFIBGVKINQKSREKEKMKDKLQKIAKMRL SKNGADSEALHVLAFLQEINBKMQQADEDSERGLESGSLIPSAS
	101	1561	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFREKDFSQLSILKELYRHMISSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLPPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTITRVWAGRHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDFSVLEGDPLKERE EDQYGMPLAIFTKGYLCLPYMALQOHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVERALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYHHALLAATLQLV LFRIVNVAKKIGNVMVIT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTPTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KABELIQQEHADQASTRSLVTMGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRISSPELDCEEGWTRLKCGGNQNERAKVCFEK ALKKKPKNPEFTSGLAIASYRLDNWPPSQMAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEGEK\LVERALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY RAKUFQVMNIRBNGHYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDABYYFQKEFSKELTPVAKQLIHLRYGN FQLYQMKCBDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRIL SKNGADSEALHVLAFLQRLNEKMQQADEDSERGLESGSLIPSAS SWNGB
	101	1561	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQBDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFBEKDFSQLSILKBLYRHMISSLGGASLEGS QVYLGLSPRDLVLHPRHKGLILFKLILLBKKVLFYISPVNKLVG ALMTVLSLPPGMIBHGLSDCSQYRPRKSMSBDGGLQESNPCADD FVSASTADVSHTNLGTITKVMAGSHGBDAAMKTBEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSEDWBTLDPSVLEDPNLKERE DQGGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVBESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVBEALIQIHDPBLRKLLNPTTADLRFADYL VRHYTENRIDVFLDGTGWEGGDBWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVWTTT\SRNVYQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDBKP TEPCRTAERCTATMSENNKNSLESSLRQLKCHPTWNLMEGENSL DDPEDKVFYRTEFQNRBFKATMCNLLAYLKHLKGQNBAALECLR KABBLIQQEHADQASIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRISSPELDCLBCWTRLKCGSQNDRERAKVCFEK ALKKPKNPBFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMRERGBBEGGEGK\LVBRALBKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY RAKVPQVMNLRBNGHYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASHALADQYEDABYYFQREFSKELTPVAKQLLHLRYGN FQLYQMKCBDKAIHHFIEGVKINGKSREKERKKNKUKLQKIAKMRI FQLYQMKCBDKAIHHFIEGVKINGKSREKERKKNKUKLQKIAKMRI SKNGADSEALHVLAFLQKLNBKMQQADEDSERGLESGSLIPSAS SWNGB AFAHSPSRGHRETHIHTPRHTPRCTMABSHLQSSLITASQPFEI
	101	1561	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLTP GDGRDSHTLPBEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDPSQLSILKELYBHMISSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLPPGMIEHGLSDCSQYRPKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMACNHGEDAAMKTEEPLPQVEDSS KGQEPNDTNQYLKPPSRPSPDSSEDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVBEALIQIHDPELRKLLNPTTADLRFADYL VRHTENRIDVFLDGTGWEGGDENIRAQFAVYIHALLAATIQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHPTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KABELIQQEHADQASIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRISSPELDCEESWTRLKCGGNQNERAKVCPEK ALEKKPKNPBFTSGLAISYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLAIKLHKMREBGEBEGGEGEK\LVBRALEKAPG\VTDV LRBAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY RAKVPQVMNLRENGUYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDABYYFQKEFSKELTPVAKQLLHLRYGN FOLYOMKCEDKAIHHFIEGVKLNQKSREKEKMKDKLQKIAKMRL SKNGADSEALHVLAFLQELNBKMQQADEDSERGLESGSLIPSAS SWNGB AFAHSPSRGHRETHIHTPRHTPRCTMAESHLQSSLITASQFFEI WLHFDADGSGYLEGKELQNLIQBLQQARKKAGLKLSPEMKTFVD

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
l .			
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
]	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /≃possible nucleotide deletion,
1	sequence	}	\=possible nucleotide insertion)
<del></del>	<del> </del>		LKLFDSNNDGKLELTEMARLLPVQENPLLKFQGIKMCGKEFNKA
ŀ	1		FELYDQDGNGYIDENELDALLKDLCEKNKQDLDINNITTYKKNI
1		1	MALSDGGKLYRTDLALILCAGDN
6002	977	81	LAPPGGGLHIPPRTPLSHSRPPPSHHAPHPSPLPLPPADLHPHS
ļ	1		SMAQRSDLLELDCQLTRDRVVVVSHDENLCRQSGLNRDVGSLDF
ļ	}	•	EDLPLYKEKLEVYFSPGHFAHGSDRRMVRLEDLFQRFPRTPMSV
l	i	1	EIKGKNEELIREQ/VLVRRYDRNEITIWASEKSSVMKKCKAANP
(	[		EMPLSPTISRGPWVLLSYYLGLLPFIPIPEKFFFCFLPNITNRT
1		}	YPPFSCSCLNQLLAVVSKWLIMRKSLIRHLEERGVQVVFWCLNE
ı	1	ļ	<u> </u>
			BSDFEAAFSVGATGVITDYPTALRHYLDNHGPAARTS
6003	140	4098	GKLRAFRGMRRLICKRICDYKSFDDBESVDGNRPSSAASAFKVP
1	Í	ĺ	APKTSENPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA
İ	l	l	FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR
1	1	1	SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA
Į.	[	i	HLSTVLGNKPDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII
	i		RHTHVPRLIPLITSNCTSKSVPVRRRSFBFLDLLLQRWQTHSLK
1		ŀ	RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY
Ì	1		
ì	· .		NSLEPSYQKSLQTYLKSSGSVASLPQSDRSSSSSQBSLNRPFSS
1	ĺ		KWSTANPSTVAGRVSAGSSKASSLPGSLQRSRSDIDVNAAAGAK
	Ī		AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV
1			RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGSPGRVLT
	1		TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSRBASPSRLSV
1		•	ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQPLASRHHSRS
1	1		TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVERA
1	ł		VADALLLGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS
	j		YSSRNGSIPTYMRQT\BDV\AEVLNRCASSNWSERKEGLIGLQN
•	•	ſ	
		Ì	LLKNORTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI
		l	QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES
	Ì		FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD
·		l	FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFBLNTPE
			FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPTP
l	1		RSPANNSSPLTSPTNTSQNTLSPSAFDYDTENMNSBDIYSSLRG
			VTRAIQNP9FR9QEDMNRPLKRDSKKDDGDSMCGGPG\MSDPRA
1	-		GGDATDSSQTAL\DNKASILHSMPTHSSPRSRDYNPYNYSDSIS
		· ·	_ · · · · · · · · · · · · · · · · · · ·
l	•		PFNKSALKRAMFDDDADQFPDDLSLDHSDLVAKLLKRI,SNHNER
			VEERKIALYELMKLTQEESFSVWDEHFKTILLLLETLGDKE2T
			IRALALKVLREILRHOPARFKNYABLTVMKTLEAHKOPHKEVVR
			SAKBAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT
			KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVAV
			HAVIGDBLKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS
			GQS
6004	140	4098	GKLRAFRGMRRLICKRICDYKSFDDEBSVDGNRFSSAASAFKVP
		10,00	APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA
			i i
			PTDVPSIQIYSSRKLEBTLNKIREILSDDKHDWDQRANALKKIR
			SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVRBACITVA
			HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII
			RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEWQTHSLE
			RHAAVLVETIKKGIHDADABARVEARKTYMGLRNHFPGEAETLY
			NSLEPSYOKSLOTYLKSSGSVASLPQSDRSSSSSGESLNRPFSS
]			KNSTANPSTVAGRVSAGSSKASSLPGSLORSRSDIDVNAAAGAK
			AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV
			RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGSPGRVLT
			TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSRBASPSRLSV
			ARSSRIPRPSVSQGCSREASRBSSRDTSPVRSFQPLASRHHSRS
			TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVERA
			VADALLLGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS
		1	YSSRNGSIPTYMRQT\EDV\ABVLNRCASSNWSERKEGLLGLQN
l i			
			LLKNORTLSRVBLKRLCRIFTRMFADPHGKRVFSMFLETLVDFI
			QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES
			PPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD
			FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFELNTPE

Predicted mind   mucleotide   mucleotide   mucleotide   corresponding   corr	_		1. GARGER	
NO: location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence solvent in the control of the cont	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cotation   Coffired	ID	beginning	nucleotide	
to first amino acid creidue of amino acid equence  seque	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first anino acid residue of amino acid dequence  #Tryptcophan, Y=Tyrosine, X=Unknown, **-Stop Codon, Y=possible nucleotide deletion, V=possible nucleotide insertion)  #Tryptcophan, Y=Tyrosine, X=Unknown, **-Stop Codon, Y=possible nucleotide insertion)  ##Tryptcophan, Y=Tyrosine, X=Unknown, **-Stop Codon, Y=possible nucleotide insertion  ##Tryptcophan, Y=Tyrosine, X=Unknown, **-Stop Codon, Y=possible nucleotide insertion)  ##Tryptcophan, Y=Tyrosine, X=Unknown, **-Stop Codon, Y=possible nucleotide insertion  ##Tryptcophan, Y=Tyrosine, X=Unknown, **-Stop Codon, Y=possible nucleotide insertion)  ##Tryptcophan, Y=Tyrosine, X=Unknown, **-Stop Codon, Y=possible nucleotide insertion  ##Tryptcophan, Y=Tyrosine, X=Unknown, **-Stop Codon, Y=possible nucleotide insertion  ##Tryptcophan, Y=Tyrosine, X=Unknown, **-Stop Codon, Y=possible nucleotide insertion  ##Tryptcophan, Y=Tyrosine, X=Unknown, **-Stop Codon, Y=possible nucleotide insertion  ##Tryptcophan, Y=Tyrosine, X=Unknown, **-Stop Codon, Y=possible nucleotide insertion  ##Tryptcophan, Y=Tyrosine, X=Unknown, **-Stop Codon, Y=possible nucleotide insertion  ##Tryptcophan, Y=Tyrosine, X=Unknown, **-Stop Codon, Y=possible nucleotide insertion  ##Tryptcophan, Y=Tyrosine, X=Unknown, **-Stop Codon, Y=possible nucleotide insertion  ##Tryptcophan, Y=Tyrosine, X=Unknown, **-Stop Codon, Y=possible nucleotide insertion  ##Tryptcophan, Y=Tyrosine, X=Unknown, Y=Stop  ##Tryptcophan, Y=Tyrosine, X=Unknown, Y=Stop  ##Tryptcophan, Y=Tyrosine, X=Unknown, Y=Stop  ##Tryptcophan, Y=Tyrosine, X=Unknown, Y=Stop  ##Tryptcophan, Y=Tyrosine, X=Unknown, Y=Stop  ##Tryptcophan, Y=Tyrosine, X=Unknown, Y=Stop  ##Tryptcophan, Y=Tyrosine, X=Unknown, Y=Stop  ##Tryptcophan, Y=Tyrosine, X=Unknown, Y=Stop  ##Tryptcophan, Y=Tyrosine, X=Unknown, Y=Stop  ##Tryptcophan, Y=Tyrosine, X=Unknown, Y=Stop  ##Tryptcophan, Y=Tyrosine, X=Unknown, Y=Stop  ##Tryptcophan, Y=Tyrosine, X=Unknown, Y=Stop  ##Tryptcophan, Y=Tyrosine, X=Unknown, Y=Stop  ##Tryptcophan, Y=Tyrosine, X=Unknown, Y=Stop  ##Tryptcophan, Y=Tyrosine,	l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to first anino acid residue of anino acid an		ccrresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
meino acid equence  ### Tryptcophan, Y=Tytosine, X=Unknown, **Stop Codon, y=possible muclectide deletion  ### Tryptcophan, Y=possible muclectide deletion  ### Tryptcophan, y=possible muclectide insertion  ### Tryptcophan, y=possible muclectide insertion  ### Tryptcophan, y=possible muclectide insertion  ### Tryptcophan, y=possible muclectide deletion, y=possible profiles profile	Į.		amino acid	P=Proline, Q=Glutamine, R=Arginine,
mino acid equence    Wednesd		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
amino acid		i .	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Pequence				
FFMILAGADETTO, CONTROL TISSUES SHOULD SHOULD SHOULD SEE SEARCH STORE AND SEARCH SHOULD SEE SEARCH SEED AND SEARCH SEED AND SEARCH SEARCH SEARCH SEED AND SEARCH SEED AND SEARCH S			bequence	
REPAINS PLATF TITE CONTINGENCY AND PARA CONDITIONS PROBLEMENT ENGINEER AND PARA CONDITIONS PROBLEMENT ENGINEER AND PARKS AND AND AND AND AND AND AND AND AND AND		sequence		I '
VTRALQNES GRADATINAS LIKINGTISS PERSONNET YKYSOSTS PONKSALKERAMFODDADQ PRODUSLUSI DLIVARILIKEUSININER VERKIANTSILMKIT LOOSES SEVENDER TILLALIKEUSININER VERKIANTSILMKIT LOOSES SEVENDER TILLALIKEUSININER SARERASVI, LANST J. SEPECTRIVLEY I (TARDY EIN LANTIGATE RALALKULER TILALIA PELINGLI QOYUMSISS VERKACVPCILVAV RUTERVERTIALLI PELINGLI QOYUMSISS VERKACVPCILVAV GOS  SOSTER GREEN LANTIG LOOSES SEVERACVPCILVAV GOS  RESGREGOLICA PEREKKIMAS GLOS PEPCAROS BEREIMBALL RIVER KROKKERMILICA QUIDIS GREED PEPVERBERVALISIOS GREED PEPVERBER PEPVER PER PER VARABELLI REVIGIOLIS CONTENSIONAL PEPVER PER VARABELLI REVIGIOLIS CONTENSIONAL PEPVER PER VARABELLI REVIGIOLIS CONTENSIONAL PEPVER PEPVER PER PER VARABELLI REVIGIOLIS CONTENSIONAL PEPVER PEPVER PEPVER PER PER PEPVER PER PER VARABELLI REVIGIOLIS CONTENSIONAL PEPVER PEPVER PEPVER PER PER PEPVER PEPVER PEPVER PER PER PEPVER PER PER PEPVER PEP PEPVER PER PEPVER PER PER PEPVER PEPVER PEPVER PEPVER PER PEPVER PEPVER PER PEPVER PER PEPVER PER PEPVER P		<u> </u>		
GODATOSSCOTALÓNIKASILLISMPTISSPESSDANIPTYNYSDISS  PPINSKALKERMEDODADOPPODISLISMBIDLVARILLISKISNINER  VERRITALYLER LIRIQUESPSYMDERRETILLILLISTIGNERP  TRALAKVILER LIRIQUESPSYMDERRETILLILLISTIGNERP  RAVERSKATALYLER LIRIQUESPSYMDERRETILLILLISTIGNERP  RAVERSKATALYLLER LIRIQUESPSYMDERRETILLILLISTIGNERP  RAVERSKATALYLLER LIRIQUESPSYMDERRETILLILLISTIGNERP  RAVERSKATALINLIDER INFOLLOGYTOMSSEKRACUPYELURAV  RAVIEDBIKAPHISCHISSBANILLINYTERRAVESGGAPPTITUS  GOS  1.33  5955  RESSERREBOLGGPFBERENSHASGLGSPSPCSANSEREDMOALL  NISLIPPPTPBEREDPEREDLSSTETPYKLKKKKUPKUPRDPKITEKS  RICKKEKKLIGPKERKSKSSKREREREDDDDDDDSKEPRSSAGLI-  BOMMODDIAVYSERDERVALTINYTARSYOPVELLANAMVIKLANS  RIMMVLGAKKRSPSTINDPKSSGASAVAAAAAAVAVVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAVAVVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVAVUESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAAVAVUESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAAVAVUESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAAVAVUESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVAVUESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAAVAVUESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAAVAVUESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAVAVESMUTA  REMANULGAKKRSPSTINDPKSSGASAVAAAAAAAAVATAVESMUTA  REMANULGAKKRSPS				
PPNESALKERMHODDADQ PEDUS LUSS DLVARILIKELS SHINDER  VEREKLAYKINGEN LOSSES SYNDERFETTILLLILES TICKET  TRAIALKYLEST LIRROPAPERNYAELTYMET. TARHICOPHES VIR SAEBASY LASTS 1 SEGCT KILLOPI (TORANY HILLALATION)?  EVI ERVISKETILLILES IMPOLICO (TORANY HILLALATION)?  EVI ERVISKETILLILES IMPOLICO (TORANY HILLALATION)?  EVI ERVISKETILLILES IMPOLICO (TORANY HILLALATION)?  EVI ERVISKETILLILES IMPOLICO (TORANY HILLALATION)?  EVI ERVISKETILLILES IMPOLICO (TORANY HILLATION)  RESERREBOLICO (TORANY HILLARI (T	i		İ	,
VERRITALYRIAMILTORESES WIDEHRITTILLILLETIGNEEP  IRAIA/XVIRRIIMIOPAPRISTUM PARTITYMIT. CHILLILLILTIGNEEP  SARRASVI LATSI INSPECTIVUCTI IQTADYPINLALTIGNEE  SARRASVI LATSI INSPECTIVUCTI IQTADYPINLALTIGNEE  SARRASVI LATSI INSPECTIVUCTI IQTADYPINLALTIGNEE  REVISERTA INLINE PRIMOGLIOCYMINESSEVERACYPCIUAV  WAY IGDELRPHISQUITGSRMKILLILYI KRAQTGSGGADPTTUS  OOS  RESGRROBOLGOPPERREKMASGLGSPSPCSAGSEEEDMOALL  NISLIPPHIPENBERDPERDILSETTPY KLIKKKORCROPAPITUS  RESGRROBOLGOPPERREKMASGLGSPSPCSAGSEEEDMOALL  NISLIPPHIPENBERDPERDILSETTPY KLIKKKORCROPAPITUS  ROMMULGARWEETSTINEPHOSGSGASVAAAAANAVVUSUMITANI  ROMMULGARWEETSTINEPHOSGSGASVAAAAANAVVUSUMITANI  ROMMULGARWEETSTINEPHOSGSGASVAAAAANAVVUSUMITANI  ROMMULGARWEETSTINEPHOSGSGASVAAAAANAVVUSUMITANI  ROMMULGARWEETSTINEPHOSGSGASVAAAAANAVVUSUMITANI  ROMMULGARWEETSTINEPHOSGSGASVAAAAANAVVUSUMITANI  ROMMULGARWEETSTINEPHOSGSKASVAAAAANAANAVVUSUMITANI  ROMMULGARWEETSTINEPHOSGSKASVAAAAANAANAVVUSUMITANI  ROMMULGARWEETSTINEPHOSGSKASSANAAAANAVVUSUMITANI  ROMMULGARWEETSTINEPHOSGSKASSANAAAANAVVUSUMITANI  ROMMULGARWEETSTINEPHOSGSKASSANAAAANAVVUSUMITANI  ROMMULGARWEETSTINEPHOSGSKASSANAAAANAVVUSUMITANI  ROMMULGARWEETSTINEPHOSGSKASSANAAAANAVVUSUMITANI  ROMMULGARWEETSTINEPHOSGSKASSANAAAANAAVVUSUMITANI  ROMMULGARVEETSTINEPHOSGSKASSANAAAANAAVVUSUMITANI  ROMMULGARVEETSTINEPHOSGSKASSANAAAANAAVVUSUMITANI  ROMMULGARVEETSTINEPHOSGSKASSANAAAANAAVVUSUMITANI  ROMMULGARVEETSTINEPHOSGSKASSANAAAANAAVVUSUMITANI  ROMMULGARVEETSTINEPHOSGSKASSANAAAANAAVVUSUMITANI  ROMMULGARVEETSTINEPHOSGSKASSANAAAANAAVVUSUMITANI  ROMMULGARVEETSTINEPHOOLOWSSOPPUNDINGARGARVEETINI  ROMMULGARVEETA LANDON TURBARVEETINI  ROMMULGARVEETA LANDON TURBARVEETINI  ROMMULGARVEETA LANDON TURBARVEETINI  ROMMULGARVEETA LANDON TURBARVEETINI  ROMMULGARVEETA LANDON TURBARVEETINI  ROMMULGARVEETA LANDON TURBARVEETINI  ROMMULGARVEETA LANDON TURBARVEETINI  ROMMULGARVEETA LANDON TURBARVEETINI  ROMMULGARVEETA LANDON TURBARVEETINI  ROMMULGARVEETA LANDON TURBARVEETINI  ROMMULGARVEETA LANDON TURBARVEETINI  ROMMULGARVEETA LANDON TURBARVEETA TURBARVEETA LANDON TURBARVE		ŀ		
IRALALKULREILIRIOPARPERTYELTIVIKTI. ZARHEDPHIKEVAL SARBASVI, LATTI VSEPCIEURT DI 107 TADPY INLALTIVOTY XVIERVISERTIJALLIPER HMOLLOGVINISESSVERACVPCLUAV. EVIERVISERSTIJALLIPER HMOLLOGVINISESSVERACVPCLUAV. EVIERVISERSTIJAL PER HMOLLOGVINISESSVERACVPCLUAV. EVIERVISERSTIJAL PER HMOLLOGVINISESSVERACVPCLUAV. EVIERVISERSTIJAL PER HMOLLOGVINISESSVERACVPCLUAV. EVIERVISERS SERVERACUPCLUAV. EVIERVISERS SERVERACUPCLUAV. EVIERVISERS SERVERACUPCLUAV. EVIERVISERS SERVERACUPCLUAV. EVIERVISERS SERVERACUPCLUAV. EVIERVISERS SERVERACUPCH PER KROKKERNILACIOLOSS GEGEVERBERVALKISIS SESSUTTUP GEKKKEKOLGPKER SINGERSERS SERVERBERVEDDIDON SERVERSSAGLI. BOMOMBO DRIVPSEDVIKTATIVAN PSQ EVIPLIAAMIRIKAN. HOMOMBO DRIVPSEDVIKTATIVAN PSQ EVIPLIAAMIRIKAN. HOMOMBO DRIVPSEDVIKTATIVAN PSQ EVIPLIAAMIRIKAN. HOMOMBO PER PREVAPER PPEVAPEL KARATKEGKOPINRAR PKASAR PREVAPELAK. GEGOSTARSSAR SERVER DAKA VARVALKAN EVIPLIAAMIRIKAN SERVER DOLLOVAS PER PER VANDER ETIMP FOR SER BOODLOVAS PEVAPEDRAS IN SINS SERVER PREVAPELAK SERVER PREVAPELAK SERVER PEVAPELAK SERVER PEVAPELAK SERVER PREVAPELAK SERVER PEVAPELAK SER	1	ĺ	ĺ	1
SARRASVI, LATST, ISPECTIKULOPI I (TIDADYPI INLANIKME)  KY I KRYNSKETIALL PRI MOGLIGOVINNESS VERKACYPCLVAV  BAY I GDELKPHLSQLTGSRMKILILYTKRAQTGSGAD PTTUVS  GOS  8 SSGROBQIGOPPGRERKMASGLGSPSPCSAGSEEEDMDALL  NNSLPPPIPSMEED PER BLEETPELKKKKKKKKKKKKKKRADDPT 1705  KRSGKRIKKKKIGPKREKRSKSKRKEREEDDDDDDDDDSKSPKSSGSVTP  GKKKKKKIGPKREKRSKSKRKEREEDDDDDDDDDSKSPKSSGSVTP  GKKKKKKIGPKREKRSKSKRKEREEDDDDDDDDDSKSPKSSGSVTP  GKKKKKKIGPKREKRSKSKRKEREEDDDDDDDDDDSKSPKSSGSVTP  GKKKKKKIGPKREKRSKSKRKEREEDDDDDDDDDSKSPKSSGSVTP  GKKKKKIGPKREKRSKSKRKEREEDDDDDDDDDSKSPKSSGSVTP  KROMPULGAKUPEKRETKKKKKRKSPKREREEDDDDDDDDSKSPKSSGSVTP  KROMPULGAKUPEKRETKKKKKERKSPRSTRUSPGKSGSVTP  KROMPULGAKUPEKRETKKKKKERKSPRSTRUSPGKSGSVTP  KROMPULGAKUPEKRETKKKKKERKERSPRSTPOLLAKMYKKAL  KROMPULGAKUPEKRETKKKKKERKERSKASANAAANAVAVUSWITAL  KROMPULGAKUPEKRETKKKKKERKERSKASANAAANAVAVUSWITAL  TEVAPPPPPVBUS TIKKATKERGKORPNARRYRETDDDDDTSKSPKSGALANAA  TEVAPPPPPVBUS TIKKATKERGKORPNARRYRETDDDDVSS  GUGSTSTRSSSSSKKRETERKOKREEVATOURSSPRVDAKKER  PRIVADLIT LIKADPPPPVBUS TIKKATKERGKERVATOURSKERDDDOTSKSPKSGALANAAANAVAVUSWITAL  GRAKERINSBEGELLERVGGOPSKRESSBODDLOVSSPPTDALSKER  GREARSTONSKERLETKKKKVKRESTERVATOURSSPRVDAKKKY  GREARSTONSKERLETKKYRETHRACHERSPRVTOURSTONSKERVETDDOTSKER  GREARSTONSKERLETKKYRETHRACHERSPRVTOURSTONSKERPTOURSCHERSPRVTANICATIONSKER  BEGEROKKIKKVKLIKKLERPPSTRUTOPTVKYEROPETDDATCH  TYPOMBIGMBYRFSWAGOTTTILADBEGGSKYRHVILTSYSE  LITTIDHAATIGS IDWACLIVDBAHERIKNNOSKYPRVLINTSYSE  LITTIDHAATIGS IDWACLIVDBAHERIKNNOSKYPRVLINTSYSLOH  TYPOMBIGMBYRFSWAGOTTTILADBEGGSKYRHVILTSYSE  LITTIDHAATIGS IDWACLIVDBAHERIKNNOSKYPRVLINTSYSLOH  TYPOMBIGMBYRFSWAGOTTILADBEGGSKYRHVILTSYSE  LITTIDHAATIGS IDWACLIVDBAHERIKNNOSKYPRVLINTSYSLOH  TYPOMBIGMBYRSHAGATATATATATATATATATATATATATATATATATATA	i		Í	· · · · · · · · · · · · · · · · · · ·
EVIERVSERTAILLIPEIMGLIQQYINGESSVRRACYPICLWAY  INVIGOBILAPHICAGINGSRIKLIAILYTERAGYGSGASSEREDMOALL  RESGRROBGLIQPFGRERKGMASGLGS PSPCSASSEREDMOALL  NISLIPPPIPERMEDDEBGLSSTRYPKLKKKKKKKPKPDDPKTPKS  KROKKERHALCAGLOSSGSGEPEVREREREVALEGISSGSGSPTPK  KROKKERHALCAGLOSSGSGEPEVREREREVALEGISSGSGSPTPK  KROKKERHALCAGLOSSGSGEPEVREREREVALEGISSGSGSPTPK  KROMMEDDRUVPSEEDVRYTUTTYKRAPSQSVRPLIAARIPKLANG  KROMMEDDRUVPSEEDVRYTUTTYKRAPSQSVRPLIAARIPKLANG  KROMMEDDRUVPSEEDVRYTUTTYKRAPSQSVRPLIAARIPKLANG  KROMMEDDRUVPSEEDVRYTUTTYKRAPSQSVRPLIAARIPKLANG  KROMMEDDRUVPSEEDVRYTUTTYKRAPSQSVRPLIAARIPKLANG  KROMPUCARMATESTANDPKGSSGSOSVANAAAAANAVVVESMVTA  KROMPUCARMATESTANDPKGSSGSOSVANAAAANAVVVESMVTA  KROMPUCARMATESTANDPKGSSGSDEPVREREREVRYDAAS VERPESSAGLI  KROMPUCARMATESTANDPKGSSGSBOLOVESSPDDAAS INSYSV  SUGSTSRSSRSRKKLRTYKKKKGEEVTAAVOGFEDDAGSTNSYSV  SUGSTSRSSRSRKKLRTYKKKKKGEEVTAAVOGFEDDAGSTNSYSV  COGGGSTILLOTPCRATHWUCHDRAFTERSKOCHLOKKUCKUGGEL  CUTCPSSTHILLICHNPLAPETSKOLORGPROOPVENGOGO  VMICKSVSSELOLLICAQVVERRUGHCEPRCTPAALGGVUCKUGGLIC  CUTCPSSTHILLICHNPLAPETSKOLORGPROOPVENGOGOS  VMICKSVSSELOLLICAQVVERRUGHCEPRCTPAALGGVUCKUGGLIC  CUTCPSSTHILLICHNPLAPETSKOLORGPROOPVENGOGOS  VMICKSVSSELOLLICAQVVERRUGHCEPRCTPAALGGVUCKUGGLIC  CUTCPSSTHILLICHNPLAPETSKOLORGPROOPVENGOGOS  VMICKSVSSELOLLICAQVVERRUGHCEPRCTPAALGGVUCKUGGLIC  CUTCPSSTHILLICHNPLATESKOLORGPROOPVENGOGOS  VMICKSVSSELOLLICAGVERRUGHCHCOCHLORGPROOPVENGOGOS  VMICKSVSSELOLLICAGVERRUGHCHCOCHLORGPROOPVENGOGOS  LILUTOPJQUNLEELGFILLINPLTPERFRHLIGGTICHNPLOVENGOGOS  CIKKLILDHIC VPIMACLICHNPLTPERFRHLIGGTICHNPLOVENGOGOS  CIKKLILDHIC VPIMACLICHNPLTPERFRHLIGGTICHNPLOVENGOGOS  CIKKLILDHIC VPIMACLICHNPLTPERFRHLIGGTICHNPLOVENGOGOS  CIKKLILDHIC VPIMACLICHNPLTTERLICAGGALLIALDHONDARICAGING  RESHINGONANDARICAGNACHAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	l			
INVIGIBILAPILISQLITGSEMELLINLYTERAQTGSGGADPYTUVS  GOS  133  5955  RESGERGEQLGQPFGEERECHISCISESPEPCEAGSEEREDMALL MISLIPPETERMERDPEREUSERTPEKLKKKKKPEREPEDMALL MISLIPPETERMERDPEREUSERTPEKLKEKTERKEREREPEDMALL MISLIPPETERMERDPEREUSERTPEKLKKKKKPEREPEDMALL REMOMBEDLINVESEEDYELTINKERSQFVERLARSDESCONTP CREAKTRUCKLGPKERKERSESEEDDDDDDDSKEPERSAGLL REMOMBEDLINVESEEDYELTINKERSQFVERLARSDESCONTP ERVAPLIKTILGARVESEEDYELTINKERSQFVERLARSDESCONTP TEVAPLIKTILGARVESEEDYELTINKERSQFVERLARSDESCONTP ERVAPLIKTILGARVESEEDYELTINKERSQFVERLARSDESCONTP TEVAPLIKTILGARVESEEDYELTINKERSGFVERLARSDESCONTP ERVAPLIKTILGARVESEEDYELTINKERSGFRENDERDDFUNGMAT ERVAPPEPPEVBEVETERATKERGSFRENDENDERDDFUNGMAT TEVAPPEPPEVBEVETERATERKERGEBETPERDEDFUCK COGGET TILCTCPRATHEVCLIPPUMERAPEGMESCPHEDROPTCS COGGET TILCTCPRATHEVCLIPPUMERAPEGMESCPHEDROPTCS COGGET TILCTCPRATHEVCLIPPUMERAPEGMESCPHEROPTEVBOORTS COTTESSYNTHICIANP PLPEI DONGENLOTECTCOALKGEVOKTLI.  CITCTPSSYNTHICIANP PLPEI DONGENLOTECTCOALKGEVOKTLI.  WERKORDPSTPVENDED PLDEI DONGENLOTECTCOALKGEVOKTLI.  WERKORDPSTPVENDED PLDEI DONGENLOTECTCOALKGEVOKTLI.  WERKORDPSTPVENDED PLDEI DONGENLOTECTCOALKGEVOKTLI.  WERKORDPSTPVENDED PLDEI DONGENLOTECTCOALKGEVOKTLI.  WERKORDPSTPVENDEN PLDEI DAT WERKORDERPSTVENDER PVENDER ERGEPEKKLERVELALOTELARSDEVELOPDERVELKERDEPSTEUD FVENDER ERGEPEKKLERVELALOTELARSDEVELOPDERVELKERVELLATURING ERGEPEKKLERVELTEREPENLARSDEVELDEN LEVELANGE  LITUDAALIGE IDMACLITYDERHEILINGSEFFENLANDLERCCHIPPT LITUDAALIGE IDMACLITYDERHEILINGSEFFENLANDLERCCHIPPT LITUDAALIGE IDMACLITYDERSEELINGSTLENDERSEELING VERTENAGENERSEELINGSERVELTERDERSEELINGSTLENDERSEELING VERTENAGENERSEELINGSERVELTERDETENGENERSEELINGSTLENDERSEELI	İ		ļ	SARKAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT
5955 RSSGRRÖBQLGOPFGRERKCHASGLGSPSPCSAGSEREDMINAL NISLIPPITEMERDPEBULSETETPKLIKKKKYPKAPDPKIPKS KROKKERMIJCAGLGISSGBGBEFVERBERVALRSDBEGSDTTP GRKKRICGISPKEKKSKSKSKEREBERDDDDDDSKEPKESSÄGLI BOMOMBDDHVFSEEDYHTLTINYKAPSGPVEPLIARKYRKANG KRIMMULGAMBEFSTRIPPKOSSGASVANAANAVVESIMVTA TEVAPPPPPVBVDIRKATKEGGSOPARRARKEGSPVEPLIARKYRKANG PREVAPLIK KLIGGGGSKRESSSGADLANAANAVVESIMVTA GRAKENGISPKETTHRIKARSGSADPARRARKEGSPVEPLAKERK PREVAPLIK KLIGGGGSKRESSSBDDLIUGSFFDDASINSTSY SDGSTSRSSRSKKLBTTKKKKIGBEBVTAVDGYETDRODYCSV CQGGSTILLOTCPRATIBHVCLIPDHEKSAPSCPPCKREGI (WRAKENSBGBBILREVGGDLEEDCHHMEFCRVCKOGGELLC CUTCPSSYHIHCIANPIDERIDPROSBROPPGGBREKK KURKENGISPSPHERPTVDPTVLOLPDHEKSAPSCPPCKREGI (WRAKENSBGBBILREVGGDLEEDCHHMEFCRVCKOGGELLC CUTCPSSYHIHCIANPIDERIDPROSBROPPGGBREKK KURKENGSPSPHERPROSPERROPPVROGGBLE  GRERINGSPREMERPTVBPDALDBERGPROSPROPPVROGGBS KSHERINGSPFARMERPTVBOTSTELBRESPROPPVROGGBEKK NIHISTROFFFARMERPTVBOTSTELBRESPROPPVROGGBEK S\RERKINGSPFARMERPTVBOTSTELBRESPROPPVROGGBEK HYNTLIKHROLPPVQABMESSBUVELQDYDLEKGSVMHERLINGS BEGGPKKLIKEVKLRELRERPSTTYDPTVLYVLYVLYSI LYBGBERGBPTVARANLARESPROPPTTVDFTVARVLYSIS HABPGMESBERTVARANLARGKRAVARANDVAVLYTYOGS BEGREKKLIKEVKLRELRERPSTTYDPTVAVLYSIS LYBGBERGAPTKARVARARGARGYASIALINGSVERSTURSTSLOPH LYBGATKURLARESPROMATERSTANDSKRAVERSAVKHULLTSYE LITTIBALIGSTDMACTLOVERARLENDGKRYFFEVLNGYSLQHK LLLITGTPIQNALEBERHLIMPITTEBEFFALISPTLSSPLSBPALOR DERAITRESPROSPETTOMATROGKRAPRIKARAVKHUSTSTELBRA LEFVAMBAPRINGSANDVEKNINGSKERSTLLVKWELSPR\Q KKYXYLYLLIBESTYRERLIGGTLSSVINGSVARGHENDELSPR\Q KKYXYLYLIBESTYRERLIGGTLANARGANGSVARHANDVANDLKKCCHNEYS LEFVAMBAPRINDLLEDGHLERGSTYRERLIGGTLANARGANGSTLANARGANGS BERGBERGVEKNINGSANDLARGANGSTLANARGANGSTLA			]	KVIERVSKETLNLLLPRIMPGLIQGYDNSESSVRKACVFCLVAV
5955 RSSGRRJGDLGOPFGRERKGMAGGLGSFEPCSAGSEKEDMALL NNSLPPHIPEMEND PEDLSKTFPRIJAKKYRDPPTI PER KROKKERMALC-GJ-GDSSGG-DEFVERREEVALR-SDSEGSDYTP GKKKKGKJG-PKKEKKSKKREBEREDDDDDDSKEPSAGLL RDMGMBDTDHVPSERDYRTLTNYKAFSG-VEPPLIJAKRYPLIANS KROMKULGARME-STINIPFKGSGASVAANANAVAVUEMVTA TEVAPPPPPVEVETIRATKERGSGNAPARTRAPVELIJAKRYPLIANS SUGSTBRS-SBS-RKKLRTTKKKKKGSEBU-VADOVETIDEODYCKY CQGGEI ILCDTCPRATHMYCLDPUMEKAPEGKWSCDPLCKEGOL UMEARDNSGGBEILERU-GSDLEKEDDHHMSFCRUCKDGELLC CDTCPSSYHILCHINPLDE I DRIGBMLCDRCTCPALKKEVGLIG WEMAGDPSSTTVPRPPDADPHTESPYRJGLEGREPROFFVKRGGMS YMHCGWSELGLEHC-QWMENTYGRKDGERBRGOFFVKRGGMS YMHCGWSELGLEHC-QWMENTYGRKDGERBRGOFFVKRGGMS YMHCGWSELGLEHC-QWMENTYGRKDGERBRGOFFVKRGGMS YMHCGWSELGLEHC-QWMENTYGRKDGERBRGOFFVKRGGMS YMHCGWSELGLEHC-QWMENTYGRKDGERBRGOFFVKRGGMS SARRIKNDPFRAMBERPYRYGIKEBM-MWIIRITAINSTVKGG BEGEPGKKLKEVKIRKERPPSTT-TDPPVKYRGDEVLIANTGG TLHPYQMEGLNWILFSUNGGTT-TILADBRGGLKGY-VANTRUCKER BEGEPGKKLKEVKIRKERPPST-TUDPPVKYRGDEVLIANTGG TLHPYQMEGLNWILFSUNGGTT-TILADBRGGLKGY-VANTRUCKLTSTE LITTIDMA'LIGS IDWACL-TUDEARRIKLKNOSKFFFVLNOSYLGUK LLLTGTPJCJNNLEELSHLIANST-TERERFFFRUNGS/LEBEALKEN- LLTTGPPLQNNLEELSHLIANST-TERERFFRUNGS/LEBEALKEN- LLTTGPPLQNNLEELSHLIANST-TERERFFRUNGS/LEBEALKEN- KYYTK'Y TILISEKTIKALM'ARGGGNOSYLIANVMULKKCCNBEY LPFVAMMER JPWHERPIKADVFRONSYENTHNOSYLGUKKCNBEY LPFVAMMER JPWHORMYGGS LITRAGSKLIANKALKANLKRLEGGE- RVLIFSGMTRNLDLLEDL-PRIBEGYKYRRIDGGITGNBGGD RSSSINTSNSKSCILDULKFGTBELFKGEATDGGGITMGGD ARSBARITGGMKKVM'I KYRYTRASVERLITGVAKKMMLHHLIV RGGGRITEKGWYNTNGS-GDBROWDODGSONSWISSENGEB SSVIHTDOKAL TREILDRINGDETBUTLGVANKKMMLHEHLIV REBMGEBEUEBEI KROBESVDDDYWKKLIRHHYGOGDBLAR RGGGRITEKGWYNTNGS-GDBROWDODGSONSVANSEGGBE DFDRESBAPRRPSRKGLRHDKKOSSG-SPSKTPTPTSTETDTOTOP NTPAPVPPAEDGI I KIERSILLSKERSI BGGEKWSKAPVASVSI- MEHLCFFGGALGATT-FADGUT FREEDERSHINGSTWANSBORGED DFDRESBAPRRPSRKGLERHDKORGSSEKKEREKKWAVSI- REBMGEBEURGI I KIERSILLERESI BGGEKWSKAPVASVSI- REBMGERGERUFLAR TREIDFYRDGESINGENDERGENDANGGD NEDFLANTYRHREBDFYTAR FTPVAVRI-QMSERNILSRLANRAP PSYMALTRPADVGLAGES I HIGHCYARGDI ONDFRAILASRLANRAP PSYMALTRPADVGRAGGS-SPSKUTPTST	ţ			HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS
5955 RSSGRRJGDLGOPFGRERKGMAGGLGSFEPCSAGSEKEDMALL NNSLPPHIPEMEND PEDLSKTFPRIJAKKYRDPPTI PER KROKKERMALC-GJ-GDSSGG-DEFVERREEVALR-SDSEGSDYTP GKKKKGKJG-PKKEKKSKKREBEREDDDDDDSKEPSAGLL RDMGMBDTDHVPSERDYRTLTNYKAFSG-VEPPLIJAKRYPLIANS KROMKULGARME-STINIPFKGSGASVAANANAVAVUEMVTA TEVAPPPPPVEVETIRATKERGSGNAPARTRAPVELIJAKRYPLIANS SUGSTBRS-SBS-RKKLRTTKKKKKGSEBU-VADOVETIDEODYCKY CQGGEI ILCDTCPRATHMYCLDPUMEKAPEGKWSCDPLCKEGOL UMEARDNSGGBEILERU-GSDLEKEDDHHMSFCRUCKDGELLC CDTCPSSYHILCHINPLDE I DRIGBMLCDRCTCPALKKEVGLIG WEMAGDPSSTTVPRPPDADPHTESPYRJGLEGREPROFFVKRGGMS YMHCGWSELGLEHC-QWMENTYGRKDGERBRGOFFVKRGGMS YMHCGWSELGLEHC-QWMENTYGRKDGERBRGOFFVKRGGMS YMHCGWSELGLEHC-QWMENTYGRKDGERBRGOFFVKRGGMS YMHCGWSELGLEHC-QWMENTYGRKDGERBRGOFFVKRGGMS YMHCGWSELGLEHC-QWMENTYGRKDGERBRGOFFVKRGGMS SARRIKNDPFRAMBERPYRYGIKEBM-MWIIRITAINSTVKGG BEGEPGKKLKEVKIRKERPPSTT-TDPPVKYRGDEVLIANTGG TLHPYQMEGLNWILFSUNGGTT-TILADBRGGLKGY-VANTRUCKER BEGEPGKKLKEVKIRKERPPST-TUDPPVKYRGDEVLIANTGG TLHPYQMEGLNWILFSUNGGTT-TILADBRGGLKGY-VANTRUCKLTSTE LITTIDMA'LIGS IDWACL-TUDEARRIKLKNOSKFFFVLNOSYLGUK LLLTGTPJCJNNLEELSHLIANST-TERERFFFRUNGS/LEBEALKEN- LLTTGPPLQNNLEELSHLIANST-TERERFFRUNGS/LEBEALKEN- LLTTGPPLQNNLEELSHLIANST-TERERFFRUNGS/LEBEALKEN- KYYTK'Y TILISEKTIKALM'ARGGGNOSYLIANVMULKKCCNBEY LPFVAMMER JPWHERPIKADVFRONSYENTHNOSYLGUKKCNBEY LPFVAMMER JPWHORMYGGS LITRAGSKLIANKALKANLKRLEGGE- RVLIFSGMTRNLDLLEDL-PRIBEGYKYRRIDGGITGNBGGD RSSSINTSNSKSCILDULKFGTBELFKGEATDGGGITMGGD ARSBARITGGMKKVM'I KYRYTRASVERLITGVAKKMMLHHLIV RGGGRITEKGWYNTNGS-GDBROWDODGSONSWISSENGEB SSVIHTDOKAL TREILDRINGDETBUTLGVANKKMMLHEHLIV REBMGEBEUEBEI KROBESVDDDYWKKLIRHHYGOGDBLAR RGGGRITEKGWYNTNGS-GDBROWDODGSONSVANSEGGBE DFDRESBAPRRPSRKGLRHDKKOSSG-SPSKTPTPTSTETDTOTOP NTPAPVPPAEDGI I KIERSILLSKERSI BGGEKWSKAPVASVSI- MEHLCFFGGALGATT-FADGUT FREEDERSHINGSTWANSBORGED DFDRESBAPRRPSRKGLERHDKORGSSEKKEREKKWAVSI- REBMGEBEURGI I KIERSILLERESI BGGEKWSKAPVASVSI- REBMGERGERUFLAR TREIDFYRDGESINGENDERGENDANGGD NEDFLANTYRHREBDFYTAR FTPVAVRI-QMSERNILSRLANRAP PSYMALTRPADVGLAGES I HIGHCYARGDI ONDFRAILASRLANRAP PSYMALTRPADVGRAGGS-SPSKUTPTST	Ì		]	GQS
NNSLPPHENBEDPERULSETETPLIKKKEPKERPDATIPES RQQKERMLLCQLGDSSGEPETPUREERPVALSBESGEDTPT GKKKRIGUGPKEKKSKSKRKREBEDDDDDDDSKEPKSSAQLL RDMGMEDDTHYFSEEDYRTITMITSGEPVRFLARRIPKASQL RDMGMEDDTHYFSEEDYRTITMITSGEPVRFLARRIPKASQL RMMVIGAKMESTETNIPFRGSGASHVAAANAVVESMYTA TEVAPPPPPVBVDTRKATKEGGASPRARRKKSSFRVEDAKKFK PRKVAPLKKIKLGGGSKRKRASSSBODDLDVGNAVVESMYTA SUGSTSRSSRSKKLETTKKKKGSEEVTANDEYETDRODYCSV CQGGSLILCTOCTPATHBUCLDPUMKERPSCPUKCKGSKVCKLIA GWERKENSBGRSTLERVGGDLEREDDHIMSCPUKCKGGELC CDTCPSSYHILCTAPPLDEVICLDPUMKERPSCPUKCKGGELC CDTCPSSYHILCTAPPLDEVICLDPUMKERPSCPUKCKGGELC CDTCPSSYHILCTAPPLDEVICLDPUMKERPSCPUKCKGGELC CDTCPSSYHILCTAPPLDEVICLDPUMKERPSCPUKCKGELC CDTCPSSYHILCTAPPLDEVICLDPUMKERPSCPUKCKGELC CDTCPSSYHILCTAPPLOPERDE PKPLGRPERPOPPVKRQCKS VMICHWESELQLELH-(QVMPRHYGRKDHERPPCDGFVKRQCKS) VMICHWESELQLELH-(QVMPRHYGRKDHERPPCDGFVKRQCKS) S\RRENKNDSPFAPMERPY VFQ IKESW\MITHIRITIANISVDKKG BEGEFGKKLKKVKLRELRSPETTVDFVKRQSVMNIRKLMG BEGEFGKKLKKVKLRELRSPETTVDFVKRQSVMNIRKLMG BEGEFGKKLKKVKLRELRSPETTVDFVKRQSVMNIRKLMG BEGEFGKKLKKVKLRELRSPETTVDFVKRQSVMNIRKLMG BEGEFGKKLKKVKLRELRSPETTVDFVKRQSVMNIRKLMG BEGEFGKKLKKVKLRELRSPETTVDFVKRQSVLANDISVLGKK LTHPYQMBLDMIRRESNAQGTDTILLDBMGLKKTVQLTVLYSTS LTHPYQMBLDMIRRESNAQGTDTILLDBMGLKKTVQLTVLYSTS LTHPYQMBLDMIRRESNAQGTROTILLDBMGLKKTVQLTVLYSTS LTHPYQMBLDMIRRESNAGGTNALLDCHARDDMY-VTVTYGKS RKYTKYLTHIBETRADVFKNNFGKTLLV\KVELSPM\Q GKKLIBDHG\PHILIBFLKADVFKNNFGKTLLV\KVELSPM\Q GKKLIBDHG\PHILIBFLKADVFKNNFGKTLLV\KVELSPM\Q KKYTKYLYTILBETRADJLLEDCHERHERNOGSKUTLVANDLKKCCNMPY LEFVAMMERPKMNFGNTDGSALIRASGKILLLQNHLKRCCNMPY RRAGAGOFCCHLISTRAGGLAINLATADTVLIVIDSDMMRPIDIQ APSSARIFGGMKKVMTYRPVTRASVELTITVANKGURMINGLE GRENGEEEVERBLIRQBSVDPDYWEKLLRHHYPQQGBDLAR NIGKGRIRRRCKVYTRDGSGRONDGDDGSUNGGBD SSVIHTDDKALTBLATTVANGGSGBDRONDDGSUNGGSDTSTYDTSTPATLGCT MIKKGRRSNBELASVERNKMSQGSSSSKRPRPTSTFTCPDTQD MITTAPPUPPABEG GRENTUTURIJARGRISTOTILCMSLEKKERSEIGEKEKAVSLAVSLAP MHICEPGGGGGATTFADGTYPGGSURGGELGRQUNTANGLIKKERSPACH REBINGERSENGLARDNINGSGGSSSTRTPTPSTFTCPDTQD MITTAPPUPPABEG AADVEKVERGSALDLTPUVERKERSEIGERGWNGLANDSLIKSERKANAP PSMALMTRADVKLLAGERIDLERDKVN	6005	133	5955	
REGRENALICAGILGDESGEGEPTVERRENZALIDGESGEGEPTT GREKKIKLIGPIKKERKERERDIDGESKEPTSAGLI KDMMEDTOHVESEEDYRTITMYKAPSQEVRPLIAAKNPKIAVS KMMAVIGAKMESPSTNIPFKGSSGASVAAAAAAVAVESMYTA TEVAPPPPPVEVETRIKAKTKEKGKEPNERREPKGSBRVPDAKKEK PRVAPIKI KIJGEGERKRESSBODLUVESDPIDJASINSTYV SUGSTERSSERSKILETIKKEKGEGEVATVADGYETDHQDYCSV SUGSTERSSERSKILETIKKKKKGEGEVATVADGYETDHQDYCSV CQGGGIILCDTCFRATHUVCLIPPMKKAPGKMSCPHCKEGII CUTCPSSYHIHCINPPLPBIPMGEWLCPRCTCPALKGKVQKILI WKMGQPESTTVPRBPDADDYTTSEVRLEGRERGFYCKGGGILG CUTCPSSYHIHCINPPLPBIPMGEWLCPRCTCPALKGKVQKILI WKMGQPESTTVPRPPDADDYTTSEVRLEGRERGFYKRQGKS YMHCSAVESLQLELHC, QUMPRNYQKINDDSPPSGDFGGDEK S\REKRINDPYKAPABERPYRYGUKPFKQCMS YMHCSAVESLQLELHC, QUMPRNYQKINDDSPPSGDFGGDEK HVHLIKMGDLPYQAASMESEDVEIQDYLFKQSYMHERSLIMG BEGEPGKKLKKYKIKKBERPFSTYVDPTVKYERCPFSTLDATAG HVHLIKMGDLPYQAASMESDFVIQOVDLFKQSYMHERSLIMG BEGEPGKKLKKYKIKKBERPFSTYVDPTVKYERCPFSTLDATAG THAPYOMESLAWIRFSMAGGTTTILLDBEAKTVYTAVELYSI IKTOBALIGSIDWAGCITALINGGKKASRMKKEASVKFHVLLTSYE BEGEPGKKLKYKIKRKLERPFSTYVDPTVKYERCPFSTLDATAG UKKLIDMIG, YHHLERIKADYFKNMPSKTELIV\RVELSFM\Q QKKELDMIG, YHHLERIKADYFKNMPSKTELIV\RVELSFM\Q QKKELDMIG, YHHLERIKADYFKNMPSKTELIV\RVELSFM\Q QKKELDMIG, YHHLERIKADYFKNMPSKTELIV\RVELSFM\Q QKKYKYK\YILHGSFILKADYKNMPSKTELIV\RVELSFM\Q QKKYKK\YIK\YILHGSFILKADYKNMPSKTELIV\RVELSFM\Q QKKYKK\YIK\YILHGSFILKADYKNMPSKTELIV\RVELSFM\Q RYLIFSOMTKMI.DILLEDPIJHBGYKYRTLIGGITCNMRQBATDR RPAPGAQQFCPILLSTRAGGIGITALADTVILYDSUMPINDIQ AFSBARITGQKKYMIXTRYTYRASVERZITQVAKKRMMIHILVV RPGIGSKTGSMSKQBLDDIDLODETEDTBLGCMNSTILSFKWAGNEGD SSVIHTDDATALBELLDRINGDFTEDTBLQCMNSTILSFKWAGNEGD SSVIHTDDATALBELLDRINGDFTEDTBLQCMNSTILSFKWAGNEGD PERRESEAPRRPSKRGLRINDKOKP.PFLLARVGGNIBSVGASHG ARBEMBEEEEVBBRIKGGESDDHOMDODSYSVAASBEGDE DPERRESEAPRRPSKRGLRINDKOKP.PFLLARVGGNIBSVGASHGEN ARDWEKVERKSAJILDTITURDLERGERKYKTAPETTAIRCT QAPAPASBOBKVVVPPPEGEBKVKKABVKRKTERFTTRICKG ARDWEKVERKSAJILDTITURDLERGERKYKTAPETTAIRCT QAPAPASBOBKVVVPPPEGEBKVKKABVKRKTERFTTRICKG ARDWEKVERKSAJILDTITURDLERGERKYKTAPETTAIRCT PSHMTVILFREPGOVAGOO  DEPLRITORIAGERGALTEGOLINGDENDITURSCOPSTROPTICHTIKT REHIGDRAGKANTARAVS BEHBE	1			
GEKKIKCHLEPKERENSKEKEREREEDDDDDDDSERFERSAGLI  ROMGRED I DHVFSEEDVYRLTHYKRAFQFYPRELIAANIPKIAVS  KMMVILGARWREFSTNIPFKGSGASVAAAAAAAVAVVESMYTA  TRVAPPPPPVEVPTIKAKKKEGKGPNARREPKGSFRVARKYK  PRKVAPLAK KLGGGGGRKRESSSENDLUVESDFDDAS INSYSV  SUGSTERSSRSKKLETTKKKKKGEEVTAVDGVETDHOPYCKSV  CQOGGET LILDTCPRATHWYCLIPPMKRAFGKMSCHPICKEK  CWEAKDINSGEET LIREVGGDLEREDDHHMSFCRVCHGGELLC  CUTCPSSYHIHCLINPPLPEIPPMERLCPRCTCPALKGKVQKILI  WKMGQPPSTFVPRPDADDPHTPSFRELGRERERGFPVKQGMS  YMHCSWVSELQLELIC CQWFRINTQRKINDDEPPSGPODEKK  S\RERKINDPKPAEMERFPYRVG KEPS\MATHRILAHISYDKKG  BEGEPGKKKKKKKKKKKKKKRKFRKBEPSTFYLVFKEROPFYLDAVISL  YKKGHSKGFFIVSAPLSTI IN\WEREFMADDHYV\VTYVCIK  BERLIERKESS\LEDHALKSVARKKAKKKKKKKKAKKKAKKKASVKFHVLLTSYE  LITIDMAILGSIDMACLIUDBAHLKRINGSKFFFKVENSSPLAKE  OIKKLIDMIG\PHARRESOLOFKNINGSKFFFKVENSSPLAKE  OIKKLIDMIG\PHARRESOLOFKNINGSKFFFKVENSSPLAKE  OIKKLIDMIG\PHARRESOLOFKNINGSKFFFKVENSSPLAKE  OIKKLIDMIG\PHARRESOLOFKNINGSKFFFKVENSSPLAKE  OIKKLIDMIG\PHARRESOLOFKNINGSKFFFKVENSSPLAKE  OIKKLIDMIG\PHARRESOLOFKNINGSKFFFKVENSSPLAKE  OIKKLIDMIG\PHARRESOLOFKNINGSKFFFKVENSSPLAKE  OIKKLIDMIG\PHARRESOLOFKNINGSKFFRKVENSSPLAKE  OIKKLIDMIG\PHARRESOLOFKNINGSKFFRKVENSSPLAKE  OIKKLIDMIG\PHARRESOLOFKNINGSKFFRKVENSSPLAKE  OIKKLIDMIG\PHARRESOLOFKNINGSKFFRKVENSSPLAKE  OIKKLIDMIG\PHARRESOLOFKNINGSKFFRKVENSSPLAKE  OIKKLIDMIG\PHARRESOLOFKNINGSKFFRKVENSSPLAKE  OIKKLIDMIG\PHARRESOLOFKNINGSKFFRKVENSSPLAKE  OIKKLIDMIG\PHARRESOLOFKNINGSKFFRKVENSSPLAKE  OIKKLIDMIG\PHARRESOLOFKNINGSKFFRKVENSSPLAKE  REPURGSCTISTSKSKELDLIKEFTERFKENSCHLILLQKMIKNLEEGGH  RULTFSQMTKMIDDLILBDFLEHGSKVINGSKLILLQKMIKNLEEGGH  RULTFSQMTKMIDDLILBDFLEHGSKVINKRESTUTIVINKSKMINGSKARK  REPURGSCTISTSKSKELDLIKEFTERFKINGSCHARRESOLOFKNINGSCALDR  RESGRESTERSTRANGSVENSCHANGVINGSCHAKKANTILLQKMITHISTUTIVINGSCHAMATHISTUTIVINGSCHAMATHISTUTIVINGSCHAMATHISTUTIVINGSCHAMATHISTUTIVINGSCHAMATHISTUTIVINGSCHAMATHISTUTIVINGSCHAMATHISTUTIVINGSCHAMATHISTUTIVINGSCHAMATHISTUTIVINGSCHAMATHISTUTIVINGSCHAMATHISTUTIVINGSCHAMATHISTUTIVINGSCHAMATHISTUTIVINGSCHAMATHISTUTIVINGSCHAMATHISTUTIVINGSCHAMATHISTUTIVINGSCHAMATHISTUTIVIN	ļ			
INDMEMDITION TO STREET YRTITITY KAPSQYPYELLAKINELINES RMMYLLAKWRISTSTNIP PEKGSGAGNAYAAAAANAVAVUSIMTYA TRYAPPEP PEVBYTRAKIKKEKGEBPRARKIKEK PRWAPLKI KLIGGIGSKRIKSISS BODDLOVESDYDAKIPK PRWAPLKI KLIGGIGSKRIKSISS BODDLOVESDYDAKIPK PRWAPLKI KLIGGIGSKRIKSISS BODDLOVESDYDAKIPK GOGGSI ILCDTCTRATHAVICLD PUMBKKAPEKINSCHECKEGI CUTCPSSYHIHCIMP PLPBI PMGKBLCPRCTCPALKEVOKILLI WIKNGOPESTPYPRP DADDNYTPS PKLOFROWYCOMS YMHCSWVSELQLELHC\QVMPRNYQRKINDDBPPSGDFOGDEKE CUTCPSSYHIHCIMP PLPBI PMGKBLCPRCTCPALKEVOKILLI WIKNGOPESTPYPRP DADDNYTPS PKLOFROYDYWGOMS YMHCSWVSELQLELHC\QVMPRNYQRKINDDBPPSGDFOGDEKK S\RRKINDDPYNASHSEDIVEI QVYDLAFQGYMNHRISLIMSG HVHILIKRINDLPYDAASHSEDIVEI QVYDLAFQGYMNHRISLIMSG REGEPGKKLKKYKLRKUBPPSTPTVDPTVYTERGPTLDATIGG HVHILIKRINGLAWIGTTHILADBELGKTUVIAVVITVOKK REGERGPFLVSAPLSTI IN\WREEPEMADDMYV\TVYOKG SARII TREBERSY\PEDDA TITGGKKASRIKKASVKFHULITSYE LITIDMAILGS IDMACLI VDEAHRLKNINGSKPFRVINGYLLGHK LLLITGTPIQINALBELGHILLINFITTERRHINLBGFLEERAD ILKEG QIKKLIDMIG\PHALBELKADVFKNMPSKREJIV\CRUSTSPM\Q QKKILDMIG\PHALBELKADVFKNMPSKREJIV\CRUSTSPM\Q QKKILDMIG\PHALBELKADVFKNMPSKREJIV\CRUSTSPM\Q KYYK\YTL\GSFFIKALM\ARGGGROYSLLINVABLKCCNMPY LPFVAMMERPHYMPGWYDGSALITANGGKLLILLQKMLKCCNMPY LPFVAMMERPHYMPGWYDGSALITANGKREJOHINGGALIRA RIGGGRI LAGGGRIGHINTATUTISDEMPHINDIQ APSRAHRIGQNKKWMIYRPVTRASVERITOVAKKMMLTHLIVV RRGIGSKTGSMSKQELDDILLEGFREHEKVENTINGGEDINEGEG SSVIHTDOKALBELLDINGDETEDTBLQCMNSTLISSFKNQVVV RREBMGEBEBVERBI IKQESSVDDDYWEKLLBHHYGQGBDINGGD SSVIHTDOKALBELLDINGDETEDTBLQCMNSTLISSFKNQVVV RREBMGEBEBVERBI IKQESSVDDYWEKLLBHHYGQGBDINGGD DPERRSBAPRPSRGGRONDKOKPLPFLLARVGGRINGGFF ANDREVKERSANDELLEVEENKOKGOGOSPSTETTSTGOTOQP NTPAPPP BERGGI ILKERGSI GREKWASTABETTA IKCT QAPAPASBDEKVVVPPPEGGEBKVKKABVKEKTBERMTERKKA ANDWEKVERKSANILDETTVADEKKEKSEBEKKWINGONGSTP KERHWINGRWSPELLAKVERSANDERSKEKKASTADETTA IKCT QAPAPASBDEKVVVPPPEGEBKVKRABVKEKTERFRITBRCGG ANDWEKVERKSANILDETTVADEKEKKEEBEKKSWINGONGSTP KERHWINGRANDELLAKESSANILGRESHKERSTLISGLINGE BERLISDINKADATI IPVAVRILOMERATITISTEDEN PEPEGD NEGHTETVI PTILKKRADICLAESBUNVANILGKETHA PEPTQOVAQOQ  DIDELERTVORTHEPPTAR	I	1		<b>1</b> —
MMMAULGARMERSPINDPEKGSGGANAANAANAVESMUTA TEVAPPPPEVEVPTRAKKTKGGKOPNARERYGSPRUPDAKTOK PKKVAPLKIKUGGPGSERRESSERDDDLDVESDFDDASINSYSV SDGSTERSSESERKIKITTKKKKKGEEVTAVDGSTETDHOVICSV CQGGSILLCTCCPRAPHUCLDPIMKKPCKUTGGEELCH CUTCPSSYHIHCLMPPLDEIPMGKELCPCTCPALKGKVGKLL UNTGSSYHIHCLMPPLDEIPMGKELCPCTCPALKGKVGKLL WEWGOPSSTPUPREPDADDNIPESPKDLGREBROPFUKGGEELL WEWGOPSSTPUPREPDADDNIPESPKDLGREBROPFUKGGEELL WEWGOPSSTPUPREPDADDNIPESPKDLGREBROPFUKGGEELCH WEWGOPSSTPUPREPDADDNIPESPKDLGREBROPFUKGGEELCH WEWGOPSSTPUPREPDADDNIPESPKDLGREBROPFUKGGEELCH WEWGOPSSTPUPREPDADDNIPESPKDLGREBROPFUKGGEELCH WEWGOPSSTPUPREPDADDNIPESPKDLGREBROPFUKGGEEL SYREKKNOPKFABMEERFYRGIKERDWIMMERLAMES SKEREKKOPKFABMEERFYRGIKERDWIMMERLAMESPDKEG BEGEPGKKKKKKUKKUKKURDPSTYDDLFUGSPWADTAGE BEGEPGKKKKKKUKKUKKUREPSPTTUPTUFUSPDATGG BEGEPGKKKKKUKKUKKURENDPSTYDLTUTAVELYSIL YKKGHISGFUVSPLSTIINWEELPEMDAVVVVTYUSPL YKKGHISGFUVSPLSTIINWEELPEMDAVVVVTYUSPL YKKGHISGFUVSPLSTIINWEELPEMDAVVVVTYUSPL YKKGHISGFUVSPLSTIINWEELPEMDAVVVVTYUSPLANGE BERAFACHOLOGIALUMELEMILINFTTDERFINLBGFLEBPADTAGE OIKKLIDMIGGIPHAACLIVDRAHELKINGSKEFEKVLASYSLOHK LLLTGTPLJOHNLEELPHLANAGGGENGYKKEASYKEPVLLTSYE LITIDMALIGSIDMACLIVDRAHELKINGSKEFEKVLASYSLOHK KYYTKYTLIHSEFLKALNIAAGGGGNOSTAWMELAWSSLOHK VKYTKYTLIHSEFLKALNIAAGGGGNOSTAWMELAWSLAGKEE LEFVAAMBAPMPWWYDGSALIRASGKLLLLOKMLEKCHBEY LEFVAAMBAPMPWWYDGSALIRASGKLLLLOKMLEKGGH RVLITSGATTRHIDLIKDFLERBYKYRRIDGGTIRGMRQEAIDR RRAGGGGCTLLISETRAGGIGIINLATADTVIIYDSDWNPINDIQ REGIGSKTGSWSKGELDILIKFUGTHARA REGIGSKTGSWSKGELDILIKFUGGGONEGGEE SSVIHYDDKALBEILULIKGTBESVDPAYWEKKMATHLUNGGGDBLAR RKGGGEEEVERBIIKGRUNGDETBELGCMNSTLGSBERKEKAMTHLUV RRGGGSKTGSWSKGEGDDWDDDCSLINGSDSWSKARKAKKAMTHLUV RRGGGSKTGSWSKGGGDDWDDDCSLINGSDSWSKARKAKAMTHLUV RRGGGSKTGSWSKGGGDDWDDCSLINGSGGDERGEGD DEDERSBAPREPSKGLRINDKKKLPPLIAAGGGINSTLGFRANST RHTUPCKRSWSPELLAWERSHAMATHTGGGGONGGETK MEHLCERGADGABTFADGVPREGISRGWVITTIGWBLIRKKUQ REFILVGRINGARGADPTTOMILVDLAGGSEKEKKAVUSLGETHA PERHONDRILAGRINGARGADTOMATHATIGKT YEIHRRHUPWHLAGIIINGTARMODIONDETPTPTIPTEMDPTOPTOP REFILVGRINGARGADPTALISTLANGEPSKGE PETOQUAQOO  DEDELBRITYPTIPTIC	ĺ	ļ		
TRVAPPPPPPVBVIKAATKEGKSPANARREPKSPRVPDAKKER PKKVAPLKI KLGGPGSIKRRSSSRDDLLDVESDFDDAS INSYSV SDGSTERSSRSKKLRITKKKKIGEBEVTAVDGYETDHODYCEV CQGGEI ILCDTCPRATHMVCLDPDMEKAPEKKNSCHCEKEGI GWEAKENDSGEGELER WEGGLEKEBHAKSCEVCGGELLC CDTCPSSYHIHCIANPELPIPORGWILCPKCTCPALKGKVQKLLI WKWGQPPSPTPVPRPDDADPNTEPSER LEGGPERGPPVKRQGMS YWHCSWVSELQLELHC\QVMFRNYQRKNDMDEPPSGDFGGBEK S\REKKNEDEFYPVRPDPDADPNTEPSERGERPEROPPVKRQGMS HVHILIKMEDLEYDQASMESGDWIGDFKGGYENGPKGGGELC ERGEPGKKLKKVKLRKLERPPETPTVDPYLVKYEOPSTLDATGG ERGEPGKKLKKVKLRKLERPPETPTVDPYLVKYEOPSTLDATGG TILHPYQMESLINIERSFNANQGTDTILDDRGGGKTVQILVAPLYSL VKEGHEKGPFLVSAPLSTIIN\WEREPEMAPDMYV\VTYVGDK DSRAIIRENEPS\FEDMAINSGKKASRWKEASVKPHVLLTSYE LITIDMAILGSTDWACTJVDEARRIKANGKSFFVLUSGYSLQHK LLLTGTPLQNNLEELFHLLMFITEPFHILKGFLEGFADIAKED QIKKLIBMLG\PHARIKADVFKNAPSKTRILV\PKVELSPH\Q KKYYK\YILHSKPLKALN\ARGGGNQVSLLNVVMDLKKCCNHPY LFFVAMMEAPKMPNGWYDGSALIRASGKLLLIQMKKNLEKGGH RVIIFSQMTYMMDLLEBLEFHUKFRILVYRTLIGGTGNMKKNLEKGGH RVIIFSQMTYMMDLLEBLEFHYRERILVYRVELSPH\Q APSAHRIGONKKWNITFPVTRASVERITJVDAKKMMTHLVV REBEMGEEREVBREII KRQBSVDPDWGMEYTLSFBYKQQCDLAR NIGGGRIRKGGRVYNTMGSGBDWQDDQSINQSDYSVASBEGDB DFDRESBAPRESRGRIRNDKDKDLPLARWGMINSTSFKVAVVUV REBEMGEEREURBEIL REQBSVDPDWGMEYTLSFBYKQQCDLAR MIGGGRIRKGMYNYMGSGBDRWQDDQSINQSDYSVASBEGDB DFDRESBAPRPRSRGRIRNDKDKDLPLARWGTHEVGMSFALIKGFANA QRKAFLNAIMRYGMPPQDAPTTQMLVRDLRGKSEKEFKAYVSLF MRHLCEFGADGABTFANDCVPREGLSRQHULTRILGVFANA QRKAFLNAIMRYGMPPQDAPTTQMLVRDLRGKSEKEFKAYVSLF MRHLCEFGADGABTFANDCVPREGLSRQHULTRILGVFANA QRKAFLNAIMRYGMPPQDAPTTQMLVRDLRGKSEKEFKAYVSLF MRHLCEFGADGABTFANDCVPREGLSRQHULTRILGVFANA CQAPAPASEDEKVVVEPPEGEEKVERKEVERTEPBHETBCKGG AADVEKVEKKSAJDLITFILVVEDKEEKEESEKKEVMLQNGETPK DLNBERGKKNIKQRFMFNIADGGFTELHSLKQNGRATATMEDPKGE MRGFLEIKNKGLIRGFARADGLOOMDRYALINSPEKGE MRGFLEIKNKGLIRGTARTGOLOOMDRYALINSPEKGE PETPOGVAQQQ  1 965  DDDFLRSBARGFRORGEREFTEPTETTGTGTGTGGIRKRARAP EPTPQOVAQQQ  6006  1 965  DDDFLRSBARGFRORGEREFTEPTRETTGRTGGIRGHARAP EPTPQOVAQQQ  CGVUPRKGREGEVETVFYQUSKYCKGEFPTEFTCRTGGIRGHAVGARAV ERHIBETTRILGKRGALTRATKTURTGTARTGGIRGHANAP	i	1	ļ	
PEKVAPLKI KLOGFOSIRKESSS SEDDLL DVSSPPDDAS INSISY  SDGSTBRSSRSRKLRTTKKKKKGEEVTAVDGYETDHODYCEV  CQQGGEI ILCDTCPRATEMUCLD PUMEKAPBEKNSCHCEKEGI  GWEAKENNSBGBEILERUGGDLEEBDHHIMBECRUCKDGGELLC  CDTCPSSYHHICINPPLBP INGEMEDTCPALKEKVQKILI  WRWGQPPSPTPVPRPPDADDPNTPSPRDLEGRPEROPPUKNGGES  YWHCSWYSELQLEIC! (QVMFRIVQKKNDHEPPSGDPGDEEK  S\REKKNKDPKPAPMERERPYRYGI KPEW\MMIHEILINISYDKKG  BEGEPGKLKKVKLRKKLKKERPPTYTVLKPEMPYLVTYREOPPYLDATGG  BEGEPGKLKKVKLRKKLKERPPTYTVLYVEROPPYLDATGG  BEGEPGKLKKVKLRKKLKERPPTYTVLYVEROPPYLDATGG  BEGRIPGKLKKVKLRKKLKERPPTYTVLYVEROPPYLDATGG  BEGRIPGKLKKVKLRKKLKREPPTYTVLYVEROPPYLDATGG  BEGRIPGKLKKVKLRKKLKREPPTYTVLYVEROPPYLDATGG  BEGRIPGKLKKVKLRKKLKREPPTYTVLYVEROPPYLDATGG  BEGRIPGKLKKVKLRKKLREPPTYTVLYVEROPPYLDATGG  BEGRIPGKLKKVKLRKKLREPPTYTVLYVEROPPYLDATGG  BEGRIPGKLKKLKVKLRKKLREPPTYTVLYVEROPPYLDATGG  BEGRIPGKLKKLKVKLRKKLREPPTTYLYVIKEOPPYLDATGG  BEGRIPGKLKKLKVKLRKKLREPPTTYLYVIKEOPPYLDATGG  BEGRIPGKLKKLKVKLRKKLREPPTTATHERUGPLEFFENDATKED  LITTOMATIGS TUMACLI VDEHERIERKLENGSKFFKLLGSTALKEN  GIKLLIDMIG \PHMLRRLKADVFKNMPSKTELIV\RVLSPM\Q  KKYYK\YILHISSFLKALM\ARGGGNOVSLLMVVMDLKKCCNMPY  LEFFUAMBAPKHPNGUNDSTGLITRHEGTPLEFTURILINGURGENDATAKED  GRAFILSFLKALM\ARGGGNOVSLLMVVMDLKKCCNMPY  LEFFUAMBAPKHPNGUNGSGLIRANDSVELTLIJOMLKLEGGH  RVL1FSOMTMILDLLEDFLEBEGYKYRRLDGGITGSMRGGBLD  FRAPGAGOPCFYLLSTRAGGIGINLATADTV1TYLYDENBPHNDIQ  AFSAMRIGGNKKVMIKFYTRASVEELTTOVAKKKMMLTHUV  RREEMGEBEBVERBEILTRQBSVDPDVWELLAHPYPQOGBDLAR  BERMGEBEBVERBEILTRQBSVDPDVWELLAHPYPQOGBDLAR  RREEMGEBEBVERBEILTRQBSVDPDVWELLAHPYPQOGBDLAR  RREEMGEBEBVERBEILTRQBSUNGDDTSVASBEGDB  DPERSBAPRRSKRIGHNDKDKLPLPLLARUGGNIEVLGFMAR  GRAFILMATMRGMPPQDAPTTOMLVRDLURGKESKEKKMYSLF  MRHLCEPGADGABTEADVPREILSBURGTERTBEMTETERBKG  GRAPHINTURFUNGMPPDAPTTOMLVRDLURGKESKEKKMYSLF  BERHIVKGRWSMPBELAEUEBKKMSQPGSPSPKTPTPSTPGDTQD  NTPAPVPPAEDGILKEENSLKERES EGERKSVKSTAPETALISCT  AADUBKVWERSALDLTPLVVERBERKEENSKNENDERAATVTKKT  YELHRERHYWLLAGI INHGYARMOODIONDRYAALINSEPDEN  NRGSFLEINKGLARGOLLARGAATINMSEDDEN  PRALATTPAPEVELLARGOLLARGAATINMSEDDEN  PRALATTPAPEVELLARGOLLARGAATINMSEDDEN  PRALATTPAPVELAR	!	!	1	
SIGSTBRSSRSKKILRTTKKKKKGEEVTAVDGYETDHOPYCKGEGI CQGGBIILCDTCPRAYHWCLDPDMKKAPEGKMCPHCKEGI QWARKENNSEGBEILBEVGGDLEESDDHHMBYCRVCKDGELLC CDTCPSSYHIHCLNPPLPIPORGWLCPKCTCPALKGKVQKILI WKKGOPPSTPVPRPPDADPNTESPKERGPBKOPPVCKQGMS YWHCSWYSKLQLELHC\QVMPRNYQKKDINDBPPSGDFGGDEKK S\RKKNKDKPKPAEMBERPYRYGIKPBW\MMIHRILDHSYDKKG HVHYLIKWRDLFYDQASWESEDVEIQDYDLFKGSYNHHRELMG EBGEPGKKLKKVKLKKLERPPETPTTOPTVYKTEQPSYLDATGG TIHPYQMEGLINHIRFSWNGGTDTILADBGGJGKTVQITAVLYSL YKEGHSKGPFLVSAPLSTIIN\MEREPEMAPDMYV\VTYVGDK DSRAIIRENFS\FEDNAIRGSKKASRWKEASVKPYLVLTSYE LITIDMALIGSIDMACLIVDEARRIKNOSKFFFVLNGYSLQHK LLLTGTPLQNNLEELFHILLBFLTFERFHILKSPLEEPADIAKED QIKKLIBMIG\S\PHINLERFKADVFKNHOPSKTBLIV\RVELSPH\Q KKYYK\YTLHISKFLKALN\ARGGGNQVSLLMVVMDLKKCCNIPPY LFPVAAMBAPKMPNGMYDGSALIRASGKLILLQKMLKNLLEGGH RVLIFSQMTKMLDLLEDFLBHEGYKYRKIDGGITGMRQBAIDA KKYYK\YTLHISKFLKALN\ARGGGNQVSLLMVVMDLKKCCNIPPY LFPVAAMBAPKMPNGMYDGSALIRASGKLILLQKMLKNLLEGGH RVLIFSQMTKMLDLLEDFLBHEGYKYRKIDGGITGMRQBAIDA RRGGGSKTGSMSKQELDDILKFGTBELFKDGATDAKEND RRGGGSKTGSMSKQELDDILKFGTBELFKDGATDAKEND RRGGGSKTGSMSKQELDDILKFGTBELFKDGATDAKEND RRGGKSKTGSMSKQELDDILKFGTBELFKDGATDAKEND RRGGKEEBEVBRBIIKQBSVDDPJWEKKLERHYEQQGDLAR NIGGGKIIRKQVNYNDGSGBDRWQDDQSJNGYSTVASBEGDB DFDRRSBAPRFSRKGLENNDKDEDPLPLLARVGGNIBVLGFBAR QRKAFINALMRYGMPPQDAPTTOMLVROLRGKESKBFKAYVSLF MRHCEPGADGAETFANGVPREGLSRQHVLTRIGVMSLIRKKVQ BFFHINVARSMPELLAEVBROKKSGGSPSKTPTPSTFGDTQD NTPAPVPPAEDGIKIERNSLKERESIBGEKSVKSTAPETAIRCT QAPAPASBERKVVSLEYBERGKKNSKGRETBEPHSTFBCKG AADVEKVEBKSAIDLTPIVVEDKEKKEEBERKKEVMLQNGETPK DIANBKQKNINKQRFMFNIADGGFTELHSIAQNBERRAATVTKKT YEINHRHHPWILAGIIHGKGARWGDRYRATLINSEPKGE AADVEKVEBKSAIDLTPIVVEDKERKEEBERKKEVMLQNGETPK DIANBKQKNINKQRFMFNIADGGFTELHSIAQNBRRAATVTKKT YEINHRHHPWILAGIIHGKGARWGDRYRATLINSEPKGEM NEGFILEINNKLARRYKLLEQALVIERGERBRISTRANAP PSMALNTRPAEVECLAESHOHLSKESMGKNANAVALHKVLKOL BELLSDNKADVTRURBEPPVTAEPIRCLAERANKAPSPEKEM NEGFILEINNKLARRYKLLEQALVIERGERRAATLARRAP EPTQOVAQOO  DDDFLKRYTVERIBEPPVTAEPIRLEARRICHVSKYKG CRUPBKGROCETVPRGGCEVTRGCTSTGCTGURCHTATGRTGGIENDV	I	1		
CQQGGETILCDTCPRAYEMVCLDPDMKKAPRGKNSCPHCEKEGI  QWARKEINSEGRETLREVGGDLKEEDDHEMBYCRVCKDGGELLC  CDTCPSSYHHCLINPPLPAIPMGKMLCPRCTCPALIGEVQVCKLI  WKWQDPSSTPVPRPPDADPWTPSEVPLEGREPERQPFVKWQCMS  YMCSWYSELQLELHC\QWPMFNYQRKNDHDEPPSGDFGDBEK S\RKKNKDPKPAEMERPYRYGIKPEW\MIHRILNHSYDKKG  HVHYLIKMRDLFYDQASMSEDVEIQDYDLFKQSYMNHEELMRG ERGPPGKKLKVVLRKLERPPSTPVDFTVKYERQPSYLDATGG TIMPYQMEGIMWLRFSMAQGTTILLDBEMGGKTVQYLAVFLYSL YKEGHSKQFPLVSAPLSTIIN\PREPEMMAPDMYV\TYYGKK BSRAITIRENEFS\FEDNAIRGGKKASRMKEASVKPHVLLTSYE LITIDMAILGSIDWACLTVDRAHRLKNNQSKFPKVLNGYSLDHK ILLTGTPLQMNLEELHLINFLTPRINLBGFLEEFADIARED QIKKLEMMIG\PPMLRRLKADVFRMMPSKTRLIV\RVBLSPM\Q KKYYK\YILHSEFLKALM\ARGGGNQVSLLINVAMLKKCCMHPY LFVYAMMEAPKMPNGMYDGSALIRASGKILLIQKMLKNLKKGGH RVLIFSQMTTMLDLLEDFLEHBGYKYRIDGTGGMMRQBAIDR RVALFSQMTTMLDLLEDFLEHBGYKYRIDGTGGMMRQBAIDR RVALFSQMTTMLDLLEDFLEHBGYKYRIDGTGGMMRQBAIDR RVARGAQOFCFLISTRAGGIGINLATADTVIIYDSMMPHNIOL RPGIGSKTGSMSKQELDDILKGTREILFKORATIGGSTROMBGED SSVHTYDDKAIRELLDRNDDETEDTELQCMNETLSSFKVAQXVV RBEBMGEEBEVBEIIKQBESVDPPYWIKKLIRHYPQQQBDIAR RGKGEIRKQVNYNDGSQEDDWQDDQSDNQSDYSVASBEGDE DFDRESEAPRRSERKSLRNDKNKET.PFLLARVGSTEUFBARA QRRAFLMAIMYCMPPQQDAFTIGLSROHVUTRIGVBLIRKKVOL RFEHVNGRWSMPELAEVERNKKMSQPGSPSPKTPTPSTTGDTQD NTTPAPVPPAREDGIKIERSSRKKMSVAGPGSPSPKTPTPSTTGDTQD NTPAPVPPAREDGIKIERSSRKKERSERKEKKSVALPSTARCT QAPAPASEDEKVVVSPPSGEEKVKMSQPGSPSPKTPTPSTTGDTQD NTPAPVPPAREDGIKIERSSRIKKERSERKEKVNIONGSTPK PEHVNGRWSMPELAEVERNKKMSQPGSPSPKTPTTSTTGDTQD NTPAPVPPAREDGIKIERSSRLKKESIBGEKKEVNIONGSTPK PEHVNGRWSMPELAEVERNKKMSQPGSPSPKTPTSTTGDTQD NTPAPVPPAREDGIKIERSSRACHRANTINMSEDPSH NRGSFLEIRKNFLARRFKILEQALVIERGGRAATINMSEDPSH NRGSFLEIRKNFLARRFKILEQALVIERGGRAATINMSEDPSH NRGSFLEIRKNFLARRFKILEQALVIERGGRAATINMSEDPSH PSMLATTPRAFWEGLAESGHOHLSRENAAVRANAATHRANA PETTQQVAQQQ  DDMLKILNTVHRHEPPVTAEPTRLLAEREDVVVDKPSSTPHIPC GRPRHTVIFILGKRHOLKELHPLERLDRLTSGVMFARTAAVS ERHEQVRDRQLEKEVVCRVBGEPTBEVTCREPITSTAAVS ERHEQVRDRQLEKEVVCRVBGEPTBEVTCREPITGTBQIKUGU GRPRHTTUFTIGKRHOLKELHPLERLDRLTSGVMFARTAAVS ERHEQVRDRQLEKEVVCRVBGEPTBEVTCREPITSTHQIKUHLOV	1 .	}	1	
QWEAKEINSEGERILERVEGOLREEDHHMRYCRVCKTOGERILC CDTCPSSYHIHCI.NPPLPRIPNGEWLCPRCTCPALKGKVQKILI WKWQGPPSTPVPRPPDADPNYTESP KPLEGRPERQFFVKWQCMS YWHCSWYSELQLEIHC\QWFMYGRKDHDBPPSGDFGGDEK S\RKRKNKDFKRAEMERPYRYKSH\MIREILINHSVDKKG HVHYLIKWRDLPYDQASWESEDVEIQDYDLFKQSYNNHRELMRG EBGRPGKKLKKVKLRKLERPFSTPTVDFTVKJERQPEYLDATGG TIHPYQMBELMWIRFSMAGGTTTLADBWGLGKTVYLAVFLYSIL YKEGHSKGPFLVSAPLSTIIN\WEREFEMMAPDMYV\VTYVGDK DSRAITRERFS\FEDNAIRGSKKASRMKKEASVKFHVLLTSYE LITIDMAILGSIDMACLIVDRAHRLKNNQSKFFRVLNGYSLQHK ILLITGTFLOMNLEBLEHLLINFLTFERFINLBGFLEBFADIAKED QKKHLHDMLG\PHMLERLKADVFKNMPSKTELIV\RVELSPM\Q KKYYK\YILHISKFLKALM\ARGGGMQVSLLNVVMDLKKCCMHPY LIFVAAMEAPKMPNGMYDGSALIRASGGLLLLQKMLKNLEEGGH RULIFSGMTKMULLLEDPLHHEBYRRILGGILEGGDMKEGGB FNAPGAQQPCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQ AFSBAHRIGGNKKVMYTRFVTRASVERLITQUAKKEMMITHLVV REGEMGESEEVEREIIKQESSVDPDYWEKLLEHHYPQQQBDLAR NGGGKSTKGMSKGSGLDDILKFGTERLFKDEATDGGDMKEGGD SSVIHYDDKALBELLDRNQDETEDTBLQCMNRYLSSFKVAQVV REBEMGESEEVEREIIKQESVDPDYWEKLLEHHYPQQQBDLAR NGGKSTGSMSKGSGKLDDILKFGTERLFKDGATTGGDMKEGGD GRAFLNAIMRYGMPPQDAPTTQWLKHLGHYPGAPARAGGNA QRKAFLNAIMRYGMPPQDAPTTQWLKLRHYPGQQBDLAR WHHCEBGADGASTFADGVPREGLSRQHVUTRIGWSLIRKKVQ RFRHVNGRMSMPELAEVERNKKMSQGGSPSRTPTPSTFGDTQP MYPAPVPAPADGILK IERNSLKERS ISGEKEVSKTAPTAIRGT MRHCEBGADGASTFADGVPREGLSRQHVUTRIGWSLIRKKVQ RFRHVNGRMSMPELAEVERNKKMSQGGSPSRTPTPSTFGDTQP MYPAPVPAPADGILK IERNSLKERS ISGEKEVSKTAPTAIRGT DANDEKWERKSAIDLTPIVVEDKEEKKEEESKKGVMLQMGSTPK DANDEKWRKSAIDLTPIVVEDKEEKKEEESKKGVMLQMGSTPK PSMALMTPRABVELAESGHHILSHISHAOMBREAATVTKKT WEIWHRRHDYWLLAGI INHGYARWQDIONDPRYAILNSPEDSH MRGMFLEIKNKFLARRFKLLEQALVIERGGRAAYLINMSEDPSH MRGMFLEIKNKFLARRFKLLEQALVIERGGRAAYLINMSEDPSH MRGMFLEIKNKFLARRFKLLEQALVIERGGRAAYLINMSEDPSH MRGMFLEIKNKFLARRFKLLEQALVIERGRARAYLNKGEPSH BEBLIGDMKADVTRIPATTARIPPVARRLQGRARAYLNKSCDPSH BEBLIGDMKADVTRIPATTARIPPVARRLGRARAYLNKGEPSH BEBLIGDMKADVTRIPATTARIPPVARRLGRARAYLKSANG BERHINTIFFLUKHTGRESPUKKERSHKKRYCRERDILSGVANG BERHINTIFFLUKKTURGERFTEUTCKERSTLEVTCKERSTPHEDYCKSH BERHINGREGNGLEEKVVCRUGESPTEEVTCKERPILGVNGYGNG BRHHTVIFTIGKRHOLKERVVCRUGESPTEUTCRTHQIRVHLG G	•		J	
CDTCPSYHIHCINPPLPBIPMGRBILCPRCTCPALIGKVQKKLI WKWQPPSPTPVPRPPDADDPTPSPKPLEGRPBRQPFVKWQGMS YMHCSWYSELQLELHC\QWPMRNYQRKMDDBPPSGDFGGDBEK S\REKKNDPKPAPMERPYPRGIKPBN\MIHRILINHSVDKG HYNLIL HKWRDLPYDOADSWESEDDYDDLFKGSYNHRELWRG EBGRPGKKLKKVKLRKLERPPSTPTVDPTVKYBRQPBYLDATGG TIMPYQMEGIMWIRFSWAQGTDTILMDBWGGNGTVVATVFUSL XKEGHSGFFIVASPLSTIIN\WREPFEMMAPDMYV\VTYVGDK LITIDMAILGSIDWACTLIVDBAHRLKNNQSKPFPVLINGYSLQHK LILTGTPLQMMLEBLFHLINFLTPERFINLEGFLBSFADIARED QIKKLEBMIG-PPMLERLKADVFKMPBYKTLIV\RVBLSPM\Q KXYKY\THISRYLAKALN\ARGGGNQVSLLNVVMDLKKCCNMPY LIFVAMMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEGGH RVLIFSGMTTKMLDLLEGFLBBEGYKYRRIDGJTGGMRGBADDR RVLIFSGMTTKMLDLLEGFLBBEGYKYRRIDGJTGGMRGBADDR RPAGEAQQFCFLISTRAGGIGINIATADTVILITUSMEPHNIO APSRAHRIGGNKKVMYYRPVTRASVBEZITQVAKKKMMITHLVV RPGIGSKTGSMSKQELDDILKFGTBELFKDEATDGGGDMEGEGD SSVIHTDDKAIERLLDRNQDETBETBLQCMNBYLSSPKVAQVVV REBEMGEBEEVBBEIIRGBESVDPDYWEKLLRHHYQQQBDLAR MIGGKRIRKOWNYNDGSGDEDRBODGSUNGSDYSVASBEGDE DFDERSEAPRPSRKGIRNDKDKPLPPLLARVGGNIEVLGFNAR QRKAFLMAIMYGMPPQDAFTTQHIVDLDLGKSEKKEKFKAYVSI.P WRHCEFGADGASTPADGYPPRGISRGUKNGLTRGWVSL BFRIVMGRMSMPBLAEVBENKKMSQPGSPSBFYPTPSTFGDTQP NTPAPVPPAEDGIKIENSLKERESIBGKEKSKKEKPEAYVSI.P WRHCEFGADGASTPADGYPPRGISRGUKNERSEKKEYMALDKGTPK AADVEKVERKSATDLTPIVVBDKBEKKEEBEKKEVMLQMGFPK DLNDEKQKKNIKQRPMFNIADGGFPKKLESILAGGRAATITKCT VETWHRHDYMLLAGIINGGTRAKKLESILAGAGRARATITKCT VETWHRHDYMLLAGIINGGTRAKKLESILAGAGRARATITKCT PSMALATTPAFVECLAESGHOILSKENAMRARATITKTM PETPQQVAQQQ  1 965 DDDELKRAFTPAFVECLAESGHOILSKESMAGNADANAVINHEVLKOL BELLSDMKADVTRLPATTARIPPVARPLQGRRANTLINSEDPSH PSMALATTPAFVECLAESGHOILSKESMAGNADANAVINHEVLKOL BELLSDMKADVTRLPATTARIPPVARPLQGRRANTLINSEDPSH PSMALATTPAFVECLAESGHOILSKESMAGNADANAVINHEVLKOL BELLSDMKADVTRLPATTARIPPVARPLQGRRANTLINSEDPSH PSMALATTPAFVECLAESGHOILSKESMAGNADANAVINHEVLKOL BELLSDMKADVTRLPATTARIPPVARPLGRARATTTKTC GRPFHNTVIFTIGKRHOLKELHPLERLDRLTSGVMFARTAAVS BRIHEQURDRQLEKEYVCRVBGEFPTBEVTCKREILTVARPATAAVS BRIHEQURDRQLEKEYVCRVBGEFPTBEVTCKREPTHDTGVAGR GRPFHNTVIFTIGKRHOLKELHPLERLDRLTSGVMFARTAAVS BRIHEQURDRGLEKEYVCRVBGEFPTBEVTCKREPTHOTHOLWHILDVSYKVGV CRUPPRGK	ĺ			
######################################	l			
YMHCSWVSELQLEIHC\QVMPRNYQRRDMBPPGGDFGGBEK S\REKRKOP KFARMEERPYRYGIRPEM\MMIHILINHSVDKKG HVHYLINKNDLPYDQASMESEDVEIQDYDLFQSYMNIRELMRG EBGRGEKKLKVKLRKLBRPPETPTVDPYUKYERQPEYLDATGG TLHPYQMEGLWKLRFSWAQGTDTLLADEMGLGKTVQTAVFLYSL YKEGHSKGPFLVSAPLSTIIN\MEREPEMADDMYV\VTYVGDK DSRAIIRENFS\PEDMAIRSGKKASRMKKRASVKPHVLTTSYE LITIDMAILGSIDWACLIVDRAHRLKNNQSKPFRVLNGYSLQHK LLLTGTPLQNNLEELFHLLMFLTPERFHNLEGFLEEFADLAKED QIKKLHDMLG\PHHLRRLKADVFKNMPSKTELTV\RVELSPM\Q KKYYK\YILHSKPLKALN\ARGGGQVSLLINVWDLKKCCNHPY KKYYK\YILHSKPLKALN\ARGGGQVSLLINVWDLKKCCNHPY KKYYK\YILHSKPLKALN\ARGGGQVSLLINVWDLKKCCNHPY KKYYK\YILHSKPLKALN\ARGGGQVSLLINVWDLKKCCNHPY FNAPGAQQFCPLLSTRAGGGIRLATADTVIIYDDDWBHNDIQ AFSRAHRIGQNKKWHIYRPVTRASVERITTQVAKKMMLTHLVV RRGGSKTGSMSKQELDDILKFGTBELFKOEATDGGGDNKGGED SSVIHYDDKAIERLLDRNQDETEDTBLQCMNBYLSPKWAQVY REBEMGEEEVBERIIRQCSVDPDWEKLLRHHYPQQGDLAR NIGKKRIRRQVNYNDGSQBDRDWQDQSINQSDYSVASBEGDE DPDRRSEAPRRPSRKGLRNDKALPPLLALCGNIEVLGFMAR QRKAFLMAINRYCMPPQDAPTTQMLVRDLRGKSEKEFKAYVSLF MRHLCEPGADGAETFADGVPREGLSKQVLTRIGVBSLTRKVQ BFRHVNGRWSMPELARVERNKKMSQPGSPSPBTPTPSTEPDTQD NTPAPVPPABCDIKIERNSLKEESIEGEKEVKATAPBTAIECT QAPAPASEDGIKIERNSLKEESIEGEKEVANLONGSTPK BFRHVNGRWSMPELARVERNKKMSQPGSPSPBTPTPSTEPDTQD AADVEKVBEKSAIDLTPIVVEDKEEKKEEBEKKEEMMLGNGETPK PSHALNTRAEVSCLAESHUHLAGKEMAGNKANAVLHKVLKQL BELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP PSMALNTRAEVSCLAESHUHLSKESMAGNKRANAVLHKVLKQL BELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP PSPPQQVAQQQ  ODDPLRRTVERHEPPVTAEPIRLEGLKISSUSVARPAKTANVS GRPRHTYLFILKKRHAPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  FRENTYUFELBERVCRVRGESPPTEBVTCKEPILVVSYKUGV GRPRHTYLFILKKRYLKREPPTEBPTREVTCKEPILLVSYKUGV GRPRHTYLFILKKRYLRREPPTEBPTREVTCKEPILLVSYKUGV GRPRHTYLFILKKRYLREPPTEBPTTEBPTLSKGG RPHHTYLFILKKRYLRERPPTEBPTTCKEPILLVSYKUGV GRPRHTYLFILKKRYLRERPPTEBPTTCKEPILLSRLANRAP BFRINGGRAPATTYTETTERFTTTARIPPTBATARIPPTTTARIPPTBATARIPPTTTARIPPTBATARIPPTBATARIPPTBATARIPPTBATARIPPTBATARIPPTBATARIPPTBATARIPPTBATARIPPTBATARIPPTBATARIPPTBATARIPPTBATARIPPTBATARIPTBATARIPPTBATARIPTBATARIPTATARIPPTBATARIANRAP BFRINGGRAPTTTARIPTTARIPTTARIPTTARIPTTARIPTTARIP	1			
S\RRIKANDPRPAEMREPYRYGIRPEN\MMTHRILMISVOKKG HVHYLIKWRDLPYDQASWESEDVBIQDYDLPKQSYMNHRELMRG EBGRPGKKLKKVKLRKUERPEFTPTVDPTVKYERCPBYTLDATGG TLHPYQMBGLMWLRFSMAGGTDTILADEMGLGKTVQTAVFLYGL YKEGISKGPFLVSAPLSTIIN\WERPFEMMAPDMYV\VTYVGDK DSRAIIRENFFS\FEDMAIRGGKKASRMKKEASVKPHVLLTSYE LITIDMAILGSIDWACLIVDERHRIKKNOGSKFFRVLNGYSLQHK LLLTGTPIQNMLEELFHLLNFLTPERFRILKEQFLESPADIAKED QIKKLEHMIG\PHMLRRLKADVFKNMPSKTELIV\RVELSPM\Q KKYYK\YILHISKFLKALM\ARGGGMYSLLAVVMDLKKCCHHPY LPFVAAMEAPRMPMGMYDGSALIRASGKLLALIQMLKNLKEGGH RVLIFSQMTKNLDLLEDFLEHEGYKYERIDGGITGNMRQEAIDR FNAPGAQOFCFLLSTRAGGLGINLATADTVIIYDDMMPHMDIQ APSSAHRIGGNKKWMIYRFVTRASVERIITQMAKKMHITHLVV RPGIGSKTGSMSKQELDDILKFGTRELFKDEATDGGGDNKGGED SSVIHYDDKAIERLLDRNQDETEDTELQCMBEYLSFWVAQVVV REBEMGEEEEWERELIRQEESVDPPYWEKLIKHHYEQQGDLAR NLGKSKRIRKQVNYNDGSGEDRDWQDDGSDNGSDYSVASBEGDE DFDRRSBAPRFSRKGLRNDKDKFLPPLLARVGGNIEVLGFMAR QRKAFLMAIMRYGMPPQDAFTTQMLVRDLRGKSEKEKKAYVSLF MRHLCEPGADGABTFADGVPREGLSRQHVLTRIGWSLIRKKVQ EFFHVNGRWSMPELAEVERNKKMSQPSSPSPKTPTPSTPGDTQD NTPAPVPPAEDGIILIERNSLKERSSIBGEKEVKSTAPBTAIRCT QAPAPASBDERVVVEPPEGEEKVKRAQVESTBEPBMTTPRGKG AADVEKVEEKSAIDLTPIVVEDKEEEEKKEVMLQNGSTPK DLNDEKQKKNIKQRFMFNLADGGFTELHISLMQNBERAATVTTKKT YEIMHRRHDYMLAGIINHGYARWQDIONDRYAAILNSPFKGEM NRGNFLEIKNKPLARRFKLLEQALVIBEGLRRAATVITKKT YEIMHRRHDYMLAGIINHGYARWQDIONDRYAAILNSPFKGEM NRGNFLEIKNKPLARRFKLLEQALVIBEGLRRAATVITKKT YEIMHRRHDYMLAGIINHGYARWQDIONDRYAAILNSPFKGEM NRGNFLEIKNKPLARRFKLLEQALVIBEGLRRAAYLNMSEDPSH PSMALNTRPAEVECLARSHONLSKESNAGNKPANAVLHKVLKKQL EELLSDMKADVTRLPATTARIPPVARLCHGSERNILSRLANRAP EPTPQQVAQQQ GRPHHTVIFTLIGKENDLAVVENGESPPTEEVTCKEPILVVSYKVGV GRPHHTVIFTLIGKENDLAVVENGESPPTEEVTCKEPILVVSYKVGV GRPHHTVIFTLIGKENDLAVVENGESPPTETETTRETHQIRVHILQF GRPHHTVIFTLIGKENDLAVVENGESPPTETETTRETHQIRVHILQF GRPHHTVIFTLIGKENDLAVVENGESPPTETETTRETHQIRVHILQF GRPHHTVIFTLIGKENDLAVVENGESPPTETETTRETHQIRVHILQF GRPHHTVIFTLIGKENDLAVVENGESPPTETETTRETHQIRVHILQF GRPHHTVIFTLIGKENDLAVGREGETTRETHGIRVHILQF GRPHHTVIFTLIGKENDLAVGREGETTRETHGIRVHILQF GRPHHTVIFTLIGKENDLAVGREGETTRETHGIRVHILQF	i			
HVHYLIKMRÖLPYDQASMESEDVBIQDYDLFKQSYMNHRELMRE BEGRPEKKLKKVKLEKLERPPETETVDTVXYBXQPBYIDATGG TIHPYQMEGLMULFRSMAQGTDTILADEMGLKTVQITAVFLYSL YKBGHSKGPFLVSAPLSTI IN\MEREPEMMADDMYV\TYYUGK DSRAIIRENERS\PEDMAIRGSKASMKKBASVKFHVLLTSYE LITIDMATLGSIDMACLIVDRAHRIKNNAQSKFFRVLNOYSLQHK LLLTGTPLQNNLEBLFHLLNFLTPERFFRILKGPLBEPADIAKED QIKKLHDMIG PHHLERLKADVFKNMPSKTBLIV\RVELSPM\Q KKYYK\YILHSKFLKALN\ARGGGRQVSLLMVWDLKKCCMPPY LPPVAAMBAPKMPMGMYDGSALIRASGKLLLQKMLKCCMPPY LPPVAAMBAPKMPMGMYDGSALIRASGKLLLQKMLKCCMPPY LPPVAAMBAPKMPMGMYDGSALIRASGKILLLQKMLKCCMPPY LPPVAAMBAPKMPMGMYDGSALIRASGKILLLQKMLKCGMPY LPPVAAMBAPKMPMGMYDGSALIRASGKILLLQKMLKKCGMPY LPPVAAMBAPKMPMGMYDGSALIRASGKILLLQKMLKKCGMPY LPPVAAMBAPKMPMGMYDGSALIRASGKILLLQKMCKCCMPY LPPVAAMBAPKMPMGMYDGSALIRASGKILLLQKMCKCCMPY RPRIGASKTGSMSKQELDDILKFGTBELFKDGATDGGGDNKKMGH RVLIFSGMTKMLDLLEBPLBHEGYKYRELDGGTGTSMAQCALDH RPRIGASKTGSMSKQELDDILKFGTBELFKDEATDGSGDNKGGD SVIHTDDKALERLLDRNDGDETEDTBLQCMMSYLSSFKVAQYVV REBEMGEEEBVBRBIIKQEBSVDPDYWEKLLEHHYEQQQDBLAR NLGKGKRIRKQVNTDDGSGEDRDWQDQDQSDQSDYSVASBEGDE DFDRESBAPRRPSKRGLENDKDKPLPPLIARVGGMIBVLGFMAR QRKAFLNAIMRYGMPPQDAPTTQMLVRDLRGKSEKEFKAYVSLF MRHLCERGADGABTFADGVPREGLISGNVLTRIGVBLLIKTURL RFHINGRWSMPBLAEVEBNKKMSQPGSPSFRTPTPSTPGDTQP NTPAPVPPAEDGIKIERSLKKMSQPGSPSFRTPTPSTPGDTQP RFHINGRWSMPBLAEVEBNKKMSQPGSPSFRTPTBFDRGKG AADVEKVBEKSALDILTPIVYENKEBKKEMSKKMVGNGSTPK PEHNINGRWSMFALDALTRARWYCHTEBPMBTEPMGKG BURDHEKQKKNIKQRFMFNIADGGFTRLHSLWQNBERAATVTKKT YEIMHRRHDYMLLAGI HHGYARMODIONDRYAILASPFRGEM MCGMFLEIKNFLARRFKLLEGALVURGERRATINSEPPSGEM MCGMFLEIKNFLARRFKLLEGALVURGERRATINSEPPSGEM MCGMFLEIKNFLARRFKLLEGALVURGERRATILSELANRAP PSPQQUVAQQO BURDHRTVTHHBEPPVTAEPIRLDRLTSGVLMFAKTANS EPTPQQVAQQO GRPHHTVIFTLGKRHOLKBIHPLBRLDRLTSGVLMFAKTANS EPTPQQVAQQO GRPHHTVIFTLGKRHOLKBIHPLBRLDRLTSGVLMFAKTANS ERIHEGVRDRGCECTVVQRGSEVVCRVBGEPPTEEVTCKEPILVVSYKVGV CRVDFRGKPCKTVVQRGSTVVCRVBGEPTTETTRETHQTRUBLQP	l	Ĭ	}	
EBGRPGKKLKKVKLRKLERPPETPTVDPTVXYERQPEYIDATGG TIHPYQWEGLMWLRFSWAQGTDTILDBMGLGKVUTIAVFLYSI XKEGEKGSPTJVSAPLSTI IN\WEREPENMAPDMYV\TYVGDK DSRAIIRERFS\FEDNAIRGGKKASRMKKEASVKPHVLLTSYE LITIDMATLGSIDMACLIVDEAHRIKNGSKFFRVIAGYSLQHK LLLTGTPIQNIALERI-FHILDFLTPERFIRIKERPLEPFADIAKED QIKKLHDMLG\PHMLRRLKADVFKNMPSKTBLIV\RVELSPM\Q KKYYK\TILHSKPLKADN\ARGGGRQVSILMVVMDLKKCCHPYY LPPVAAMEAPKMPNGMYDGSALIRASGKILJLQMULRALEGGH RVLIFSQMTKNIDILLEDFLEHEGYKYRRIDGGITGNMRQEAIDR RVLIFSQMTKNIDILLEDFLEHEGYKYRRIDGGITGNMRQEAIDR RVLIFSQMTKNIDILLEDFLEHEGYKYRRIDGGITGNMRQEAIDR RVLIFSQMTKNIDILLEDFLEHEGYKYRRIDGGITGNMRQEAIDR RVLIFSGMTKNIDILLEDFLEHEGYKYRRIDGGITGNMRQEAIDR RVLIFSGMTKNIDILLEDFLEHEGYKYRRIDGGITGNMRQEAIDR RVLIFSGMTKNIDILLEDFLEHEGYKYRRIDGGITGNMRQEAIDR RVLIFSGMTKNIDLLEDFLEHEGYKYRRIDGGITGNMRQEAIDR RVLIFSGMTKKVMIYRPVTRASVBERITQVAKKKMLTHLVV RPGGSKTGSMSKQELDDILKRGTERLFKDEATDGGGDNKEGED SSVIHTDDKAIERLIDRNQDETEUTBLQCMMRYLSPKVAQVVV REBEMGEEEEVEREIIKQESVDPDYWEKLLRHYPEQQQEDLAR NIGKKRIRKQVNYNDGSGDRDMQDDQSDQSDYSVASREGDE DPDRRSBAPRRPSRKGLRNDKDKPLPFLLARVGGDYSVASREGDE DPDRRSBAPRRPSRKGLRNDKDKPLPFLLARVGGPNSYSVASREGDE MRCHELEGAGABTFADGVPRRGLSRQNVTRIGGMSLIRKKVQ RFFHVNGRWSMPBLAEVEENKKMSQPGSPSPKTPTPSTPGDTQP NTPAPVPPAEDGIILERNSLKERESIBGEKEVKSTAPTAIBCT QAPAPASEDEKVVVBPPEGEEKVKRAEVKERTEBPBETBCKG AADVEKVBEKSAIDLTFIVVBCKEEKKAEVKERTEBPBETBCKG AADVEKVBEKSAIDLTFIVVBCKEKRAEVKERTEBPBETBCKG NRGMFLEIKNKFLARRFALLEQALVIBEDLARAAYLMNSEDPSH PSMALNTRPAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL EELLSINKADVTRLPATTARIPPVAVRLQMGERRILLSRLARRAP PSMALNTRPAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL EELLSINKADVTRLPATTARIPPVAVRLQMGERRILLSRLARRAP PSMALNTRPAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL GRPRHNTVIFILGKKHOLKBIHPLHRLDRLTSGVLMFAKTAAVS BRIHEQVRDRQLEKEYVCRVEGEBPTEEVTCKBPILTWFAKTAAVS GRPRHNTVIFILGKKHOLKBIHPLHRLDRLTSGVLMFAKTAAVS BRIHEQVRDRQLEKEYVCRVEGEBPTETEVTCKBPILTVVSKYGGV CRVDFRGKPCKCTVVQRLGSVVCRCPLTGRTHGTRUHLQL	•		}	
TLHPYQMEGLNWLRFSMAQGTDTILADEMGLGKTVQTIAVFLYSL YKECHSKGP FTVSAPLSTI IN\MERPEMMAPDMYV\VTYGDK DSRAITRKERFS\FEDNATRGGKKASMKKEASVKPHVLLTSYE LITIDMATLGSIDWACLIVDBAHRLKNNQSKPFRVLNGYSLQHK LLLTGTPIQNNLEBLFHLLNFLTPERFHNLSGFLEBFADIAKED QIKKLHMIG.PHMLERLADVFKNMPSKTELIV\RVELISPM\Q KKYYK\YTLHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNHPY LFFVAAMEAPKMPNGMYDGSALIRASGKLILLQKMLKNLKBGGH RVLIFSQMTKMIDLLIGHBEGYKYKRIDGGITGNMRQBAIDR RVLIFSQMTKMIDLLIGHBEGYKYKRIDGGITGNMRQBAIDR RVLIFSQMTKMIDLLIGHBEGYKYKRIDGGITGNMRQBAIDR FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQ AFSRAHRIGGNKKVMIYRFVTRASVERITQUXKKKMMLITHLVV RPGGGSXTGSMSQKGLDULKFGTBELFKDEATHGGGINKBGGD SSVIHYDDKAIERLLDRNQDETBDTBLQCMNBYLSSPKVAQYVV REBEMGEEBVERBIIKQESVDPDYWEKLLRHHYFQQQBDLAR NLGKGKRIRKQVNYNDGSQBDRWQDDQSUNGSDYSVASBEGDB DFDRRSBAPRRPSRKGLRNDKDKPLPPLLARVGGNIBVLGFNAR QRKAFLNAIMRYGMPPQDAFTTQMIVRDLRSKSEKKEKAYVSLP MRHLCEPGADGABTPADGVPREGLSRQHVITRIGVMSLIRKKVQ EFFRIVNGRWSMPBLAEVEBNKKNSQPGSPSPKTPTPSTPGDTQP NTPAPVPPAEDGIKIERSKKNSQPGSPSPKTPTPSTPGDTQP NTPAPVPPAEDGIKIERSKKNSQPGSPSPKTPTPSTPGDTQP NTPAPVPPAEDGIKIERSKKVERFEBPMSTRGKG AADWEKVERKSAIDLTPIVVEDKERKEEBEKKSVMLQNGSTPK PADMENVERKSASIDLTPIVVEDKERKEEBEKKSVMLQNGSTPK PADMENVERKSASIDLTPIVVEDKERKEEBEKKSVMLQNGSTPK PADMENVERKSASIDLTPIVVEDKERKEEBEKKSVMLQNGSTPK PEINHRRHDYWLLAGIINGYARWODIONDFRYALINSEPPKGEM NRGGNELIKNKPLARRFKLLEQALVIEGCJRRAAYLMMSEDPSH PSMALNTRPAEVBCLAESHOHLSKESMAGNKPANAVLHKVLKQL EELLSDMKADVTRIPATIARIPPVAVRLQMSERNAILBRLANRAP PSTPQQVAQQQ  6006 1 965 DNDFLRNTVHRHBPPVTAEPIRLLAENBDVVVDKPSSIPVHPC GRPRHNTVIFTILGKRHQLKELHPLHRLDRLTSGVIMFAKTAAVS ERIHGQVRDRQLEKEYVCRVEGEPPTEEVTCKBPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGGSSVVECRELTGRTRAITMAVS ERIHGVRDRDLEKEYVCRVEGEPPTEEVTCKBPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGGSSVVECRELTGRTRAITHAVS			ì	
YKEGHSKGPFLVSAPLSTI IN\MEREPEMAPDMYV\TYVGDK DSRAIIRENEPS\FPACINAIRGKASRMKKASVKPHVILITSYE LITIDMAILGSIDWACIJVDRAHRLRNNGSKPFRVINGYSLQHK LLLTGTPIQNNLEELFHLLNFLTPERFHNLEGPLEEPADIAKED QIKKLHDMIG\PHMLERLRADVFKNMPSKTELIV\RVELISFM\Q KKYYK\TILHSKPLKADVFKNMPSKTELIV\RVELISFM\Q KKYYK\TILHSKPLKADVFKNMPSKTELIV\RVELISFM\Q KKYYK\TILHSKPLKADVFKNMPSKTELIV\RVELISFM\Q KKYYK\TILHSKPLKADVFKNMPSKTELIV\RVELISFM\Q KKYYK\TILHSKPLKADVFKNMPSKTELIV\RVELISFM\Q KKYYK\TILHSKPLKADVFKNMPSKTELIV\RVELISFM\Q KKYYK\TILHSKPLKADVFKNMPSKTELIV\RVELISFM\Q KKYYK\TILHSKPLKADVFKNMPSKTELIV\RVELISFM\Q KKYYK\TILHSKPLKADVFKNMPSKTELIV\RVELISFM\Q RVLIFSQMTKNIDILLEDFLAHBGYKYRRIDGGITGNNRQKBIDR RVLIFSQMTKNITYRRVITRASVEERITQVAKKKMMLTHLIV\ RPGIGSKTGSMSKQELDDILKFGTERLFKDEGENNKBGED SSVIHYDDKALERLLDRNQDETBUTBLQCMNBYLSFKVAQYVV REEMMEBEEVBEEIKGEVNDPYMELILIHHYPQQQBDLAR NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNGSDYSVASBEGDE DPDRRSBAPRRPSRKSLRNDKDKPLPPLLARVGGNIBVLGFNAR QRKAFLNAIMRYGMPPQDAFTTQMLVRDLKGKSEKEFKAYVSL; MRHLCEPGADGABTFADGYPREGLSRQHVUTRIGVMSLIRKKVQ REFRINGRWSMPBLAEVERNKKMSQPGSPSPKTPTPSTPGDTQP NTPAPVPPAEDGIKLEENSLKEESISEGEKEVSTAPETAIECT QAPAPASADDEKVVVBPPEGGEKVBKABVKERTEEPMBTEPKGKG AADVEKVEBKSAIDLTPIVVEDKEBKKEEBSKKEVMLQNGETPK DLNDBKQKKNIKQRMFNIADGGFTELHSLMQNBKRAATVTKKT YEIMHRRHDYWILLAGIINHGYARWQDIQNDPRYALINSPFKGEM NRGMFLEIKNKPLARRFKLLEQALVIEEQLRRAAYLMMSEDPSH PSMALNTRPAEVECLAESHOHLSKESNAGNKPANAVLHKVLKKOL BELLSDMKADVTRLPATTARIPPVAVRLQMSERNILSRLANRA PSTPQQVAQQQ  6006 1 965 DNDFLRNTVHRHBPPVTAEPIRLLAENBEDVVVVDKPSSIPVHPC GRPRHNTVIFTILGKRHQLKELHPLHRIDRITSGVIMFAKTAAVS BRIHBQVRDRQLEKEYVCRVEGEPPTEVTCKBPILVVSYKVGV CRVDPRGKPCSTVPQRLSYNGGSSVVRCRELTGRTHGIRVHLQF		<b>!</b>		
DSRAIIRENBFS\FEDMAIRGGKKASRMKKEASVKPHVLLTSYE LITIDMATLGSIDMACLIVDEAHRLKNNOSKFPRVLNGSYSLOHK LLLTGTPIQNNLEBLEHILINFLTPERFHNLEGFLEBFADIAKED QIKKLHMIG\FHMLRRLKADVFKNMPSKTBLIV\RVELSPM\Q KKYYK\YILHSKFLKALN\ARGGGRQVSLINVVMDLKKCCHPY LFPVAAMBAPKMPNGMYDGSALIRASGKILLLQXMLKNLKEGGH RVLIFSOMTKMLDLLEBFLBHIBGYKYBRIDGGITGNMRQBAIDR FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQ AFSRAHRIGQNKKVMIYRFVTRASVBERITOVAKKKMMLTHLVV RPGLGSKTGSMSKQKLDDILKFGTBRLFKDEATDGGGDNKBGED SSVIHYDDKAIBRLLDNNQDETEDTBLQCMNSYLSSFKVAQVVV REBEMGEEEBVBRBIIKQBSSVDPDWDBKLLARHHYEQQGBDLAR NLGKKRIRKQVMYNDGSQBDWQDDQSLNQSDYSVASBEGDB DFDRRSBAPRPSRKGLRNDKDKPLPFLLARVGGNIBVLGFNAR QRKAFLNAIMRYGMPPQDAPTTQWLVRDLRGKSEKEFKAYVSLF MRHLCBFGADGABTFADGVPREGLSRQHVLTRIGVMSLIRKKVQ BFEHVNGRWSMPBLAEVENKKMSQPGSPSPKTPTPSTPGDTQP NTPAPVPPAEDGIKIENSLKEBESIBGEKBVKSTAPBTAIECT QAPAPASEDEKVVVBPPEGEEKVEKKEREBEKKSVMLQNGETPK AADVEKVBEKKSAIDLTPIVVBCKBEKKBEBERKSVMLQNGETPK AADVEKVBKKSKAIDLTPIVVBCKBKKKBEBERKSVMLQNGETPK YEIMHRRHDYWLLAGIINHGVGARMQDIONDFXYAILNSPFKGEM NRGNFLEIKNKPLARRFKLLEQALVIBEQLRRAAYINMSEDPSH PSMALNTRFABVUCLAESHQHLSKESMAGNKPANAVLHKVLKQL BELLSDNKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP PSMALNTRFABVECLAESHQHLSKESMAGNKPANAVLHKVLKQL BELLSDNKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP PSPPQQVAQQQ  6006 1 965 DNDFLRNTVPHRHEPPVTAEPIRLLABNEDVVVDKPSSIPVHPC GRPRHNTVIFILLKKRPLJKBLLBRLDRLITSGVIMFAKTANAS BRIHBQVRDRQLEKEYVCRVBGKPPTBEVTCKBPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQF		f	Į.	•
LITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQHK LLLTGTPFLQNNLEELEFHLLMFLTPERFHRLRGFLEBEADIAKED QIKKLHDMLG\PHMLRRLKADVFKNMPSHTELLV,VEVLSPM\ KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNHPY LFPVAAMRAPKWPNGMYDGSALIRASGKLLLLQKMLKNLKEGGH RVLIFSQMTKMLDLLEDFLBHEGYKYBRIDGGTGNMRGEAIDR FNAPGAQQFCFLLSTKRGGLGINLATADYVIIYDSDWNPHNDIQ AFSRAHRIGQNKKVMIYRFVTRASVBERITQVAKKKMMLTHLVV RPGLGSKTGSMSKQELDDILKFGTBELFKDEATDGGGDNKKGEB SSVIHYDDKAIFRLLDENQDETEDYBLQCMNBVLSFKVAQVVV REBEMGEEEBUBREIIKQEESVDPDYWBKLLRHHYEQQQEDLAR NLGKSKRIRKQVMYNDGSQBDRWQDDQSINQSDYSVASBEGDE DFDERSBAPRPSKKGLENDKDKPLPPLLARVGGNIKVLGFNAR QRAFIANIMRYGMPPQDAPTTQMLVRDLRGKSEKEFKAYVSILF MRHLCEPGADGABTFADGVPREGLSRQHVLTRIGVMSLIRKKVQ EFRHVNGRWSMPELAEVEBNKKMSQPGGSPSKTPTPSTPGDTQP NTPAPVPPAEDGIKIENSLKKERESIEGREVKSTAPETAIRCT QAPAPASBDEKVVVEPPEGEEKVKKAEVKERTEEMBTBPKGKG AADVEKVBEKSAIDLTPIVVEDKEEKKEEBEKKEVMLQNGETPK DLNDEKQKKNIKQRFMFNIADGFTELLSLQNGERAATTIKKT YEIMHRRHDYMLLAGIINGFTRALBILQNBERAATTIKKT YEIMHRRHDYMLLAGIINGFTRALBILQNBERAATTIKKT YEIMHRRHDYMLLAGIINGFTRALBILQNBERAATTIKKT YEIMHRRHDYMLLAGIINGFTRALBILQNBERAATTIKKT YEIMHRRHDYMLLAGIIINGFTRALBILGNBERAATTIKKT EBLLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP PSMALNTRPABVECLAESHOHILSKESMAGNKPANAVLHKVLKQL EBLLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENBEDVVVVDKPSSIPVHPC GRFRHNTVIFIIJGKRHJLKBLHRLDRLITSGVIMFAKTAAVS ERIHGVRDRQLEKEYVCRVKGEPPTBEVTCKEPILVVSYKVGV CRVDPRGKPCETVYQKLSYMGQSSVVRCRPLTGRTHQIRVHLQP		ł		YKEGHSKGPFLVSAPLSTIIN\WEREFEMWAPDMYV\VTYVGDK
LLLTGTPIQNNLEBLFHILNFLTPERFHNLRGPLBEPADIAKED QIKKLHDMIG PHMLRRIKADVEKNNPSKTBLIV\RVELSPM\Q KKYYK\TILHSKFIKALN\ARGGGNQVSILNVVMDLKKCCNHPY LFPVAAMBAPKMPMGYDGSALIRASGKILLIQKMLKRILKEGGH RVLIFSQMTKMLDLLEDFLBHBGYKYBRIDGGITGNMRQBAIDR RVLIFSQMTKMLDLLEDFLBHBGYKYBRIDGGITGNMRQBAIDR RNAPGAQQPCFYLLSTRAGGIGINIATADIVIIYDSDWNPHNDIQ APSRAHRIGQNKKVMIYRPVTRASVBERITQVAKKKMMLTHLVV RPGIGSKTGSMSKQELDDILKFGTBRIFKDEATDGGGDNKEGED SSVIHYDDKALBRILLDRNQDETEDTBLQCMNBYLSSPKVAQYVV RBRBMGEEBKVBRBIIKQBESVDPDYMEKLLRHHYPEQQEDLAK NIGKGKRIRKQVMYNDGSQEDRDWQDDQSINQSDYSVASBEGDB DFDKRSBAPRRPSKGLRNDKDKPLPPLLARVGGNIBVLGFNAR QRKAFLNAIMYGMPPQDAFTTQMLVRDLRGKSEKKFKAVVSLP MRHLCEPGADGABTFADGVPREGLSRQHVLTRIGVMSLIRKKVQ BFPHNURGMSMPBLIAVEBNKKMSQPGSPSRTPTPSTPGDTQP NTPAPVPPAEDGIKIEENSLKEBESIBGEKEVKSTAPBTAIECT QAPAPASBDEKVVVBPPSGEEKVKARSVKERTBEPMSTRPKGKG AADVEKVEBKSAIDLITPIVVEDKEBKKEBEBEKEVMLQNGBTPK DINDBKQKKNIKQRPMFNLADGGFTBLHSLMQNBERAATVTKKT YEIMHRRHDYWLLAGIINHGYARWQDIONDFRYAILNSPPKGEM NRGNFLEIKNKFLARRFKLLEQALVIBEQLRRAAYLMMSEDPSH PSMALNTRPABVBCLAESHQHLSKESMAGNKPANAUHKVLKQD BELLGDMKADVTRLPATTARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFTRNTVHRHBPPVTAEPIRLLAENBDVVVVDKPSSIPVHPC GRPRHNTVIFILGKRHQLKBLHPLHBLDRLTSGVLMFAKTAAVS ERIHGQVRDRQLEKEYVCRVEGEPPTBEVTCKBPILVSVKVGV CRVDPRGKPCETVPQRLSYNGGSSVVRCPPLTGRTHQIRVHLQP	1		ì	
QIKKLHDMLG\PHMLRRLKADVFKNMPSKTBLIV\RVELSPM\Q KKYYK\YILHISKFLKALM\ARGGGNQVSLLNVVMDLKKCCNHPY LFPVAMBAPKMPNGMYDGSALIRASGKILLLQKMLKNLKEGGH RVLIFSQMYKMLDLLBDFLBHBGYKYRRLDGGITGMMRQBAIDR FNAPGAQQPCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQ APSRAHRIGGNKKWMIYPFVTRASVERZITQVAKKKMMLTHLVV RPGLGSKTGSMSKQELDDILKFGTBELFKDBATDGGGDNKEGED SSVIHYDDKALBELLDRNQDETEDTBLQCMMYLSSPKVAQYVV REBEMGEEEKVERELIKQBESVDPDYWEKLLRHHYEQQQEDLAR MLGKGKRIRKQVMYNDGSQBDRDWQDDQSDNQSDYSVASBEGDE DFDRRSBAPRRPSRKGLANDKDKPLPPILLARVGGNIEVLGFMAR QRKAFLNAIMMYGMPPQDAFTTQMLVRDLAGKSEKEFKAYVSLF MRHLCEPGADGABTFADGVPREGLSRQHVLTRIGVMSLIRKKVQ BFEHVNGRWSMPBLAEVEENKKMSQPGSPSPKTPTPSTPGDTQP NTPAPVPPABGGIKIERNSLKERESIBGEKEVKSTAPBTAIBCT QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMBTEPKGKG AADVEKVBEKKSAIDLIPPLVVEDKEEKKEEBERKEWMLQNGETPK DLNDEKQKKNIKQRFMFNIADGGFTBLHSLMQNBERAATVTKKT YEIWHRRHDYWLLAGIINGGYARWQDIONDPRYAILNSEPFKGEM NRGWFLEIKNKFLARRFKLLEQALVIBEQLRRAAYLNMSEDPSH PSMALNTRPAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL RELISDMKADVTRILDATTARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFLRNTVHRHBPPVTAEPIRLLABNBDVVVDKPSSTPVHPC GRFRHNTVIFILGKRHQLKBLHPLHRLDRITSGVLMFAKTANVS ERIHGQVRDRQLEKEYVCRVEGEPPTEEVTCKBPLVVSKKVGV CRVDPRGKPCETVPQRLSYNGGSSVVRCPPLTGRTHQIRVHLQP		1		LITIDMAILGSIDWACLIVDKAHRLKNNQSKFFRVLNGYSLQHK
KKYYK\YILHSKPIKALN\ARGGGNQVSILNVVMDLKKCCNHPY LFPVAAMBAPKMPNCMYDGSALIRASGKILLIQKMLKNIKEGGH RVLIFSQMTKMLDILEDPLBHEGYKYBRIDGGITGNMRQBAIDR FNAPGAQQPCFILSTRAGGIGINLATADIVIIYDSDMDPHNDIQ AFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVV RPGLGSKTGSMSKQELDDILKFGTBELFKDEATDGGDNKBGED SSVIHYDDKAIERLLDRNQDETBDTBLQCMNBYLSSPKVAQYVV REBEMGEEERWERBIIKQBESVDPDYWEKLLRHHYEQQQBDLAR NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASBEGDE DFDRBSBAPRPSRKGLRNDKDKPLPPLLARVGGNIBVLGFNAR QRKAFLNAIMRYGMPPQDAPTTQMLVRDLRGKSEKKFKAYVSLF MRHLCEPGADGABTFADGVPREGLSRQHVLTRIGVMSLTRKKVQ BFRHVNGRWSMPBLAEVEBNKKMSQPGSPSPKTPTPSTPGDTQP NTPAPVPPABDGIKIERBSLKEERSIBGBKEVKSTAPETAIBCT QAPAPASBBEKVVVEPPEGEEKVEKAEVERTBEPMBTBFKGKG AADVEKVBEKSAIDLTPIVVEDKEEKKEERBFBFBFBFKGKG AADVEKVBEKSAIDLTPIVVEDKEEKKEERBFMSTBFWGKG AADVEKVBKKSAIDLTPIVVEDKEEKKERMLQNGSETPK UNGNFLEIKNKFLARRFKLLEQALVIEQLGRAAFLNMSEDPSH PSMALNTRPAEVECLAESHOHLSKESMAGNKPANAVLHKVLKQL BELLSDMKADVTRLPATTARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFLRNTVHRHBPPVTAEPIRLLAENBDVVVVDKPSSIPVHPC GRPRHNTVIFILGKKHQLKELHPLLERLDRLITSGVLMFAKTAAVS ERIHEQVRDRQLEKEYVCRVEGEPPTBEVTCKBPILVVSYKVGV CRVDPRGKPCETVYGRLSYNCQSSVVRCRPLTGRTHQIRVHLQP	!	<b>!</b> .		LLLTGTPLQNNLEBLFHLLNFLTPERFHNLEGFLEBFADIAKED
LFFVAAMBAPKMPNGMYDGSALIRASGKILLLQKMLKENGKE RVLIFSQMTKNIDLIEDFLBHBGYKYBRIDGGTGSMRCBAIDR RVLIFSQMTKNIDLIEDFLBHBGYKYBRIDGGTGSMRCBAIDR FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQ APSRAHRIGQMKKVMIYRFVTRASVBERITQVAKKKMMITHLVV RPGLGSKTGSMSKQELDDILKFGTBRLFKDEATDGGGDNKEGED SSVIHYDDKAIERLLDRNQDETEDTBLQCMNBYLSSFKVAQYVV REBEMGEBEBVERBIIKQBESVDPDYWEKILRHHYEQQQBDLAR NIGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASBEGDE DFDRBSBAPRRPSRKGLRNDKDKPLPPLLARVGGNIBVLGFNAR QRKAFLNAIMRYGMPPQDAFTTQMLVRDLRGKSEKEFKAYVSLF MRHLCBPGADGABTFADGVPREGLSRQHVLTRIGVMSLTRKKVQ EFRHUNGRMSMPELAEVEBNKKMSQPGSPSPKTPTPSTPGDTQP NTPAPVPPAEDGIKIERSLKERESIEGEKEVKSTAPBTAIECT QAPAPASBOBKVVVBPPEGEEKVEKABVKEKTEPMBTEPKGKG AADVEKVBEKSAIDLTPIVVEDKEEKKEEESKKEVMLQMSETPK DLNDEKQKKNIKQRFMFNIADGGFTBLHSLMQMBERAATVTKKT YEIWHRRHDYWILLAGIINHGYARWQDIONDFRXAILNSPFKGEM NRGNFLEIKNKFLARRFKLLEQALVIBEQLRRAAYLNMSEDPSH PSMALMTRFABEVBCLAESHQHLSKESMAGNKPANAVLHKVLKQL RELLGDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFLRNTVHRHBPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRPRHNTVIFILGKRQLKBLHPLHRLDRLTSGVLMFAKTAAVS ERIHBQVRDRQLEKEYVCRVEGEPPTBETTCKBPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGGSSVVRCRPLTGRTHQIRVHLQP	1			QIKKLHDMLG\PHMLRRLKADVFKNMPSKTELIV\RVELSPM\Q
RVLIPSQMTKNLDLLEDFLEHEGYKYERIDGGITGNMRQEAIDR PNAPGAQQFCFLLSTRÄGGIGINLATADTVIIYDSDWNPHNDIQ AFSRAHRIGQNKKVMIYRPVTRASVERZITQVAKKMMLTHLVV RPGLGSKTGSMSKQELDDILKFGTBRLFKDEATDGGGDNKEGED SSVIHYDDKALTERLLDRNQDETEDTBLQCMNEVLSSFKVAQYVV REKEMGEEEBVEREIIKQEBSVDPDYWEKLLRHHYEQQQEDLAR NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASBEGDE DFDRBSBAPRRPSRKGLRNDKDKPLPPLLARVGGNIBVLGFNAR QRKAFLNAIMRYGMPPQDAPTTQMLVRDLRGKSEKEFKAYVSLF MRHLCEPGADGABTFADGVPREGLSRQHVLTRIGVMSLIRKKVQ EFRHVNGRWSMPELABVEENKKMSQPGSPSPKTPTPSTPGDTQP NTPAPVPPAEDGIKIEENSLKEEESIBGEKEVKSTAPBTAIECT QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMBTEPKGKG AADVEKVBEKSAIDLTPIVVEDKEBKKEERSKKSVMLQNGETPK DLNDEKKKNIKQRFMFNIADGGFTBLHSLMQNBERAATVTKKT YEIWHRRHDYWLLAGIINHGYARWQDIONDPRYAILNSEPKGEM NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDPSH PSMALNTRPAEVECLAESHOHLSKESMAGNKPANAVLHKVLKQL KELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFTENTVERHEPPVTAEPIRLLAENBDVVVVDKPSSIPVHPC GRPRHNIVIFILGKRHQLKBLHPLHRLDRLTSGVLMFAKTAAVS ERIHKQVRDRQLEKEYVCRVEGEPPTBEVTCKEPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP	1	ł	1	KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNHPY
RVLIPSQMTKNLDLLEDFLEHEGYKYERIDGGITGNMRQEAIDR PNAPGAQQFCFLLSTRÄGGIGINLATADTVIIYDSDWNPHNDIQ AFSRAHRIGQNKKVMIYRPVTRASVERZITQVAKKMMLTHLVV RPGLGSKTGSMSKQELDDILKFGTBRLFKDEATDGGGDNKEGED SSVIHYDDKALTERLLDRNQDETEDTBLQCMNEVLSSFKVAQYVV REKEMGEEEBVEREIIKQEBSVDPDYWEKLLRHHYEQQQEDLAR NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASBEGDE DFDRBSBAPRRPSRKGLRNDKDKPLPPLLARVGGNIBVLGFNAR QRKAFLNAIMRYGMPPQDAPTTQMLVRDLRGKSEKEFKAYVSLF MRHLCEPGADGABTFADGVPREGLSRQHVLTRIGVMSLIRKKVQ EFRHVNGRWSMPELABVEENKKMSQPGSPSPKTPTPSTPGDTQP NTPAPVPPAEDGIKIEENSLKEEESIBGEKEVKSTAPBTAIECT QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMBTEPKGKG AADVEKVBEKSAIDLTPIVVEDKEBKKEERSKKSVMLQNGETPK DLNDEKKKNIKQRFMFNIADGGFTBLHSLMQNBERAATVTKKT YEIWHRRHDYWLLAGIINHGYARWQDIONDPRYAILNSEPKGEM NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDPSH PSMALNTRPAEVECLAESHOHLSKESMAGNKPANAVLHKVLKQL KELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFTENTVERHEPPVTAEPIRLLAENBDVVVVDKPSSIPVHPC GRPRHNIVIFILGKRHQLKBLHPLHRLDRLTSGVLMFAKTAAVS ERIHKQVRDRQLEKEYVCRVEGEPPTBEVTCKEPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP			i	LFPVAAMRAPKMPNGMYDGSALIRASGKILLLIQKMLKNLKEGGH
FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQ APSRAHRIGQNKKVMIYRFVTRASVBERITQVAKKKMITHLVV RPGLGSKTGSMSKQELDDILKFGTBELFKDEATDGGGDNKBGBL SSVIHYDDKAIERLLDRNQDBTBDTBLQCMNBYLSSFKVAQYVV REBEMGEEEBURBEIIKQBESVDPDYWEKLLRHHYPQQQEDLAR NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASBEGDE DFDRRSBAPRRPSRKGLRNDKDKPLPPLLARVGGNIBVLGFNAR QRKAFINAIMRYGMPPQDAFTTQMLVRDLRGKSEKBFKAYVSLLF MRHLCBFGADGABTFADGVPREGLSRQHVLTRIGVMSLIRKKVQ RFEHVNGRWSMPBLAEVEBNKKMSQPGSPSPKTPTPSTTPGDTQP NTPAPVPPAEDGIKIERNSLKEBESIBGEKBVKSTAPETAIECT QAPAPASEDEKVVVBPPEGEEKVBKABVKERTEEPMBTBPKGKG AADVEKVBEKSAIDLTPIVVEDKEBKKEEBEKKEVMLQNGBTPK DLNDEKQKKNIKQRFMFNIADGGFTBLHSLWQNBERAATVTKKT YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNSPFKGEM NRGNFLEIKNKPLARRFKLLEQALVIEEQLARAAYLMMSEDPSH PSMALNTRFAEVBCLAESHOHLSKBSMAGNKPANAVLHKVLKQL BELLSDMKADVTRLPATTARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFLRNTVHRHBPPVTAEPIRLLAENBDVVVVDKPSSIPVHPC GRFRHNTVIFILGKKHQLKBLHPLHRLDRLTSGVLMFAKTAAVS ERIHBQVRDRQLEKEYVCRVEGKEPPTBEVTCKRPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP		]		
APSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKRMMLTHLVV RPGLGSKTGSMSKQELDDILKFGTBRLFKDEATDGGGDNKBGED SSVIHYDDKAIERLLDRNQDETDTBLQCMNBYLSSFKVAQYVV REBEMGEEEVERBIIKQEBSVDPDYWEKLLRHHYEQQQEDLAR NLGKGRRIRKQWNYNDGSQEDRDWQDDQSDXQSDYSVASBEGDE DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFNAR QRKAFLNAIMRYGMPPQDAFTTQMLVRDLRGKSEKEFKAYVSLF MRHLCEPGADGABTFADGVPREGLSRQHVLTRIGVMSLIRKKVQ EFEHNURGWSMPBLAEVEENKKMSQPGSPSPKTPTPSTFGDTQP NTPAPVPPAEDGIKIERNSLKEEESIBGKEVKSTAPETAIECT QAPAPASEDEKVVVEPPEGEEKVBKABVKERTEEPMBTEPKGKG AADVEKVBEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGSTPK DLNDEKQKKNIKQRFMFNIADGGFTELHSLMQNBERAATVTKKT YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNSPFKGEM NRGNFLEIKNKPLARRFKLLEQALVIBEQLERAAYLMMSEDPSH PSMALNTRFAEVUCLAESHQHLSKESMAGNKPANAVLHKVLKQL EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRFRHNTVIFILIGKKHQLKELHPLHRLDRLTSGVLMFAKTAAVS ERIHEQVRDRQLEKEYVCRVEGEEPPTEEVTCKRPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP		ł	1	
RPGLGSKTGSMSKQELDDILKFGTBRLFKDEATDGGGDNKEGED SSVIHTDDKAIRRLLDRNQDETEDTBLQCMNRYLSSFRVAQYVV REBEMGEEEBVERBIIKQBESVDPDYWEKLLRHHYEQQQEDLAM NLGKGKRIRKQVMYNDGSQENDWQDDQSDNQSDYSVASBEGDE DFDRRSEAPRRPSRKGLINDKDKPLPPILARVGGNIBVLGFNAR QRKAFLNAIMRYGMPPQDAFTTQMLVRDLRGKSEKEFKAYVSLF MRHLCEPGADGABTFADGVPREGLSRQHVLTRIGVMSLIRKKVQ EFRHWNGRWSMPELAEVEENKKMSQPGSPSPKTPTFSTPGDTQP NTPAPVPPAEDGIKIERNSLKERESIBGEKEVKSTAPETAIECT QAPAPASEDEKVVVEPPEGEEKVEKABVKERTEEPMBTEPKGKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEKKEVMLQNGSTPK DLNDEKQKKNIKQRFMFNIADGGFTBLHSLMQNBERAATVTKKT YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNSPFKGEM NKGNFLEIKNKFLARRFKLLEQALVIBEQLRRAAYLMMSEDPSH PSMALNTRFAEVUCLAESHQHLSKESMAGNKPANAVLHKVLKQL BELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRFRHNTVIFILGKKHQLKELHPLLRCLTSGVLMFAKTAAVS ERIHEQVRDRQLEKEYVCRVEGEFPTBEVTCKRPILVVSYKVGV CRVDPRGKPCETVYQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP		į.		
SSVIHYDDKATERLLDRNQDETEDTELQCMNEYLSSPKVAQYVV REKEMGEEEVERBIIKQEBSVDPDYWEKLLRHHYEQQQEDLAR NLGKGRRIRKQVNYNDGSQEDRDWQDDQSURQSDYSVASBEGDE DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIBVLGFNAR QRKAFLNAIMRYGMPPQDAFTTQMLVRDLRGKSEKEFKAYVSLF MRHLCEPGADGABTFADGVPREGLSRQHVLTRIGVMSLIRKKVQ BFKHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDTQP NTPAPVPPAEDGIKIERNSLKERESIBGEKEVKSTAPETAIECT QAPAPASEDEKVVVEPPEGEEKVEKABVKERTEEPMBTTEPKGRG AADVEKVEKKSAIDLTPIVVEDKEEKKEEERKEKVMLQNGSTFK DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNBERAATVTKKT YEIWHRRHDYWLLAGIINGGYARWQDIONDPRYAILASPFKGEM NRGNFLEIKNKPLARFKLLEQALVIEEQLRRAAYLNMSEDPSH PSMALNTRPAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL RELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFTENTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRPRHNTVIFILGKKHQLKELHPLHRLDRLTSGVLMFAKTAAVS ERIHEQVDROGLEKEYVCRVEGEEPPTEVTCKEPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP	1	ŀ		1
REBEMGEEEVEREIIKQEESVDPDYWEKLLRHHYPQQQEDLAR NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDYSVASBEGDE DFDRRSEAPRRPSRKGLIRNDKDKPLPPLLARVGGNIBVLGFNAR QRKAFLNAIMRYGMPPQDAFTTQMLVRDLRGKSEKEFKAYVSLF MRHLCBPGADGABTFADGVPREGLSRQHVLTRIGVMSLIRKKVQ EFRHVMGRWSMPELAEVERNKKMSQPGSPSRTPTPSTPGDTQP NTPAPVPPAEDGIKIEENSLKEBESIEGEKEVKSTAPETAIECT QAPAPASEDEKVVVBPPEGEEKVEKABVKETEEPMBTEPKGKG AADVEKVBEKSAIDLTPIVVEDKEEKKEESEKKEVMLQNGSTPK DLINDEKQKKNIKQRFMFNIADGGFTELHSLWQNBERAATVTKKT YEIWHRRHDYWLLAGIINHGYARWQDIONDPRYAILNSPFKGEM NKGNFLEIKNKPLARRFKLLEQALVIEEQLARAAYLMMSEDPSH PSMALNTRPAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL BELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFTENTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRPRHNTVIFILGKKHQLKBLHPLHRLDRLTSGVLMFAKTAAVS ERIHEQVRDRQLEKEYVCRVEGBEPPTEVTCKEPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP			Į	
NIGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEGDE DPDRRSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIBVLGFNAR QRKAFINAIMRYGMPPQDAFTTQMLVRDLRGKSEKEFKAYVSILF MRHLCBPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKKVQ RFEHVNGRWSMPBLAEVEENKKMSQPGSPSPKTPTPSTTPGDTQP NTPAPVPPAEDGIKIERNSLKERESIBGEKEVKSTAPETAIECT QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMBTEPKGKG AADVEKVBEKSAIDLTPIVVEDKEBKKEEBEKKEVMLONGSTPK DLNDEKQKKNIKQRFMFNIADGGFTBLHSLWQNBERAATVTKKT YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNSPPKGEM NRGNFLEIKNKPLARRFKILEQALVIEEQLARAAYLMMSEDPSH PSMALNTRFAEVECLAESHOHLSKESMAGNKPANAVLHKVLKQL BELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRFRHNTVIFILGKKHQLKBLHPLHRLDRLTSGVLMFAKTAAVS ERIHEQVRDRQLEKEYVCRVEGKEPPTEEVTCKRPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP	1	1	j.	<u> </u>
DFDERSEAPRRPSRKGLENDKDKPLPPLLARVGGNIEVLGFNAR QRKAFLNAIMRYGMPPQDAFTTQMLVRDLRGKSEKEFKAYVSLF MRHLCEPGADGABTFADGVPREGLSRQHVLTRIGVMSLIRKKVO EFFHUNGRWSMPBELAEVEENKKMSQPGSPSRTPTPSTTPGDTQP NTPAPVPPAEDGIKIERNSLKEBESIEGEKEVKSTAPETAIECT QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMBTEPKGKG AADVEKVBEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGBTPK DLNDEKQKKNIKQRFMFNIADGGFTELHSLMONBERAATVTKKT YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNSPFKGEM NRGNFLEIKNKPLARRFKLLEQALVIBEQLERAAYLMMSEDPSH PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL BELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRFRHNTVIFILGKKHQLKELHPLHRLDRLTSGVLMFAKTAAVS ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKRPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP				
QRKAFLNAIMRYGMPPQDAFTTQMLVRDLRGKSEKEFKAYVSLF MRHLCEPGADGABTFADGVPREGLSRQHVLTRIGVMSLIRKKVQ BFRHUNGRWSMPBELAEVEENKKMSQPGSPSPKTPTPSTPGDTQP NTPAPVPPAEDGIKIEBNSLKEBESIBGKEVKSTAPBTAIECT QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMBTEPKGKG AADVEKVEBKSAIDLTPIVVEDKEEKKEEKKEVMLQNGBTPK DLNDEKQKKNIKQRFMFNIADGGFTELHSLMGNBERAATVTKKT YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKGEH NRGNFLEIKNKFLARFKLLEQALVIBEQLERAAYLMMSEDPSH PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL BELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRFRHNTVIFILGKKHQLKELHPLHRLDRLTSGVLMFAKTAAVS ERIHEQVRDQLEKEYVCRVEGEFPTBEVTCKEPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP	Ì			
MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKKVQ  BFEHVNGRWSMPBLAEVEBNKKMSQPGSPSPKTPTPSTPGDTQP  NTPAPVPPAEDGIKIERNSLKEBESIBGEKEVKSTAPBTAIECT  QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMBTEPKSGR  AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGETPK  DLNDEKQKKNIKQRFMFNIADGGFTRLHSLMGNBERAATVTKKT  YEIWHRRHDYWLLAGIINHGYARMQDIQNDPRYAILNSEPFKGEM  NRGNFLEIKNKPLARRFKLLEQALVIEEQLRRAAYLNMSEDPSH PSMALNTRPAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL  EBLLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRPFHNTVIFILGKKHQLKBLHPLHRLDRLTSGVLMFAKTAAVS ERIHEQVRDQLEKEYVCRVEGEFPFREVTCKRPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP	1	]	<u> </u>	
BFEHVINGRWSMPELAEVEENKKMSQPGSPSRTPTPSTPGDTQP NTPAPVPPAEDGIKIEENSLKEESIBGEKEVKSTAPBTAIECT QAPAPASEDEKVVVEPPEGEEKVEKABVKERTEEPMETTEPKGKG AADVEKVEKKSAIDLTPIVVEDKEEKKEEREKEVMLQNGETPK DLNDEKQKKNIKQRFMFNIADGGFTELHSLWONBERAATVTKKT YEIWHRRHDYWILLAGIINEGYARWODIONDPRYAILASPFKGEM NRGNFLEIKNKPLARRFKLLEQALVIEEQLRRAAYLNMSEDPSH PSMALNTRPAEVECLAESHOHLSKESMAGNKPANAVLHKVLKQL RELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRPFHNTVIFTIGKKHQLKBLHPLHRLDRLTSGVLMFAKTAAVS ERIHEQVRDRQLEKEYVCRVEGEFPFREVTCKEPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP	1	l	Į.	
NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIECT QAPAPASEDEKVVVBPPEGEEKVEKABVKERTEEPMBTTEPKGKG AADVEKVEEKSAIDLITPIVVEDKEEKKEEBEKKEVMLQNGSTPK DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTKKT YEIWHRRHDYWILLAGIINHGYARWQDIQNDPRYAILNSPKGEM NRGNFLEIKNKPLARRFKILLEQALVIEEQLARAAYLAMSEDPSH PSMALNTRPAEVECLAESHOHLSKESMAGNKPANAVLHKVLKQL EBLLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFIENTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRFRHNTVIFILGKKHQLKELHPLHRLDRLTSGVLMFAKTAAVS ERIHEQVRDRQLEKEYVCRVEGEEPPTEEVTCKEPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP	)	1	i	
QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKGKG AADVEKVBEKSAIDLTPIVVEDKEBKKEEBEKKEVMLQNGETPK DINDEKQKKNIKQRFMFNIADGGFTELHSLMQNBERAATVIKKT YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNSPPKGEM NRGNFLEIKNFLARRFKILEQALVIEEQLARAAYLMMSEDPSH PSMALMTRFAEVECLAESHOHLSKESMAGNKPANAVLHKVLKQL BELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  ONDFIRMTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRFRHNTVIFILGKKHQLKELHPLHRLDRLTSGVLMFAKTAAVS ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKRPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP			l	
AADVEKVEEKSAIDLTPIVVEDKEEKKEVEKKEVMLQNGBTPK DINDEKQKKNIKQRFMFNIADGGFTELHSLMGNBERAATVTKKT YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKGEM NRGNFLEIKNKFLLEQALVIBEQLERAAYLMMSEDPSH PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL BELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRFRHNTVIFILGKKHQLKELHPLHRLDRLTSGVLMFAKTAAVS ERIHEQVRDRQLEKEYVCRVEGEFPTEVTCKEPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP	1	{		
DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNBERAATVTKKT YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKGEM NRGNFLEIKNKPLARRFKLLEQALVIBEQLRAAYLMWSEDPSH PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL BELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ ONDFLRNTVHRHBPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRPRHNTVIFILGKKHQLKBLHPLHRLDRLTGGVLMFAKTAAVS ERIHEQVRDRQLEKEYVCRVEGEFPTBEVTCKEPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP	!	1	]	
YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPPKGEM NRGNFLEIKNKFLARRFKLLEQALVIBEQLRAAYLNMSEDPSH PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL EELLSDMKADVTRLPATTARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  ONDFLRNTVHRHBPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRPRHNTVIFILGKKHQLKBLHPLHRLDRLTSGVLMFAKTAAVS ERIHBQVRDRQLEKEYVCRVEGEFPTBEVTCKBPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP	1	[		
NRGNFLEIKNKPLARRFKLLEQALVIEEQLRRAAYLNMSEDPSH PSMALNTRPAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL EELLSDNKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  6006 1 965 DNDFRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRPFHNTVIFILGKKHQLKBLHPPLHRLDRLTSGVLMFAKTAAVS ERIHEQVRDRQLEKEYVCRVEGEPPTREVTCKEPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP	l	1		
PSMALNTRPAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL BELLSDMKADVTRLPATIAR I PPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  ONDETERNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRPRHNTVIFILGKKHQLKBLHPPLHRLDRLTSGVLMFAKTAAVS ERIHEQVRDRQLEKEYVCRVEGEPPTREVTCKRPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP	]	1	1	YEIWHRRHDYWLLAGIINHGYARWODIONDPRYAILNEPFKGEM
PSMALNTRPAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL BELLSDMKADVTRLPATIAR I PPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ  ONDETERNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRPRHNTVIFILGKKHQLKBLHPPLHRLDRLTSGVLMFAKTAAVS ERIHEQVRDRQLEKEYVCRVEGEPPTREVTCKRPILVVSYKVGV CRVDPRGKPCETVPQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP		1		NRGNFLEIKNKFLARRFKLLEQALVIBEQLRRAAYLNMSEDPSH
EPTPQQVAQQQ  6006 1 965 DNDFTRNTVHRHBPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRFRHNTVIFILGKRHQLKBLHPLHRLDRLTSGVLMPAKTAAVS ERIHBQVRDRQLEKEYVCRVEGEFPTBEVTCKEPILVVSYKVGV CRVDPRGKPCBTVFQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP	[		İ	
EPTPQQVAQQQ  6006 1 965 DNDFTRNTVHRHBPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRFRHNTVIFILGKRHQLKBLHPLHRLDRLTSGVLMPAKTAAVS ERIHBQVRDRQLEKEYVCRVEGEFPTBEVTCKEPILVVSYKVGV CRVDPRGKPCBTVFQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP	1	1	}	
6006 1 965 DNDFLRNTVHRHBPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRFRHNTVIFILGKRHQLKBLHPLHRLDRLTSGVLMPAKTAAVS ERIHBQVRDRQLEKEYVCRVEGEPPTBEVTCKEPILVVSYKVGV CRVDPRGKPCBTVFQRLSYNGQSSVVRCRPLTGRTHQIRVHLQP	i	l	(	
GRFRHNTVI FILGKRHOLKBLHPLHRLDRLTSGVLMFAKTAAVS BRIHBQVRDRQLEKEYVCRVEGEFPTBEVTCKEPILVVSYKVGV CRVDPRGKPCBTVFQRLSYNGQSSVVRCRPLTGRTHQIRVHLQF	2002	ļ	0.55	
ERIHBQVRDRQLEKEYVCRVEGEFPTBEVTCKEPILVVSYKVGV CRVDPRGKPCBTVFQRLSYNGQSSVVRCRPLTGRTHQIRVHLQF	P00P	1 1	765	
CRVDPRGKPCETVFQRLSYNGQSSVVRCRPLTGRTHQIRVHLQF	<b>J</b>	ì	j	GKERMYTVI FILMKKHQDKKHMPLHKDJKDISGVIMFAKTAAVS
CRVDPRGKPCETVPQRLSYNGQSSVVRCKPLTGRTHQIRVHLQF LGHPILNDPIYNSVANGPSRGRGGYIPKTNEELLRDLVAEHQAK	ŀ	1	1	RKTHRÜAKDKÜTEKKA ACKARÜKEALEKRALCKRATTAARAKACA
LGHPILNDPIYNSVAWGPSRGRGGYIPKTWSKLLRDLVAEHQAK	1	l	[	CRVDPRGKPCETVFQRLSYNGQSSVVRCRPLTGRTHQ1RVHLQF
		L		LGHPILMDPIYMSVAWGPSRGRGGYIPKTNEKLLRDLVAEHQAK

Do   Deginning	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cocresponding to first amino acid residue of amino acid residue of amino acid acid amino acid acid acid acid acid acid acid acid		beginning	nucleotide	
corresponding to first mino acid amino acid anino acid anino acid sequence and control to the cesidue of anino acid sequence and control to the cesidue of anino acid sequence and control to the cesidue of anino acid sequence and control to the cesidue of anino acid sequence and control to the cesidue of sequence and control to t	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid am	1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid aequence  Godon, /-possible mucleotide deletion, Codon, /-possible mucleotide deletion, Codon, /-possible mucleotide deletion, Codon, /-possible mucleotide deletion, Codon, /-possible mucleotide deletion, SIAPRCDVPTCPTI  GODOT 3  2351  BEGGURADICEGUIS POINTSTAPS SEGRODIESCAARA QUME RYARANGELDITIALS ERAVETUWNO() ROTYTLCRVPAGATC SLAPRCDVPTCPTI  BEGGURVPTORTOTITEREMOPERCS INGENETIGE GPTPOSSEGHISTIALS SISHINNISHITTSSSFRTS PRETELIK BEIDLPYKANJALITYQUINVOTOTICEDEWISH ASSOLVEN BEIDLYKWANJALITYQUINVOTOTICEDEWISH ASSOLVEN BEIDLYKWANJALITYQUINVOTOTICEDEWISH ASSOLVEN BEDDERRANGIATILCIA PREVENTER SETTEM THE LIKE BEDDERRANGIATILCIA PREVENTER SETTEM THE LIKE BEDDERRANGIATILCIA PREVENTER SETTEM THE LIKE BEDDERRANGIATILCIA PREVENTER SETTEM SETTEM THE LIKE BEDDERRANGIATILCIA PREVENTER SETTEM SETTEM THE LIKE BEDDERRANGIATILCIA PREVENTER SETTEM SETTEM THE LIKE SESSIOLOGIA GUARALTE HAVO REGIONAL PROMETISH AND ASSOCIATIVA SETTEM WINTOTICHEM THE AND ASSOCIATIVA PREVENTER SETTEM SETTEM LICENSEN SETTEM THE AND ASSOCIATIVA PREVENTER SETTEM SETTEM UNIVERSIANDA SETTEM THE AND ASSOCIATIVA SETTEM THE AND ASSOCIATIVA SETTEM THE AND ASSOCIATIVA SETTEM THE AND ASSOCIATIVA SETTEM THE AND ASSOCIATIVA SETTEM THE AND ASSOCIATIVA SETTEM THE AND ASSOCIATIVA SETTEM THE AND ASSOCIATIVA SETTEM SETTEM THE AND ASSOCIATIVA SETTEM SETTE	1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
residue of anino acid sequence (200m, 1-possible mucleotide deletion) (200m, 1-possible mucleotide deletion) (200m, 1-possible mucleotide deletion) (200m) (			amino acid	
amino acid aequence  Codoni, /-possible mucleotide insertion)  GEDWINICEGUIS POINTERTAPSE GERODIASCIANA QUME  WYREAN PORCHIOTIAL SERVEY DWING) ROT TILCEV PROGRET  SLAPRCDVP CTPTI  BEGOVEY TO THE THE SERVEY PROMONON ROT TILCEV PROGRET  GOTTO 3  2351  BEGOVEY TO THE THE SERVEY PROMONON ROT TILCEV PROGRET  GPTPOSSEGILISTICS LIGHINICATION ROT TILCEV PROGRET  BEDLIP REVISION ROT THE BEDLIP REVISION ROT TO THE SERVEY PROGRET ROT THE SERVEY PROGRET ROT THE SERVEY PROGRET ROT THE SERVEY PROGRET ROT THE SERVEY PROGRET ROT THE SERVEY PROGRET ROT THE SERVEY PROGRET ROT THE SERVEY PROGRET ROT TO THE SERVEY PROGRET ROT THE SERVEY PROGRET ROT THE SERVEY PROGRET ROT TO THE S	1		residue of	S=Serine, T=Threonine, V=Valine,
Sequence   N-possible nucleotide insertion			amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
GSLDWIDLCEGGLSPELITISTAPSSETGGDDLEELAAAA QOMME  WARAAPQERDITLAISEKAAVETUMON QRQTYLTEVPAGATG  SLAPRRCOVETOPTI.  BELGGVEVVETOTTOTT.TENEMOPBEGSLINGHKYQETIGGLVPE  GPTPDSSEGRILSVILSSLSHINMINGHLITSSSPRTJEPRINTELLIK  BEDLEVRAVSLGHTVUDINVOTTOTGEGMOMOSIAABSOLEVYAS  SPDEKALVRAAARIGJVFICRSSETMEVATIGHLERYKLIHILLE  PDDDRERNSTVONDERSETMEVATIGHLERYKLIHILLE  PDDRERNSTVONDERSETMEVATIGHLERYKLIHILLE  BEDLEVRAVSLGHTULLAYRKPTSKYEETIDRE.TEVARTALOGON,  KKLANAPGPIEKULI LIAGATAVERDLORVERTERALGHAGON,  WILTGORHETANSVSLSCHEMETHINLELINGKSDERCARGLER  GLARETTENHIVORGUVOTOTISLIAGHERIKLPHOEVRICHSCANGLUK  WILTGORHETANSVSLSCHEMETHINLELINGKSDERCARGLER  LCCRMAPLOKARVIRLIKI SPERPITTANGGORANDVSHIQEAHV  ULTVAVVANALE-HEMVIRHINTUNGLIAGHERIKLPHOEVRICHSCANGLUK  LCCRMAPLOKARVIRLIKI SPERPITTANGGORANDVSHIQEAHV  ULTVAVVANALE-HEMVIRHINTUNGLIAGHERIKLPHOEMPITIELIT  SEPLILYSLLEGOUPHVILONGRUTISLIGURGWGOMFFOTLVFTVM  ULTVAVANALE-HEMVIRHINTUNGLIAGHERIKLPHOEMPITIELIT  HESSENAPISHGSHADDFYTNIDSILILISTNOSSYC  GROSPIHISSISHBASDFYTNIDSILILISTNOSSYC  GROSPIHISSISHBASDFYTNIDSILILISTNOSSYC  GROSPIHISSISHBASDFYTNIDSILILISTNOSTYC  RCSPERPIPHIASTHADVALMOSILIKLDSNOCTEAPPEHAGPAR  ASKPSOCHMOLPFOLINGRICHANGARVERALERVIL  BETSTECKALLTANDORTHUNGHLERARICH STRONGURKTULGTH  IKIPHAPMASARSISTSTYNINKINGLERKROARVERGANYTICK  KCTYRDPIARITANGNINGHTANGURKARRATYKILLISDICLBYCCKRILE  DEROKERPIPHIASTHADVALMOSISTYRUNGHTANGURVANGURVANIC  SURRESSITLICRCHYNKHILYRHIPHONAPYTIAKAGERSLANGAVPIC  KCTYRDPIARITANGURKHANGURVANAVILORNINGVAVCOGYSV  OQMMILGIJGRANPYSTPOGROSVKGLERROGONINGKUNGGSTV  GOMMILGIJGRANPYSTPOGROSVKGLERROGONINGKUNGGSTV  GOMMILGIJGRANPYSTPOGROSVKGLERROGONINGKUNGGSTV  ANANYTHIARDAABASSISTYRONINGHURGONINGVAVCOGYSV  OQMMILGIJGRANPYSTPOGROSVKGLERROGONINGKUNGGSSIDAAA  ATOPPOGRITSTYNKILITICH LIAGHERIKARROV  ANANGURLSTPENDING PELAPVAKTYROHDERBERGRICH SERDESO  OQMMILGIJGRANPYSTPOGROSVKGLERROGONINGKUNGGSSIDAAA  ATOPPOGRITSTYNKILITICH LIAGHERIKARROV  ANANGURLSTPORTHUNGKORTHUNGRICH KORTINGKUNGONINGKUNGGSSIDAAA  ANTOPPOGRITSTYNKILITICH LIAGHERICH LIAGHERIKARROV  GORMALSTRIDENDA JARGHERICH PROPROVORICH LIAH			sequence	
BYARAROPEUTUTALLS:REAVETDVING\RGT\TLCRVPACATC SLAPRECOVETOTIC SLAPRECOVETOTICS SLAPRECOVETOTICS BELGOVETOTICS PERSONAL SILLS SLINAMISHINITISS SPETIOPHETE TILL BELGOVETOTICS SILLS SLINAMISHINITISS SPETIOPHETE TILL BELGOVETOTICS SILLS SLINAMISHINITISS SPETIOPHETE TILL BELGOVETOTICS SHOWS SHOW SHOWS SERVED SHOWS SHOW SHOWS SPERKALVERANT GUT YET KINSETERE TILLS SPETIOPHETE TILL BELGOVETOTICS SHOWS SHOW SHOWS SHOW SHOWS SHOW SHOWS SHOW SHOW	L	sequence		1
SLAPRICUPY CYTL  REGOVER OF THOS SEGNIL STATEMEND PRICES INCHINYGE TIGELUPE  GPTPOS SEGNIL STATISLISHINANI SHILTESS PETT GPTRATELLING  REDUPE PRANSLET UN DINNOTO THE CORPON GRANGE AND SOLE YYAS  SPORKALVRAJARIGUY L'EXREST PREVITTIGALERY KLILHILLE  REDUPER RESPONDANT OF THE CONTROL OF THE CO	ł			
### ##################################		İ		
OPTPOSSERILEYLSSISHIANISHITTSSYTPENRITERINE REDLEPRAVALED (VOLD VINCED CONTROL PROMITA PSOLETY AS SPERKALVRANAR (GIVY IGNSETHEWATLIGHERY KILLIH REDLEPRAVOLA POR SERRILIAN CONTROL PROMITA SPERKALVRANAR (GIVY IGNSETHEWATLIGHERY KILHIH POSDER RING) AND SPERKALVRANAR (GIVY IGNSETHEWATLIGHERY KILHIH POSDER RING) AND SPERKALVRAN RING AND SPERKALVRAN				
REDLEPERAVILLENGUNTOCTOCTOCOPOGNILADSOLUTIONS SPORKALVEARANG (SUPTIGINS RETWEVITLIGALERY KILLHILE PUSDRENNSVIVOADSCRULLIFAKGASSS ILPKCIGGETETETIL HVDEFALKGIRETICLATREPERS KEYETETICE —PERPTALOORINE RKLAAVPOPTEKOLLLIGATAVEDETIGIOKVRETTERLENHOLTRU WILTGORHETZAVSVLSCCHEPETETMILLELINGKSDESCARGUR (GLARRITTEDHIVOGRILVPORTSISIALAREIBELPHEVEUNICSEN LCCRADELGRAKVITLIKISPERUTTAVOGGAMONSHIQDAHU GIGINGKSGRQABANISDITAINETETISRULTVERGORMONSHIQDAHU GIGINGKSGRQABANISDITAINETETISRULTVERGUSTATIAVALUTE WULTGORINETVETTOCHTOCHTOCHTOCHTOCHTOCHTOCHTOCHTOCHTOC	6007	3	2351	1
SPEKALIVBASRIGIVFIGNEETHEVITAGLERYKLLHILE PDEBRANSVIVOLPSCERLIPAGEASSILPTGELERYKTE HVDEPALIGIETICLTAYREYTSKEYETIGKEETYTETH HVDEPALIGIETICLTAYREYTSKEYETIGKEETYTETH HVDEPALIGIETICLTAYREYTSKEYETIGKEETYTETHAGAIKV HVLTGDKHETAVSVISLSCGHFRETMITLELLINGKSDEBCABQLE GLARRITEDHVIQHGLVYDSTSJALALREHEKLPHEVCHNEYS LCCRAPADGARVITLIKISTSERVETJALALREHEKLPHEVCHNEYS LCCRAPADGARVITLIKISTSERVETJALALREHEKLPHEVCHNEYS LCCRAPADGARVITLIKISTSERVETJALALREHEKLPHEVCHNEYS LCCRAPADGARVITLIKISTSCGALDRIVALVALGEFT SLETLIVSLLEGHUDERVIQHETLIRDISKRELLSIKTFILWIG UVYPYRNVCETTOPTATYOTLIGHTONGANTATURYTLIVALGEFT SLETLIVSLLEGHUDERVIQHETLIRDISKRELLSIKTFILWIG LIGHBYRSGVALLIGKOTSIGANTYTTIVALD LGGGNYPPYIGLISSSGAMPATILUTVOTCLEDITIKAVOTCHPU LGGGNYPPYIGLISSSGAMPATILUTVOTCLEDITIKAVOTCHPU LGGGNYPPYIGLISSSGAMPATILUTVOTCLEDITIKAVOTCHPU LGGGNYPPYIGLISSSGAMPATILUTVOTCLEDITIKAVOTCHPU LGGGNYPPYIGLISSSGAMPATILUTVOTCLEDITIKAVOTCHPU LGGGNYPPYIGLISSSGAMPATILUTVOTCLEDITIKAVOTCHPU LGGGNYPPYIGLISSSGAMPATILUTVOTCHPUTTIKAVOTCHPUT LGGGYPPHTHISSBANDSPYTTMBUTLITATUROTCHPUTTIKAVOTCHPUT LGGGYPPHTHISSBANDSPYTTMBUTLITATUROTCHPUT LKEVAPPARATETYTTARUTCHMUTSTILTSTMOSTICTSTACKTLETH LKEVAPPAGASSSILTTTONGKNOTGLAREGARDVICA SARRESSIHCKRCLPMPKSYBALVQHVIGDHERIOYQVTAMIG HTWVVPREFEIMLIAPKUQUKSMGLEPPIGSLASGNVADA ASPAPTSLQGAMASSILSSGGLASSVHLQOMNYSVSUGGSSKAAA ATGPPEGRTSSTQKKLCTICNKEPPERVYSHPEKSHDAKVI GQMURLGIJERHISTGVAMHASPYLAGOGSSKAAAA ATGPPEGRTSSTQKKLCTICNKEPPERVYSHPEKKEHDAKVI AVANYMKINHTSKCLCYNNYLTUTTILTHILLIGGSCPYCRS TPRODVERMADHRAWNILDSRGPRTDSTLEPDLTLQGGSHVIDHIL LLUTTYINLIDADASSVANHAGAMPEYPPIRAGRICAGSSKAAAA ATGPPEGRTSSTQKKLCTICNKETPPERVYSHPEKKEHDAKVIT LGGDDSSSDSPELBESSINSGSGPDDVPVERVERKINGGSSKAAAA ATGPPEGRTSSTQKKLCTICNKETPPERVYSHPEKKEHDAKVIT SPRAAVERVARDVERKERGAPSVANHAGAMPEYPPIRAGRICAGSSKAAAA ATGPPEGRTSSTQKKLCTICNGGSTCAGASVANKAGANGSSKAAAAA ATGPPEGRTSSTQKKLCTICNGGSTCAGASVANKAGANGSKAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	)			1
### POSDRENNSVITOADSCREULPANGARSSILLDTGGESTERTH ### POSDRENNSVITOADSCREULPANGARSSILLDTGGESTERTH ### POSDRENNSVITOADSCREULPANGARSTERAL PRACTACOGN   ### POSTRENSVITOADSCREULPANGARS   ### POSTRENSVITOADSCREULPANGA	1			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
HVDEPALIGLETT.CLAYRKTSEKYERIDRE.PERAPALOOR\S EKIAAPOPOT EKULLLAGATAVEROLIGUNENIELARMAOJKV WULTIGKBETAVSVSLSCGIPBETHINITLELIBQESGISEAGOLE OLARRITISHVIJOHULVOUTSLSLALREBELIPBEVCENGSAV LCCRMAPIQKAKVIRLIKISPEKPITLAVGDCANDVSMIQEAHV GIGIMRGRQAARKSDTATARPKFLSKLLFVHGHFYITALTLI WOVPYFRINGETTEPOPITOPTICLESQCIPTISOVINTITALTLI WOVPYFRINGETTEPOPITOPTICLESQCIPTISOVINTITALTIL WOVPYFRINGETTEPOPITOPTICLESQCIPTISOVINTITALTIL WOVPYFRINGETTEPOPITOPTICLESQCIPTISOVINTITALTIL WOVPYFRINGETTEPOPITOPTICLESQCIPTISOVINTITALTIL WOTTOPTIVAMAECTHPYMINILITMGS LIPFVPGISTYGILIMPE LISGSMIPTYPOSTILLIGUNGMORTHISTILUTURGITALITMUT ULTYTVIVAMAECTHPYMINILITMGS LIPFVPGSLAGOULIMPE LISGSMIPTYPOLILISSGSAMPAILIMUTUCLEDITIKKUPORHIL HPISTEKAQLITETMAGITKCLOBMCCPPEGRAACASVERLERVI GROSPIHLISSMASADPYTIMOSILLIMITAMS LIPFVPGSLEVGOLIMPE LISGSMIPTINGSHAADATILIMUTUCLEDITIKKUPORHIL HPISTEKAQLITETMAGITKCLOBMCCPPEGRAACASVERLERVI GROSPIHLISSMASADPYTIMOSILLITMONYTKEPCCSACP PSKEPSAYKSHARANDASILITMONYSTUPTICACACP ASPROSPENDELVANITIMEDUGLADESLITMONYTKEPCCSACP PSKEPSAYKSHRAWHSENDERNILLIMONYTKEPCCSACP PSKEPSAYKSHRAWHSENDERNILLIMONYTKEPCCSACP PSKEPSAYKSHRAWHSENDERNILLIMONYTKEPCCSACP PSKEPSAYKSHRAWHSENDERNILLIMONYTKEPCCSACP PSKEPSAYKSHRAWHSENDERNILLIMONYTKEPCCSACP PSKEPSAYKSHRAWHSENDERNILLIMONYTKEPCCSACP GQMIRILISTERRENINGSPELAGATIVE LITTARRIDAS SISTEMARIA TENGALERVANITYENDICHARANICANISTAS LITTARRIDAS SISTEMARIA TENGALERVANITYENDICHARANICANISTAS ANAPERSISTICHARIA CTICHELPERNIVSUHERKEHERIKANIVA ANAPENSALSHANINANINANINANINANINANINANINANINANINANI	ł			9
HILANPOPTERUILLIGATAVEDELODAVERTIEALEMBAIKV   WULTGIBEERTAVUSLISCISTEPTINTILEILISCISTECASOLE				
WILTGRIETAVSVSLSCGIPTERTHNILLELINGGESISCARQLE QUARRITEMPLOHOLVOMIC JOHAND TO SLALARERISELIPSWYCENGAN LCCRMAPIQKAKVIRLIKISPEKPITLAVGIGANDVSMIQEAHV GIGIMMGRGKQAARNSDYAINEPKILSKLIFVHGHEYTIRLATL WYPFYRNUCETTPOFILIGETURSQYTINGVYMIGEAHV GIGIMMGRGKQAARNSDYAINEPKILSKLIFVHGHEYTIRLATL WYPFYRNUCETTPOFILIGETURSKGLIPSWYTHOLYNIGETE SLEILLIYSLLEGGRUPPHYLONKEPILYRDISKRRLLSIKFILWT LIGPSHAPIEPFGSYLLIGGGRUPSHLGROWNFORTLYTIVM VITVYVKHALE-THPWHINILWTMGSLIFFYFSLEFTURTIVETY WYTYYVKHALE-THPWHINILWTMGSLIFFYFSLEFTURTIVETY UTTYVKHALE-THPWHINILWTMGSLIFFYFSLEFTURTIVETY HPSTEKAQITETNAGITKCLDSMCCPPEGBAACASVGRMLERVY GRCSPHILSBRAGDPPYTMDSILIKUTMGSTC GRCSPHILSBRAGADPYDRIBSITCLDSIKCUTPHSSTC GRCSPHILSBRAGADPYDRIBSITCLDSICHTWORTH CONTROL HPSTEKAQITETNAGITKCLDSMCCPPEGBAACASVGRMLERVY GRCSPHILSBRAGADPYDRIBSITLLIGDIGLEFVCKHIE HPSTEKAQITETNAGITKCLDSMCCPPEGBAACASVGRMLERVY GRCSPHILSBRAGADPYDRIBSITLLIGDIGLEFVCKHIE DFRQFERMDFYLLNITHBURGSLIRGHESITANDGDITKEPFCCSACC PSSKFFSAYKSHERNWISGDFRURSILLIGDIGLEFVCKHIE DFRQFERMDFYLLNITHBURGSLIRGHESITANDGDITKEPFCCSACC SNARESSILLIKGELPHSKYSRLJOGITKEDBRIGGOVTANTIG HTWVVPBSKEIMLICAPPPGDKKSMGLIPPTIGSLASGNV\RSLP GQMMRILSITERNINHSTGNURMSVULLOGHRISTIGGERGO APARYSLOGANASSILSSGULKSPELSQGOSKULOGSSKPAAA ATDPPGMTSSTQRKKICTI CURELPPRHVYSWFRERHEABKVP AVANYINKLINHFSKCICYCRRLPTUFLLINHHLIHGLSGUPCS GROWNERLSTRURMWHOLDSHOPKTOSTISPTUFLQGGSHTNIT LLUTTTNIRDADABSVAJHIQANDPUP PROPKVQEKADIPVKS SPOAMPYSKUNOKKTLCPLCFSILKGE ISBAHCHLOFKUDGGSHTNIT LLUTTTNIRDADABSVAJHIQANDPUP PROPKVQEKADIPVKS SPORAPYSKUNOKKTLCPLCFSILKGE ISBAHCHLOFKUDGGSHTNIT LLUTTTNIRDADABSVAJHIQANDPUP PROPKVQEKADIPVKS SPORAPYSKUNOKKTLCPLCFSILKGE ISBAHCHLOFKUDGGSHTNIT LLUTTTNIRDADABSVAJHIQANDPUP PROPKVQEKADIPVKS SPORAPSKERANVANYA GENSHERABRETUKYPT\QDP TREETELAJATAVWAY GENSHERABRETUKYPT\QDP TREETELAJATAVAYAY GENSHERABRETUKYPT\QDP TREETELAJATAVAYAY GENSHERABRETUKYPT\QDP TREETELAJATAVAYAY GENSHERABRETUKYPT\QDP TREETELAJATAVAYAY GENSHERABRETUKYPT\COCOCCANAGRE ULUTUROKCHANAGATATATAGGGCCLGARXVRASVFTGNOPOVYGGL NGKRASAGRARGATHOPTICAGGCCCAGRASVRASVFTGNOPOVYGGL NGKRASAGRARGATHOPTICAGGCCCAGRASVR	1			
GLARRITEDHYLOHGLUVDOTTSLSLALREHBELDPBWCNICSAN     LCCRMAPLIGARVIRLIA ILS PERPITTANGUADNOSMIOGRHU     CIGHMONGORGARINSDYALRERIS KLLPPGEHEYY ILATI.     WYPFYRWCFITPQFLYDYTYCLPSQGTLYDSVIATLY \NICPT     SLFILLYSLLEGHUDPRYLQINGRETI-SRCLIPGENGYTHIA     TILEFSBAPIFFPRSYLLIGGDTSLLGGGGRGWHTESTLYTUW     VITYTYMALE-THEWTWINILITHMSSLIFYPYSPSLEYGOLINEP     LGSQRWFPVFLOLLSSGSAPFAILLWYTGLFLDITKKYPPRHL     HPYSTEKAQLIPETHAGYKICLDGMCPFPEGBACVGRWHLERVI     LGSQRWFPVFLOLLSSGSAPFAILLWYTGLFLDITKKYPPRHL     HPYSTEKAQLIPETHAGYKICLDGMCPFPEGBACVGRWHLERVI     GRGSPHITSRSWASDPYTNDRSILTLSTMDSSTC     GRGSPHITSRSWASDPYTNDRSILTLSTMDSSTC     GRGSPHITSRSWASDPYTNDRSILTLSTMDSSTC     GRGSPHITSRSWASDPYTNDRSILTLSTMDSSTC     GRGSPHITSRSWASDPYTNDRSILTLSTMDSSTC     GRGSPHITSRSWASDPYTNDRSILTLSTMDGSTC     ASKPOSGTWPOLEVANICSLEKRRYTYKKLLSDIGLEYCKERIE     DPKQRPRDPYLANTIPEDGELDPSILTRYDCHYPCFCCSACD     SARPASSALSSILTSTWDRWNDSULLDDIGLYCKERIE     DPKQRPRDPYLANTIPEDGELDPSILTRYDCHYPCFCCSACD     SARRESSSILTWRENTHISTRYDMANDSULLDDIGLYCKERIE     FUNDVYPEKKILTNTERGURDPSILTRYDCHAGRESLANGAPILC     SARRESSSILTWRENTHISTRYDMANDSULLODINGUVUS     SARRESSSILTWRENTHISTRYDMANSSULLODINGUVUS     GROWNLIGHT     HTWVVPRSKENLLAPRRYDUKSKRIGP PRICES     GQMWALGIGGRAPVS IPQGGSVKOLLPGSSSSVADAA     ATROPPGRITSSTCHALTAPROGVKORSHOLPGISLASGNV     SQMWARLSIPRENTISTGWNMSSVLILQUNNYOVES VCQCYSTS     GQMWALGIGGRAPVS IPQGGSVKOLLPGSSSVADAA     ATROPPGRITSSTCHALTAPROGVKORSHOLPGISLASGNV     SQMWALGIGGRAPVS IPQGGSVKOLLPGSSSVADAA     ATROPPGRITSSTCHALTAPROGVKORSHOLPGISLASGNV     AVANYIMKI:RNFSKCLYCRRV.PTDTLLINHILLHELSCLGCYCS     TREILEKALSIWV,WK.SDILASPSILSGORSKVADA     AVANYIMKI:RNFSKCLYCRRV.PTDTLLINHILLHELSCLGCYCS     TREILEKLASSIWV,WK.SDILASHSSRKKKCVDCCEK/KRGJL     LGRIDDSSGSSPENLESSNRGSSPPDYPERRERISHTAPROGSSWADA     TREILEKLASSIWV,WK.SDILASHSSRKKKCVDCCEK/KRGJL     LGRIDDSSGSSSSSPENLESSNRGSSPPDYPVEVERRISHNIPSER     VLKYJEBDASESSRENLOKKGRAPAKKGTHYCKSKVOLCEK/KRGJL     LGRIDDSSGSSSSSPENLESSNRGSSPPDYPVEVERRISHNIPSER     VLKYJEBDASESSRENLOKKGRRATMAKKSKVOLCEK/KRGJL     GROSSSGSBASSSRANAKARTHYCH	ł			The state of the s
LCCRMAPLORANVIRLALTSPERCTITLAVGICANDUSMIQRAHU GIGIMAKERGARARSDYALTARPRISARLIPTYATELYTE GIGIMAKERGARARSDYALTARPRISARLIPTYATELYTATI VOYPPYRNVCFITPQFLYGPYCLFSQQTLYDSVYLTLY\NICPT SLFILITSALLEGHUDPHYLQNRCFILTADISKRILLSTRIFTAYT ILGFSEAFIPFRSYLLIGGUSTLALGRGGMANNIFGTLIVTYW VITYTVAMALE-HPWTWINILTYMSS LIFYFYFSLFYGOLLIMPE LGSGRWFYPVIGLASGGSAPHAT LIMWYCLFLDITLKCHDFRIHL HPTSTEKAGLIFTHNGSIKCLDSMCCFPFGEAACASVGRMLERVI GRCSPTHISSRAMASDPYTHNGSILTLATMOSTC GRCSPTHISSRAMASDPYTHNGSILTLATMOSTC GRCSPTHISSRAMASDPYTHNGSILTLATMOSTC GRCSPTHISSRAMASDPYTHNGSILTLATMOSTC GRCSPTHISSRAMASDPYTHNGSILTLATMOSTC GRCSPTHISSRAMASDPYTHNGSILTLATMOSTC GRCSPTHISSRAMASDPYTHNGSILTLATMOSTC GRCSPTHISSRAMASDPYTHNGSILTLATMOSTC GRCSPTHISSRAMASDPYTHNGSILTLATMOSTC GRCSPTHISSRAMASDPYTHNGSILTLATMOSTC GRCSPTHISSRAMASDPYTHNGSILTLATMOSTC GRCSPTHISSRAMASDPYTHNGSILTLATMOSTC GRCSPTHISSRAMASDPYTHNGSILTLATMOSTC GRCSPTHISSRAMASDPYTHNGSILTLATMOSTALTMOSTC GRCSPTHISSRAMASDSICTANAPSILTLATMOCHTARPOTALTMOSTC GRCSPTHISSRAMASSILTATANAPSILTLATMOCHTARPOTALTMOCHTARPOTALTMOSTLATMOST KCTYRDPLYRITURKHI YRRHPGHVARPY TAKAGEKSIANGAPLG SNARESSILTRKCLJPMKSYRBALVOGNICHBEIGVGVTAMIG HTMVVVPBSKEIMLLAPPRODIKSNAGLPPRIGSLASGNV\ASLA GQMRILGIGGRAPVSI PQOSQVYKOLLPGGNGSVGGLEGASGNVAANA ATGPPGGRTSSTOJWKILCTICURELPPHNVSVHJEKSHEAKRVP AVANYIMKIRNPTSKCLYCNTYLPPTOTILINMILIGSCPYCRS TPRODVERMAJARHANVHLUBERGPKTOSTISPOLTLQGGSHTNILL LLVTTHINGDAPASSVAYHAQNNPPUP PROPRVQEKADILTVES SPORAPYKKOMOSTLOPHCHOTSTISPOLTLQGGSHTNILL LLVTTHINGDAPASSVAYHAQNNPPUP PROPRVQEKADILTVES SPORAPYKKOMOSTLOPHCHOTSTISPOLTLQGGSHTNILL LGFRMEELINAVANGHBND-DAGGLFRIMIDERGGRVABASCADAKKAM GGCKTARPSKINAVANGASPESGEPCOQVODEROMTCGKKGTOM GGCKTARPSKINAVANGASPESGEPCOQVODEROMTCGKKGTOM GGCKTARPSKINAVANGASPESGEPCOQVODEROMTCGKKGTOMOCHAL ULKUPEDDASESSERLOQKROGSSYRFTHITHSTILMINGSD SKOSGDAPASKARDOTAROTARGGRCCHORGCKGGGVUGABER ULKUPEDDASESSERLOQKROGSSYRFTHITHSTILMINGSD SKOSGDAPASKARDOTAROTARGGRCCHORGTUGARSVAGSPOTARABCGGRC GRCHABSTANAGGAGGRCCHORGTUGARSVAGSPOTARABCGGRC GRCHABSTANAGGAGGAGGACARAPACHAGGAGGACHAGAGGAGGACHAGACHAGGAGGACHAGACHAGAGAGAG	ĺ			
GIGIMOKEGRQAANSDYALTARFEIT,SKILFVEIGHFYTJRLATI. VOYPPYKNUCTITQPILOPYCLFSQOTLINSPULTILAVINCPP SLPILIYSLLEQHVDPHVLQNRPTLYRDISKNRLLSIKTFILYWT TILFFSSIAPITFFFSSYLLIGKDTSLLAGEGGWWTFTTLVTFVM VITTYTVANGLTHFWYMSILFYYWSIFFYGGILINPP LGSQRNYFVFJQLISSGSANFAILITMVTGGILFYYWSIFFYGGILINPP LGSQRNYFVFJQLISSGSANFAILITMVTGGILFYYWSIFFYGGILMPP LGSQRNYFVFJQLISSGSANFAILITMVTGGILFYYWSIFFYGGILMPP LGSGRYFYTDRSILTLSTMDSSTC GROSPHILSRSWASJDPYTTDRSILTLSTMDSSTC GROSPHILSRSWASJDPYTTDRSILTLSTMDSSTC GROSPHILSRSWASJDPYTTDRSILTLSTMDSSTC FSSKFFSANKGFGRALFAGATAVPPPSARRERCFAPFERGAPA ASRPSQETMPQLPVNNLGSLRKARKTYKKLIDIGLFYCKEHIE DFKQFSPHDDFYLLNITTMKNVGLIMDFSLTTRKQDITKFFCCSACT FSSKFFSANKSHFRANNEGDFPRRILLIAGFYCCTFNADKKTLEFT IKLFHAPAASAPSSSLSTFTKDRWKNNGLKPKQADSVEQAVYTCK KCTYRDPLYELTVKRHITYRHFQUVAAPYTJAKAGEKSLNGAVPLG SNARESSIHCKRCLFMPKSTRALVQHVIEDHERIGYQVTAMTIG HTMVVVPRSKLILAFRYGVAAPYTJAKAGEKSLNGAVPLG SNARESSIHCKRCLFMPKSTRALVQHVIEDHERIGYQVTAMTIG HTMVVVPRSKLILAFRYGVKAAPYTJAKAGEKSLNGAVPLG SNARESSIHCKRCLFMPKSTRALVQHVIEDHERIGYQVTAMTIG HTMVVVPRSKLILAFRYGVKAAPYTJAKAGEKSLNGAVPLG SNARESSIHCKRCLFMPKSTRALVQHVIEDHERIGYQVTAMTIG HTMVVVPRSKLILAFRYGVKAAPYTJAKAGEKSLNGAVPLG SNARESSIHCKRCLFMPKSTRALVQHVIEDHERIGYQVTAMTIG HTMVVVPRSKLILAFRYGVKAAPYTSVANGASVELQGISTSGORSV GQSRRLGIGGRAPVSIPQAKSVALDPKSTYGLGSGRSVGLGSGRSCYGGSV APARTISLGSANASSLISSGLKSPSLSGCASAVVLCGSSKRAA ATGPPGGTTSSTLYKMICTI CINKLIPPBUVYSVHFRKEHKARKY AVANYIMKLIMFTSKCLLCHKTYLTYLTILHHLGIGLGCCYCGS TFROUGKMAAAMAMAVULDEBGGPKTDSTLSFDLTLQGSSHTNIH LLITTNILADAPASSVALAHQANSPYPPERVOGKORKJCHAVKA SPQAAVPYKKDVCKTLCFLCTSILKGPISDALAHHARRHQVIQ GQDKTNAPSRLNQSPSLAPVKRTYBQMEPPLLKKRKLDDDSDS SFREKER SEPVULALDPKSHI BODSYEARKSFLTKYFFYKQFP TRREIEKLAASIAVVAKVSBUDSABHSNIKGRRGCKGCKGVANGKCKGCANGCKCCKGVANGKCKGCANGCKCCKGVANGKCKGCANGCKCCKGANGCKCCKGANGCKCCKGANGCKCCKGANGCKCCKGANGCKCCKGANGCKCCKGCANGCKCCKGCANGCKCCKGCCKCCKCKCCK	į.			, –
OVPPYKNIVETTPOPLYOPYCLESQOTIANDSVYLITAVNICET SLPILIYSLLEQHYDPHVLQNKPTLYRDISKNILSIKTPLYWT ILGPSIAPITPPSSYLLIGKDTSLLANDCANGGWYTEGTLYPTW VITYTYMALETHEWWINHLYTMGSITFYFYSTEGOLIMPP LISGNMYPYUPJQLLSSGSAMPAILHUVTCHEDITIKKVPPRHI. HPISTEKAQLITETNASIKCLDSMCCYPEGBAACASVGRMLERVY GRCSPHISRSWASDSPYTDRISHITLTNOSTC GRCSPHISRSWASDSPYTDRISHITLTNOSTC GRCSPHISRSWASDSPYTDRISHITLTNOSTC GRCSPHISRSWASDSPYTDRISHITLTNOSTCHARDSTC ANTWERGREGEGALFAGATAVFPYSARRERRCPAPEHAGPAR ASRPSQETWPQLPVNILGSIRKRATVXKILISGIGLEVCKEHIR DFRQFERPDFYLLNTTWEDVGLADDBSLTRMQDYRTCPCCSACP FSKFPSAYKSHFRNUHESDFBRRILLIANCPYCTFNADKKTLETH IKIFHAPPASAPSSISSTFYKNKNINGLERANDVPLG SNARESSIELKCHCLPWRSVERALUQUSVGQAVYTCK KCTYRDPLYBLTVRKHTYRHPQHVAAPYIAKAGEKSLANAVPLG SNARESSIELKCHCLPWRSVERALUQUSVGGAVYGCC KCTYRDPLKHTYRTVRHOPHVAAPYIAKAGEKSLANAVPLG SNARESSIELKCHCLPWRSVERALUQUSVGGAVYGCGSV GQMKILGIGGRAPVSIPQGSGVVGLLPSGGRSVGLSSGRSVALGSGRSV APARYSLGSANASSISSGGLKSPSISGGSARVLICGSSKRAAA ATGPPFGHTSSTQKWRICTICHCRIKPTRVSVVHFRERIKARKVP AVANYIMKINFTSKCLYCNRYLDTTJLINIMLIHGLIGCPYCRS TFROVEKNAAAMRAWVILIBERGCPTCTSTLOFLIQOGSHYNL LLUTTYNIRDAPASSVAYHAQNNPPVPPRPQPKVQEKADLPVKS SPQAAVPYKKDVCKTLCPLCTSILKGFISDALAHHLRRRGVGTON GQOKTNAPSRINGSPSLAPVKRTYBMFFFLKKKCVRDCEXYRGVU. LGFMKELNKVKHBMDPJABGLFRNIBERGRYCNSKCWASK"ADKKU. LGGDDSSSDSFRNLESSNSSGSPPDVPVRURKISNDNPERH VLKVIFEDASSSBERLDQKRDGSKYKTHILTEEPTCRKRCTWSDE SSGSEDARSSRPAAKKATMGGDRRGLKNRASSYGRVESPHSKN QSOKNABSBIRDELSRPQIERDFTTDSEDGRGPUNNTDGVAEP NIGGLGLETPFREIMISIGG*BPH*AA*QAVRESEKSIC*GSPSC NICHHVAGVULPARGSSHSAGPAQGAPR*TOTGSGTPKAAEGGGW EATTLGHQHMMPFJGRPLJMKGRIKKGCKG*VSDSVTGS RAVAGCAGAGGGREVAPARGGGRGGGGGAGASTOTRORGWGGLL NGKRGCCPESGYLFGFIVJGKIQSLERAVPLPVNGQTGERASRG NCZHIHVDAVC*SBHH*DHFIAAAFLENSTIIS*VAGSWQGIA VLKKUKSAVQRRYSTITSSIHVDTKIQGLHDWYNAGAGGVYGG EATTLGHQHMMPFJGRPLJMLGTUCSFFRANGGGCTHAGLFHIAGEFULGEPHTTSVSL FVLAQDGGGGGREVAPCRGGGRGGGGGAGASTTHADLFARGUDIA VLKKUKGAVCRGFBSYDTARAFRANGGRACKGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC				15
SLPILIYSLLEDGHUDDHVLQNEPTLYRDISSNRILSLIFTLYWT  HLGFGRAFT JEPPFGSYLLI GENTSLLANGLQMGGWMFGGTLVFTVW  VITVTV XMALE"HFWTWINHLVTWGS I IFYFWFSLFYGGILNPF  LGSQMNFYPF JGLJESGSAWFAI ILMVYTCLFLDI ITKKYFDRIH- HPTSTEKAQLIETINAGIK KLDSMCCFPEGACSWGRMLERVI  GRCSPTHISSRWABSDPFYTDMSSILTLSTMDSTG**  GRCSPTHISSRWABSDPFYTDMSSILTLSTMDSTG**  GRCSPTHISRSWABSDPFYTDMSSILTLSTMDSTG**  ASPRESGETMFGLFVNNLGSLEKRARVTVKLISDIGLKYCKBHIK  DPKQFFPBDFYLRVTTWBUOLGNPBLITTMDDVSTTCPFCCSACP  FSSKPFSAYKSHPRUVESDPFNRILINCYCYTFNADKKTLETH  IKIFHAPRAGASSSILSTKDNRKNDGLKERQLGVYCKPKHIK  KCTYRDPLYSLTVKKHI YRRHGUNAPPT JAKAGEKSLAKGAVPLG  SNAREBSSINCKGCLFMPKSTBALUQHVIEDHBRIGVYQVTAMIG  EHTWLVVPRSKELMIAPRYCPKKSMGLIPPGLAGGENSGLASGWV, SGLP  SQMWRILSIFKPNLHSTGVMMYSVHLQGNNGVKSVGGTSV  GQGMRIGGGRAPVGI FORGUKSMGLIPPGLAGGENSGLAGGRVASGLP  APARYSLQSAMASSILSGGLKSPSLSQSQASRVLQGSSKDAAA  ATGPPGGTTSSTJVKKICTI CINICHPENVYSVHFRERHREKEVP  AVANYIMKLINNPTSKCLLGURSTLDFDLTLQGGSHTNIH  LLVTTVILDAPABSVAFHAROMFPPP PERVORGABILVYKS  SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRRRHQVTQ  GQORTABPSRLNQSPSLAPVKRTYBOMFPPLLKKRRLDDGSDPS  SPPREKYBLEKLAASILWV\KKV,SDIASHFSNKKKCVRDCEKYKRGVI  LGFNMKELINVVKHEMDFJABGLFFNIDEKGSRVANSKCORDCEKYKRGVI  LGFNMKELINVVKHEMDFJABGLFFNIDEKGSRVANSKCORDCEKYKRGVI  LGFNMKELINVVKHEMDFJABGLFFNIDEKGSRVANSKCORDCEKYKRGVI  LGFNMKELINVVKHEMDFJABGLFFNIDEKGSRVANSKCORDCEKYKRGVI  LGFNMKELINVVKHEMDFJABGLFFNIDEKGSRVANSKCORDCEKYKRGVI  LGRODSSDSPFNLESSBFSNGSSPPDFURSKKSTIDEERGERJOKYMDFFNIDEKG  FULDULGVLUPVARGSSHSAGFGGGGGGGGGGOFTOTTMTGVARGFTRSDB  SQSGEDARSSKPAAKKKATMGGDRGLKWRNSSYGKVEGFWSKD  GGGRKRAGERGFRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1			
VITYTYMALETHMYMINHLYMGSIIFYPYBSLEPYGGILMPP   LGQNMYPVPIQLISGGSAPFAIILMVVTCLPIDIIKKVPDRHL   HPTSTEKAQLITETMAGIKCLOSMCCTPEGGSACASVGRMEERVI   GRCSPTHISGBWARSDPTTMINGSILTASTMSSTC    AVVRRAGREGGGALGAGATAVPPBERRRCCAPAPHAGPAR   ASKPSQETMPQLPVNNLGSLRKARKTVKKLISDIGLBYCKKHIK   DFKQFEPNDFYLRNTWBUNGLIRKARKTVKKLISDIGLBYCKKHIK   DFKQFEPNDFYLRNTWBUNGLIRKARGAFRAKTAKTHISDIGLBYCKKHIK   LKIFHAPNASAPSSISSTFKDNKNNDGLRKKAGDVFLKY   KCTYRDPLYLVRHITYRBEPQHUKANGPIGLBYCVTAMIG   HTNVVPBRSKEIMLIAN-HVDRIKSGHFROSLAGAVPLG    SNARESSIHCKRCLPMPKSYBRALVQHVIEDBERIGYQVTAMIG   HTNVVPBRSKEIMLIAN-HVDRIKSGHFROSLAGAVPLG    SNARESSIHCKRCLPMPKSYBRALVQHVIEDBERIGYQVTAMIG   HTNVVPBRSKEIMLIAN-HVDRIKSGNASKULGQSSKVLAGSSSKRAAA    ATGPPGRTSSTOWKKICTICRILPPRIOGLAGGRAY/NSIB-   SQCMVNRLSIPKPNLNSTGVNMMSSVHLQQNNYGVKSVGGGYSV    GQSMRLGLIGGBARVSIFQQLKSPBLSQSQASKULGQSSSKRAAA    ATGPPGRTSSTOWKKICTICRILPPRIVGSAGSSKULGQSSSKRAAA    ATGPPGRTSSTOWKKICTICRILPPRIVGSAGSSKULGQSSKRAAA    ATGPPGRTSSTOWKKICTICRILPPRIVGLAGGASTHLOGASSKRAAA    ATGPPGRTSSTOWKKICTICRILPPRIVGSQASKULGQSSKRAAA    ATGPPGRTSSTOWKKICTICRILPPRIVGSQASKULGQSSKRAAA    ATGPPGRTSSTOWKKICTICRILPPRIVGSQASKULGQSSKRAAA    ATGPPGRTSSTOWKKICTICRILPPRIVGSQASKULGQSSKRAAA    ATGPPGRTSSTOWKKICTICRILPPRIVGSQASKULGQSSKRAAA    ATGPPGRTSSTOWKKICTICRILPPRIVGSQASKULGQSSKRAAA    ATGPPGRTSSTOWKKICTICRILPPRIVGSQASKULGQSSKRAAA    ATGPPGRTSSTOWKKICTICRILPPRIVGSQASKULGQSSKRAAAA   ATGPPGRTSSTOWKKICTICRILPPRIVGSCAGAKHARASTICVAGA   CTVILPPRIKMINGSAGASPRIVGTAGKTACKACKAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1			
LGSQNMYPVPIQLISSGSAMPAI LIMVYTCLFADITIKKVPDRIIL HPSTEKADJETAMAGIKCLDSMCCPPEGBACASVGRMLERVI GRCSPTHISRSWSASDPYTNDRSILTLSTMDSSTC AGVGRAGARGGGGRALPAGATAVPPFSARRARGCAPEHAGPAR ASRPSGETMPQLPVNNIGSIRRARGTVKKLISDIGLBYCKSEHI DFKQYBPNDFYLRNTTMBDVGLMDPSIJTKNQDYRTKPPCCSACP FSSKPFSAVKSHPRNVBKSDPRNRILLOVCYTFMADAKKTLBTH IKIFHAPNASAPSSSLSTPKDKNKNDGLKPKQADSVEQAVYYCK KCTYRDPLYELTVRHIYTRBPUGLMOPSIJTKNQDYRTKPPCCSACP FSSKPFSAVKSHPRNVBKSDPRNRILLOVCYTFMADAKKTLBTH IKIFHAPNASAPSSSLSTPKDKNKNDGLKPKQADSVEQAVYYCK KCTYRDPLYELTVRHIYTRBPGGHAPAPYTAKAGERSLAGGAVYGK SOMWARISJTEVRHIMATGVANFSYTBALVQRIV EDBERIGYCYTAMIG HTMVVVPRSKPLMILAPKPQDKKSMGLPPRIGSLAGGAVYRIG SOMWARISJTEVRHIMATGVANFSYTBALVQRIV EDBERIGYCYTAMIG HTMVVPRSKPLMILAPKPQDKKSMGLPPRIGSLAGGAVYRIG SOMWARISJTEVRHIMATGVANFSYTBALVQRIV GQBRRIGLIGGRAPVSITPQGSGSVKQLLPSGNGKSYGLGSBQRSO APARYSLQSANASSLSSGQLKSPSLSQSARVLGQSSSKPAA ATGPPEGBTSSTQKMKICTICNBEPLOSPLOKGSSKVAGAS ATGPPEGBTSSTQKMKICTICNBEPLOSPLOKGSSKVAGA ATGPPEGBTSSTQKMKICTICNBEPLOSPLOKGSSKVAGA ATGPPEGBTSSTQKMKICTICNBEPLOSPLOKGSSKVAGASKVAG VANAYMKLIMPTSKCLYCNRVLPTDTLIMHILIBGLSCPYCRS TFRODVERMABHERNVLYDLCPSILKGFDLAHHILARRHQVIQ TVHPVEKKLTYKCHCLGVYTSMMTASTITHLVHCKGGVGKTQN GQDKTNAPSRINOSPELAPVKRTYRQHEPPLLKRKLDDDBISP SPFEREPEEPVULALDPLCPSILKGFDLAHHILARRHQVIQ TVHPVEKKLTYKCHCLGGVYTSMMTASTITHLVHCKGGVGKTQN GQDKTNAPSRINOSPELAPVKRTYRQHEPPLLKRKLDDDBISP SPFEREPEEPVULALDPLAGAFSHTATYT*\CQPY TRREIEKLAASLWV\MK\GDIASHFSMKCVRDCEKYKGGVL LGFMREINKVHEHMDPABGLFRHMSGRWARSKYGKPGFMSKI GGBDSSDSFBRLERSSNRSGSPPDPVEVERPRISMDNPERH VLKVIPDEDASESBEKLDQKBDGSKYFFTIHLTEPTKLMINASDS EVODDVVENKDGASPSEGGFGGQVSDFRDMTCEMKRGTKMINDSDABE SSGSEDARSSRPAAKKATMQCDRRQLKMNASSYGKVEGFMSKI GSGMTABSENDERLSNPGTBGHTUNGKKGKGKG*VSDDVTGS RAVAGGDARTHTPTAGGGGCLGARSVFTONGOTGERSSC NCCHIVUTAVC*SEHNAPGGGGCLGARSVFTIGSPGTHKABCGGWGM LUKGKULPVULARGSSRSVDTAPAGGARHABFSPGIQGEPTTTSVSL FVLAPQDGGGGVPFVEGQLVTVLUGUVPOGSTRITFPHHTQLFLAFUN AVTRGSAVQRSPCTTTSSTHVDTKLQGELDWAVAGADGVVQMG DPFVVGLAGIFPHLIDDFLHQIBLSFQRRV-EQCGCVKPDLGPUP REPRIGULQVGPLVRGGGRRVAGGGCLGRICHDLDFMRMGLSHHT				ILGPSHAFIPPPGSYLLIGKDTSLLGNGQMFGNWTFGTLVFTVM
HPTSTEKAJL/TETTAGIKCLOSMCCFPEGBAACASVGRMLERVI GRCSPTHISRSWSASDPYTNIDRSITIC AGVERAGARRGEGRATAVPPSARRERRCPAPEHAGPAR ASRPSGETMFOLDYNNIGSLERARRITYEKULSDIGLEVCKEHIE DFKQFENDFYLANTTHEDVGLIMDESILOSLOSKYCKEHIE IKIFHAPNASAPSSLSTPKDNKNNDGLKPKQADSVEQAVYYCK KCTYRDPLYELVRHUT YREHFQHVADPYIAKAGEKSLAGAVPLG SNAREBSSIHCKRCLFMPKSYBRALVQHVI DDIBERTOYQVTAMIG HTMVVPPRSKPIMLIAPROPDKEMBELPYIGLAGGRVYNSLG SQMWIRLSIPKPBLINSTGVINNASVHLQQDNYGSVGGGSYS GQMWIRLSIPKPBLINSTGVINNASVHLQQDNYGSVGGGSYS APARYSLGSARASSLSSGQLKSPSLSGSGASKVLGGSSGRAS ATGPPPGHTSSTJWKKICTICRELPPENVISVHPBKRHKALKAVP AVANYMKKHPTSKCLYCRFLIPTDTLIAHHILIBGLSCYCES TFANOVEWAALHERWATHDEBMGPKTDSTLSFDLTLQQSHTPIH LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQPKVGBKADIPVKS SPQAAVPKKUDVEKTLCFLCFSILKGFISDALAHHLARRHQVQ GQKTATAPSRINGSPSLAPVKRTVEGPLCKKRKLDDSDSP SPFRERPEEPPULALDPKSH\ADDSYBARKSHTKYTY\CQPYP TRREIKLAASLWV\WK\SDIASHFSNKKKCVRDCEKYKFGVL LGFNMGELNKVRHEMPFJARGJFRENDEKSKVNASK-NOKKLM LGGNDSSSDSFFNLEESSNRSGSPPPVPEVEWERKISNDMFERH VLKVIFBDASSBEKLDQKGGSKYFTITHEBPTKKMINNASDS KVDQDVVENKDGASPSBSGSPDSQVSDFRDTCERKFGTWSBS SSQSEDARSSISPAAKKATMQGDREQLKMNNSSYGKVEGFWSKD GOMKNASENDBELSNPQIEMMSTTSBGGGFTNSHD SSQSEDARSSRPAAKKATMQGDREQLKMNNSSYGKVEGFWSKD GOMKNASENDBELSNPQIEMMSTSTSBGGFTNSHD SSQSGARASSKPAAKKATMQGDREQLKMNNSSYGKVEGFWSKD GSGKRASSKPAAKKATMGGGRCLGAKSVARSVFTONDGFWGLI NGKRGGCFESGYLFGFTVTGKTGSLBAKVFLFWONGTGERASEG NCRIHLVDAVC+SEHIH-DHYLAAAFLENSTITSVAACSODJAG VLQKEVQASVRCRGFFSVDTAPAGPHAHSPPGLGEPTTTSVSL FVLAPQDGEGGVFVEGGLVTVLGLVUQGSTRRIFFHHTQGFLAFUN AVTRGSAVQRSPSTTTSSIHVDTKLQGURGSTHTCHTGLFAEN AVTRGSAVGRSFSTTTSSIHVDTKLQGURGTHTTGFLAFAU AVTRGSAVGRSFSTTTSSIHVDTKLQGURGTHTTGFLAFAU AVTRGSAVGRSFSTTTSSIHVDTKLQGURGTHTGFLAFAU AVTRGSAVGRSFSTTTSSIHVDTKLQGELDDWAAGAGGVPQHGL FVLARGGALGVGLAFFUNGGGRCLGAKVELDVHTHTQGFLAFAUN AVTRGSAVGRSFSTTTSSIHVDTKLQGELDDWAAGAGGVPQHGL DPFVVGLAGIFFHLIDDFLHGIELSFQRRV-EQCGVKPDSGPVP RERREILLQVGPDLWGGGRRVAGKGKCWRDLLFFNENGLSHHT				vitytykmale:"hfwtwinhlvtwgsiifyfyfslfyggilwpf
GRCSPTHIGRSWASDPYTYDRSJLTLSTMDSSTC  ASPRSQETMFQLPVWNLGSLTRARTVYKLLSDIGLEYCKEHLE DFKQFEPNDFYLKYTTWEDWGLMDDSLTKNQDYRTKPFCCSACP FSKFPESAVKSHFRVNJESDFRSTLLINCPYCTPRADAKKTLRTH DFKQFEPNDFYLKYTTWEDWGLMDDSLTKNQDYRTKPFCCSACP FSKFPESAVKSHFRVNJESDFRSTLLINCPYCTPRADAKKTLRTH IKIFHAPNASAPSSSLSTFKDKNKNDGLKPKQADSVEQAVYYCK KCTYRDPLYBLYDRKHITYBHRUGHVAPFILKAGEKSLNGAVPLG SNAREBSSTHCKCLYMPKSYBLAVUQHVIEDHERIGYVTAMTG HTMVVVPRSKFLMLLAPKPQDKKSMGLPPRIGSLASGNV\RSLD SQQMVRRLGILGGNAPVSIPQOKGSMGLPPRIGSLASGNV\RSLD SQQMVRRLGILGGNAPVSIPQOKGSMGLPPRIGSLASGNV\RSLD SQQMVRRLGILGGNAPVSIPQOKGSMGLPPRIGSLASGNV\RSLD APARYSLGSNANSSLSSGQLKSPSLSQSGSSKULQGSSSKPAAA ATGPPGBYTSSTQVKKICTICNLEPMVSWHPEKERIKABKVP AVANYINKTHNFTSKCLYCHRYLPTDTLLINHLHGLSCPYCRS TFNOVEKMAAHMRNVHLDEMGPRTDSTLSPDLTLQQSGHTNIH LLJTTINLRDAPABSVAYHAQNNPPVPPRPQPKVQBRADLPVKS SPQAAVPYKKDVGKTLCPLCPSILKGPISDALHHLARRHQVIQ TVEPVSKKLTYKKIRCLGVYTSMTSTTLHLUNKGSVGKTON GQDKTNAPSRLNQSPSLAPVKRTYBQMEFPLLKKRKLDDDSDS SFFEREFEEPVULALDPKGH\EDSYLARKKCVRDCKSVKKTON LGGEDDSSSDSFENLEBESNESGSPPDVPVPVBVERKLYKKYLT\LCPYT TREIEKLAASLWV\MK\SDIASHFSNKKKVCVRDCKYKFGVL LGFNMGELMKVKHRMDFJABGLFENIDEEKDSRVANSKTADKKLN LGGEDDSSSDSFENLEBESNESGSPPDVPVPVBVERKLYMRNEDS SQSGBARSSRFARKKATNTGGGREQKKWASSTGWGFBSND GSGSBARSSRFARKKATNTGGGREQKKWASSTGWGFBSND GSGSBARSSRFARKKATNTGGGREQKAWNSSTGWGFFBSND GSGSBARSSRFARKKATNTGGGREQKAWNSSTGWGFFBSND GNGNGASENDBRLSNPOIEMONSTIDSEDGSPDNTCMKRFGTWSDR SQSGBARSSRFARKKATNTGGGREQKAWNSSTGWGFFBSND HULGGLUDVARAGSNGARVRATGGTGRASEG NCHHUDVAV*SREHP+PHTALAAGLENSTIIS*ARGSNGDTWGMGLL NGKRGCCFESGYLGGFYVIGKIQSLEAKVPLPWGGTGBRASEG NCHHUDVAV*SREHP+PHTALAAGLENSTIIS*ARGSNGDTWGMGLL NGKRGCCFESGYLGGFYVIGKIQSLEAKVPLPWGGTGBRASEG NCHHUDVAV*SREHP+PHTALAAGLENSTIIS*ARGSNGDTWGAL VLQKEVQASVRCRGFESVDTAPAGPWAHSPPGLQGEPTTTSVSL FVLAPQDEGGVFYVGGGVFVPGGGCKKGKGTKVARGUSHTLUPARGUPHA AVTRGSAVGREPSTTISSIHVDTKIQQGELBDWTWAGADGVVGG DPFVVGLAGIFEHLIDDPJHOIELSFQRXV*EQCGVVPDSQQPVP	İ			LGSQNMYFVFIQLLSSGSANFAIILMVVTCLFLDIIKKVFDRHL
AGVRRAGARRGGRALÞAGATAVFPFSARRRRCFAPEHAGPAR ASRPSGETMFQLPVINLIGSBURRARKTVKILLDIGLEYCKEHLE DFKQFSPINFYLMYTTMEDUGLIDDESLITKINQDYSTKFCKEHLE DFKQFSPINFYLMYTTMEDUGLIDDESLITKINQDYSTKFCKEHLE DFKQFSPAKSHFRNVHSEDFRIR ILLINCPYCTFNADKKTLÆTH IKIFHAPNASAPSSLSTFKOKNKIDGLKPKQADSVEQAVYCK KCTYRDPLYELVRKHIVRBHFQHVARAPYTAKAGEKSLINGAVPLIG SNARESSSTHCKRCLFMFKSYBALVQHVLEDHBRIGYQVTAMIG HTWVVVPBSKFMLLAFRPQDKKSMGLPPRIGSLASGNVASLD SQMVNRLSIPKPNLINSTGVNMMSSVHLQQNNYGVKSVGGGYSV GQSMRLGLGGRAPVSIPQQGSGVKQLLPSGRARSYGLGSBQRSQ APARYSLQSANASSLSSGQLKSPSLQSQASKULGQSSKPAAA ATGFPPGNTSSTQKMKICTI CINKLFPRNVSVMFKKRIKABKVP AVANYIMKINHFTSKCLYCNRYLPTDTLLINHMLIGLSCPYCRS TYRDVEKMAAHMRWHLDEBMGFKTDSTLSFDLATLQQSSHTNIH LLUTTTINLDAPASSVAYHAQNBPPVP FREDRVQSKRADLPVKS SPOAMPYKKDUGKTLCPLCTS LIKGFISDALAHHLBRRIGVIQ TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTMAPSRLNQSPSLAPVKRTYBQMEPPLKKRKLDDDSDSP SFFEREPEPEVVALADPKGH; HODSVEARKKSFLYKTVT\QXPYP TRREIEKLAASIMV\WK\SDIASHFSNKKKCVMCCKKYKGUL LGFNKEKLAASIMV\WK\SDIASHFSNKKKCVMCCKKYKGUL LGFNKEKLAASIMV\WK\SDIASHFSNKKKKCVMCCKKYKGUL LGFNKEKLAASIMV\WK\SDIASHFSNKKKKCVMCCKKYKGUL LGFNKEKLAASIMV\WK\SDIASHFSNKKKKCVMCCKKYKGUL KKVIPEDASSSBERLDQKRGGSKYRTIHITEPTKLMHNASIS EVODDVURHKOGJAPSESGERGGQVSDPEDMTCEMKFGTMSDS SQSEDARSSKPARKKATMQGDRRQLKMKNSSYGKVEGFMSKD GSQKRABSENDERLSNPQIEMONSTIDSEDGGFUNNTDGVAEP MKSLLAGVKLSSOG AVAGEQASGRRTVFTAGGGRCLGAKSVRASVFTONQFGWGLIL NGKRGGCFBSGYLGFFIVIGKTGGKKGKGVSDVTOG RAVAGEQASGRRTVFTAGGGRCLGAKSVRASVFTONQFGWGLIL NGKRGGCFBSGYLGFFIVIGKTGGKKGKGVSDSVTOG RAVAGEQASGRRTVFTAGGGRCLGAKSVRASVFTONQFGWGLIL NGKRGGCFBSGYLGFFIVIGKTGGKEGSTYLAPGFSRQUHA VLQKKVQASVRCRGFBSVDTAPAGFMAHSPPALGGGETTTSVSL FVLAPQDEGGVPFVVEQUVTULGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFIHLLTLVCSSFMYNYGG*GKRGGFTTTSVSL FVLAPQDEGGVPFVVEQUVTULGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFIHLLTLVCSSFMYNYGG*GKRGGFTLHQLFASVN AVTRGSAVGRRPSTTISSIHVDTKLQGRLKGKGGKTGKGRDGLSHT	1			_
ASRPSQBTMPQLPVNNLGSLRKARKTVXKLLSDIGLBYCKEHIE DFRQFBSNDFYLKNTTMEDUSLMDDSLTKNDQDXTKFDFCCSACP FSSKFPSAVKSHFRWNGSLDWSGLLUDPSLTKNDQDXTKKFDCCSACP FSSKFPSAVKSHFRWNGSLDWSGLLUDPSLTKRKDRKKTLRTH IKLFHAPNASAPSSSLSTFKOKNNNDGLKPKQADSVEQAVYYCK KCTYRDDLVELTVRKHIY YREHFQHVAAPYLAKAGEKSLNGAVPLG SNAREBSS IHCKRCLFMPKSYBALVQDVICHDERIGYQVTAMIG HTMVVVPRSKFLMLLAPRPQDKKSMGLPPRIGSLASGNV (RSLP SQMVMRLSIPKPHLNSTGVMMSSLUQQNSYGVLSGGSYSV GQSMRLGLGSNAPVSIPQQGSVKQLLPSGNGRSYGLSSBQRSQ APARYSLQSANASLSSGQLKSPSLSQQASKVLQGSSKPAAA ATGPPGBNTSSTQKKKLCTICNLFPBNVYSVHPEKBHKABKVP AVANYIMKTHNFTSKCLYCNRYLPTDTLIMHLHGLSCPYCRS TFROVERMAAHMRWVHIDERMGPKTGSTLSFDDLTQGSHTNIH LLVTTYNLRDAPABSVAYHAQNNPPVP PKPQPKVQEKADLPVKS SPQAAVPYKKDUGKTLCPLCPSILKGP ISDALAHHLRERHQVIQ TVEPVSKKLTYKKIHCLGVYTSSMTSTTLHLHVRGVGKTON GQDKTMAPSRLNQSPSLAPVKRTYBGMEPPLLKKRKLDDDSDSP SPFEEKPEPVVLALDPKGH\EDDSYBARKSFLTKKYFT\KQPVF TRRIIEKLAASLMV\WK\SDIASHFSNKKKKCVRDCCKYKRGVI LGFNMELINKVGHRNDPABGLFENIDBERGVRASKTARKLN LGKEDDSSSDSFENLESSNNSGSPDPVPVEVERKISNDMFERK VLKVIPBDASESERKLDQKEDGSKYFTTHILTEEPTKLMHNASDS EVDQDUVVERNGGASPBSESPDPVPVEVERKISNDMFERK VLKVIPBDASESERKLDQKEDGSKYFTTHILTEEPTKLMHNASDS EVDQDUVVERNGGASPBSEGFGSQVSDFENDTCSMKPGTWSDR SSQSEDARSSNRAAKKRATNGGGRRQLKNWRSSTGVVGFGWSN QSOKNASENDBRILSNPQIEMONSTIDSEDGBQFDNMTDGVAEP MHGSLAGVKLSSQQA  6009 4272 1534 CHGLQILLTPFRELNISLGG*BPH*NA*QAVRSEEKSIC*GSPSC HLVLGULUDVARQSSBRAGFDQSAFF*TOTTGSTPKAAEGSGW EATYLLGHDWMMPFJQRPDLWMGRGKEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGBCLGAKSVRASVFTGNQPGVMGLL NGKRGCCFRSGYLEGFTVICKIQSLBAVRYLPWGGTGBRASEG NCHHLVDAVC*SEHR+PHILAARJENSTIIS*VARGSGOWSDFDG NCHGLDAVCHUDVAVSKHHPH-PHILAARJENSTIIS*VARGSGOW EATYLLGHDWMMPFJQRPDLWMGGAGKEKGVSDSVTGG NVARGSAVGREPSTTISSIHVDTKLQQGLHDWMAGADGVVONG DPFVVGLAGIFHLIDDPJHQIKLSFQRV*BQQQGVKPDSQDVVG PVVGLAGIFHLILDDPJHQIKLSFQRV*BQQQGVKPDSQDVVG DPFVVGLAGIFHLILDDPJHQIKLSFQRV*BQQQGVKPDSQDVP RPLRVGLLQVGGIGRAVAGGGKRCARGLISHTVHTQCLSHVR			1	! ·
DPKQPEPNDPYLENTTHEDVGLMDPSLTKNQDYRTKPPCCSACP PSKFPSAYKSHFRNVHSEDPRIRLILNCPYCTFNADKKTLETH IKLFHAPNASAPSSLSTFYKNKNKDGLKPKQADSVEQAVYYCK KCTYRDPLVELTVRKHLYRBHFQHVAAPYLAKAGEKSLINGAVPLG SNAREBSIHCKRCLPMPKSYEALQMIVLEDHERLGYQVTAMIG ENTWVVPRSKFLMLTAPKPQDKKSMGLPPRIGSLASGNVARSLP SQMVIRLSIPRPILLAPKPQDKKSMGLPPRIGSLASGNVARSLP SQMVIRLSIPRPILLAPKPQDKKSMGLPPRIGSLASGNVARSLP SQMVIRLSIPRPILLAPKPQDKKSMGLPPRIGSLASGNVARSLP SQMVIRLSIPRPILLAPKPQDKKSMGLPPRIGSLASGNVARSLP SQMVIRLSIPRPILLAPKPQDKVGLLPSCHGRISYGLSSDRSQ APARYSLQSANASSLSSGQLKSPSLSQSQASRVLQQSSSKPAAA ATGPPPGINTSSTQKMKLCTICNELPBRIVSVAVHERGHKABKVP AVANYIMKT:HNFTSKCLYCHNYLPDTTLLHIML.HGLSCPYCRS TPRIVERMAHPRINVILDEBMGPKTDSTLSFDLTLQQGSHTNTH LLUTTYNLRDAPAESVAYHAQNNPPVPKPQPKVQBKADLPVKS SPQAAVPYKXDUGKTLCPLCYSILKGPISDALAHHLRERRQVIQ TVIPVERKKLTYKCIHCLGYYTSIMTASTITHLUHCKGVGKTON GQDKTNAPSRLNOSPSLAPVKRTYRGMFPPLKKRKLDDDSDS SFFREIRCBEPUVLALDPKSHIKDDFDAEHTKKYTTIKQPYP TRREIRKLAASLWVJKK,SDLASHESSRKCVRDCEKXPGVL LGKEDDSSDSPENLBESSNRSGSPPDPVPEVBRKINNASDS FVDQDDVUSKNGASPSSEGSGVQSSPFENTERKRCVRDCEKXPGVL LGKEDDSSDSPENLBESSNRSGSPPDPVPEVBRKINNASDS FVDQDDVVBKNGASPSSEGSGVQSSFFENTERKRCVRDCEKXPGVL LGKEDDSSDSPENLBESSNRSGSPPDPVPEVBRKINNASDS SQSGDARSSKPAAKKATMQGDRSQLKWKNSSYGKVEGFWSKD QSQKRABERDDRLSINPQIEMQNSTIDSEDGEPINNTTGVAEP WIKSLAGVKLSSQQA CHGLQHLTPPRELNISLQS*BPH*AA*QAVRSEEKSIC*GSPSC HLVIGVLVPVRQSSHRSGPAQASP*TGTGSGTPKAAEQSGYW PHESLAGVKLSSQQA CHGLQHLTPPRELNISLQS*BPH*AA*QAVRSEEKSIC*GSPSC HLVIGVLVPVRQSSHRSGPAQASP*TGTGGTPKAAEQSGYW PKSLAGVKLSSQQA CHGLQHLTPPRELNISLQS*BPH*AA*QAVRSEEKSIC*GSPSC HLVIGVLVPVRQSSHRSPFTISSTIDKNSTIIS*VAPGSWQDHA VLQKKVQASVGCRGFESVDTAPAGGMRCKGMCVGDLGEPTTTSVSL FVLAPQDGBGVPVPCGQLEVTUGLQVVQSIRTPTFWHTQLFLHP LYLKQALGVPLAGGRRVAGFRCYTHRQGCRERASGG NCSHTVDAVC*SBHH*DHFLIAAAFLENSTIIS*VAPGSWQDHA VLQKKVQASVGCRGFESVDTAPAGGRKCHGNLDLFPRRWGLSHRT AVTRGSAVQRRPSTTISSTHVDTKIQQELBUWWAGADGVVQMG DPFVVGLAGIPHLILDDPLHQTILCQCKVPQCQCQVXPDSQPVP RPLRVGLAGIPHLILDDPLHQTILCGCRCWCDLLFPRRWGLSHRT	6008	4554	1089	
FSSKPPSANKSHERNVHSEDPRILLINCPYCTPNADKRTLETH  IKTHAPNASAPSSLSTPKDRINDGLKPKQADSVEQAVYYCK  KCTYRDPLYETURKHI YREHPQHVASPYIAKAGEKSLINGAVPLG  SINARERS THCKRCLFMPKSYRALUQHYLEDHRELGYQVTAMIG  ETNVVVPRSKETMLLAPKPQDKKSMGLPPRIGSLASGNV\RSLP  SQMVIRLSIPRPILMSTGVMMSSVHLQQNIYGVKSVGGGTSV  GQSMRILSIGGNAPVSIPQOSQSVKQLLPSGMGRSYGLGSBQRSQ  APARYSLQSANASSLSSGQLKSPSLSQSQSRVLGQSSSKPAAA  ATGPPBGNTSSTQKMKICTICNKLPPRIVYSVHPRKEHKABKVP  AVANYIMKINFTSKCLYCNRYLPPDTLLINIMLHGLSCPYCRS  TFINDVERMAAHPRINVHIDEBMCPKTDGTLSFDXTLQQGSHTNIH  LLITTINLRDAPASSVAHAQNNPPVPPKQPKVQEKADIPVKS  SPQAAVPYKKDVGKTLCPLCTSILKGFISDALAHHLRERRQVTQ  TVHPVVEKKLTYKCHICLGVYTSMTASTITLHLVHCKGVGKTQN  GQDKTNAPSRLNOSPSLAPVKRTYBQMEFPLLKKRILDDDSDS  SPFERPEREPVULALDPKSH\RDDSYSARKSFLTKYFT\KQPYF  TRREIBKLAASLWV\WK\SQLSHSMRKKTKYCHCKCKYKYGN  LGFNMKELNKVKHENDFDABGLFRHDEKDSRVNASKTADKKLN  LGKDDSSSDSFENLESSNISGSPFPDVVFEVRRKISINDPEEK  VLKVIPEDASSESREKLDQKRGSVKYTHTHETEFTKLMINNASDS  EVDQDDVVENKDGASPSESRLDQKRGSVKYTHTHETEFTKLMINNASDS  SSGSBARSSKPAAKKKATMGGDRGQLKMKNSSYGKVEGFWSK  GSOKKAASKNDRAKLSNOQIEMONSTIDSEDGEQFUNNTDGVAEP  NHGSLAGVKLSSQQA  6009  4272  1534  CHGLQHLTPFREINLSLQS*BEH*AA*QAVRSEEKSIC*GSPSC  HLVLGULVPVARGSSHSAGPAGAFR*TGTSSGFPKAAEQSGW  EAYTLGHQHMMPFIQRPLVMKGRRIMCGKCKG*VSDSVTGG  RAVAGRQASQRRTVFTAGGGBCLGAKSVRASVFTGNQFGYMGLL  NGKRGCFRSGYLFGFFIVIGKIDSLARVPLPWGGGGRABGS  NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA  VLQKKVQASVRCRGFESVDTAPAGGBRLGAKSVRASVFTGNQFGYMGLL  FVLAPQDGEGVPFVEGQUFVULGURPHTQGGERASU  AVTRGSAVQRRPSTITISSIHVDTKIQQELHDVWAGADGVVQMG  DPFVVGLAGIPHLLIDDPLHQIELSFQRRV*GCQCYKPDSQPVP  RPLRVGLLQVPLVBGGGRRAGGKKCWBOLLFPWRWGLSHRT		. ,		
IKTEHAPNASAPSSSLSTERDKNKNDLKERKQADSVEQAVYYCK KCTYRDPLYEIVRKHIYREHFGYNARFITAKAGEKSLINGAVPLG SNAREBSSINCKRCLFMPKSYPALVQRVI EDHERIGYQVTAMIG HTWVVPRSKPLMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLD SQMVNRLSIPKPNLNSTGVNMMSSVHLQQNNYGVKSVGGYSV GQMRIGLGGNAPVSIPQQGSVKQLLPSGNGRSYGLGSEQRSQ APARYSLQSANASSLSSGQLKSPSLSQSQASRVLGSSSKPAAA ATGPPGNTSSTQKWLICTICNKLPPBNVSVHPKREHKABKVP AVANYIMKHNFTSKCLYCNRYLPTDTLLNHMLHGLSCPYCRS TFROVERMAHMENVHIDEEMGPKTDSTLSFDLTLQQGSHTNIH LLVTTNIRDAPBSVAVHAQNNPPVP PKPQPKVOEKADIPVKS SPQAAVPYKKDVGKTLCPLCPSILKGP ISDALAHHLRERHQVIQ TVHPVERKLTYKCHELGGVYTSMMTASTITLHLVHCRGVGKTQN GQDKTNAPSRIANGSPLAPVKRTYEGMEFPLLKKRKLDDBSDSP SPFEERPEEPVLALDPKGH\EDDSYEARKSPLTKYFT\KQPYP TRREIEKLASLINV\WK\SDIASHSNKKKCVRDCEKYKRGVL LGRMGKLINVKHEMDFJABGLFRINDEKDSRVNASK*LADKKLN LGKEDDSSSDSPENLERSSNRSGSPDPVPVEVERRISNNDPERH VLKVIPEDASESERKLDQKEDGSKYFTIHLTEEPTKLMINASDS EVQQDDVVEKKDGASPSSEGPSQQVSDFEDNTCENKPGTWSDE SQSEDARSSKPAAKKATMQGDRGLKMNASYGKVEGFWSKD QSQKNASENDERLSNPQIEMQNSTIDSEDGBGPDNMTDGVAEP MHGSLAGVKLSSQA  6009 4272 1534 CHGIGHITPFREINLSLQG*BPH*AA*QAVREBEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EATTLCHQHWMPFIQRPLVMKGRRIMGKKKKG*VSDSVTOG RAVAGEQASGRTVFFTAGGGGCLGARSVRASVFTCNOPGVMGLL NGKRGGCFRSGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPC NCEIHTVDAVC*SEHH*DHFLAAFLENSTIIS*VAPGSWQHA VLQKEVQASVRCRGFESVDTAPAGFWAHSSPGIQGEPTTTSVSL FVLAPQDGBGVPFVEGGLVTVLGLVVPQSTRHTFVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSENVANG*KRKGTHFQLFARVN AVTRGSAVQRRPSITISSHVDTKLQQEHDVMVAGADGVVQMG DPFVVGLAGIFHLIDDPLHOIRISFGRRV*EQCGVKPDSQPVP RPLRVGLLQUFUNGGGFINTESFQRRV*EQCGGVKPDSQPVP RPLRVGLLQUFUNGGGFINTESFQRRV*EQCGGVKPDSQPVP RPLRVGLLQUFUNGGGFINTESFQRRV*EQCGGVKPDSQPVP RPLRVGLLQUFUNGGGFINTESFQRRV*EQCGGVKPDSQPVP RPLRVGLLQUFUNGGGFINTESFQRRV*EQCGGVKPDSQPVP RPLRVGLLQUFUNGGGFINTESFQRRV*EQCGGVKPDSGPVP	l	·		1
KCTYRDPLYETURKHIYRBHPQHVARPYTAKAGEKSLNGAVPLG SNAREBSSTHCKKCLPMPKSYRALUQHVIEDHERIQYUTAHIG HTMVVVPRSKPLMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLP SQMVRLSTPKPNLMSTGYMPMSSVHLQQMNYGVKSVGGGYSV GQSMRLGLGGNAPVSTPQGGSVKQLLPSGHGSGYGSGGYSQ APARYSLGSANASSLSSGJLKSPSLSQSQASRVLGGSSGYBAA ATGPPONTSSTQKWKICTICNKLPPBNVYSVHFRKEHKABKVP AVANYIMKINNFTSKCLYCNRYLPTDTLLNHHLIHGLSCPYCRS TFMOVEMAAHMENVHIDEMGPKTDSTLSFDLTLQQGSHTNIH LLVTTYNLRDAPABSVAYHAQNMPPVPPROPKVDEKADLPVKS SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLEREHQVIQ TVHEVEKKLTYKCHCLGYVTSMMTASTITLHHVHCRGVGKTQN GQDKTNAPSRLNGSPSLAPVKRTYBQMEPPLLKKRKLDDDSDSP SFFEKPEBPVLALLDPKGH\EDDSYBARKSPLTKYFT\KQPYP TRREIKLAASLAV\WK\SDIASHFSNKKKCVNDCEKKRCGVL LGFMMKELNKVHEMDPJABGLVENHIDEKDSRVNASKTADKKLN LGKEDDSSDSFENLESSNHSGSPPDPVFVEVRFKISNDNPEH VLKVIPEDASESSEKLDQKEDGSKYFTIHHTBEPTKLMINASDS EVDQDDVVENKOGASPSESGPGGQVGFBDMTCRKFCTWSDB SQSEDARSSKPAAKKKATWQCDREQLKWNNSSYGKVEGFWSKD QSOWKNASKBDRELSNPQIEMONSTIDSEDGROFDNMTDGVAEP MHGSLAGVKLSSOQA CHGLGHILTPFREINLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVUGULVPVARGSSRIAGFAGSAFR*TGTGSGTFRAARQSGWW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGARSVRASVFTCNQPGVMGLL NGKRGGCFBSGTLGFITVGTGJSLAVRDPNGTGFRASEG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKKVQASVRCRGFBSVDTARGFWARSPERASEG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKKVQASVRCRGFBSVDTARGFWARSPERASEG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKKVQASVRCRGFBSVDTARGFWARSPERASEG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKKVQASVRCRGFBSVDTARGFWARSPERASEG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKKVQASVRCRGFBSVDTARGFWARSPFVAHSPEGLQCEPTTTSVSL FVLAPQDGSGVAPVSVEGGLVILVLOVQDSIRHFFVHHTOLFFLHP  I*KLGALDVAPLHLLTLVCSSPNVAYG*GKNGGTTLHQLPAEVN AVTRGSAVQRRPSITISSHVDTKLQQGLHDVMVAGADGVVQNG BDFVVGLAGIFHLIDDPLHOIELSFQRRV*EQCQGVKDPSQPPP RPLRVGLLQVGFLUVKGGGRRVAGGGRCRAGGLTLHQLFAEVN	ł			
HTNVVPRSKPLMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLP SQMVNRLSIPKRNLNTGVMMSSVHLQQNSVGVSGTSV GQSMRLGLGGRAPVSIPQSGSVKQLLPSGNGSVGLGSEQRSQ APARYSLQSANASSLSSGQLKSPSLSQSQASKVLGQSSSKPAAA ATGPPBONTSSTQKMKICTICNKLPPBRVYSVHPBKEHKABKVP AVANYIMKINFTSKCLYKRYLPDTULINHALIBLSCPYCRS TFNDVEKMAAHMRNVHIDEBMGPKTDSTLSPDLTLQQGSHTNIH LLVTTYNLRDAPABSVAYHAQNINPPVPPRQPKVQEKADLPVKS SPQAAVPYKKVOWEKTLCPLCPSILKGPISDALAHHLRRHQVIQ TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVRRTYSQMEPPLLKKRKLDDDSDSP SFPREKEEBEVVLALDPKS,BDOSYEARKSPITKYFYTKQDYF TRREIEKLAASLWVWK\SDIASHFSNKRKCVRDCEKYKPGVL LGFNMKELNKVKHEMDFJABGLFRHDEKOSRVANSKCADKKUN LGKEDGSSDSFFINLEESSNESGSPPDPVPVENRFISINDNPEH VLKVIPEDASESEBKLDQKEDGSKYFTIHLTEEPTKLMHNASDS EVVQDDVVENKDGASPSESGPSGQVSDFEDNTCEMKPGTWSDR SSQSEDARSSRPAAKKRATMGGDRRQLKWKNSSYGKVEEFWSKD QSGWKNASENDERLSNPGJENQOSDREQLKWNSSYGKVEEFWSKD QSGWKNASENDERLSNPGJENQOSDRFTNTESEDGEGFDNMTDGVAEP MHGSLAGVKLSSQQA  6009 4272 1534 CHGLQHLTPFREINLSLQG*REPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGFRAQSAFR*TGTGSGTFKAABQSGYW EATTLEHQHNNMFPIQRPPLVMKGRRIMGKCKKS*VSDSVTGG RAVAGEQASQRRTVFTAGGGELGAKSVRASVFTGNOPGVMGLL NGKRGGCFESGYLFGFTVIGKIQSLEAKVPLPVNAQTGERASEG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFBSVDTAPAGFWAHSPPCLGGEPTTTSVSL FVLAPQDGSGVPYVEGGLYTGLGVVTGLGVPQSIRTFVHHFTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQREPSTTISSIHDDTKLQGELHDVMVAGADGVVQNG DPFVVGLAGITHLIDDPLHQIELSFQRRV*ECGCGVKVPDSQFVP RPLNVGLLQVGPDVRGGGGRRVAGGGKCWRDLLFPNRWGLSHRT	Ì			
SQMVNRLSIPKPNLNSTGVNMMSSVHLQQNNYGVKSVGGYSV GQSMRLGLGGNAPVSIPQQSGVKQLLPSGNRSVGLGSEQRSQ APARYSLGSANASSLSSGQLKSPSLSQSGASRVLGGSSKPAAA ATGPPPGNTSSTQKWKICTICNELFPRNVYSVHFEKEHKAEKVP AVANYIMKINFTSKCLYCNRYLPTDTLLINIHLLIGLSCPYCRS TFNDVERMAAHMRAVHIDERMGPKTDSTLSPDLTLQGSHTNIH LLJTTYNLRDAPAESVAYHAQNNPPVPP KPQPKVQEKADLFVKS SPQAAVPYKKDVGKTLCFLCTSILKGPISDALAHHLRERHQVIQ TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTNAPSRINGSPSLAPVARTYBQMEPFLLKKRKLDDDSDSP SPFEERBEEPVVLALDFKGH\EDDSYEARKSFLITKYFT\KQPYP TRREIEKLAASLWV\WK\SDLASHFSNRCKKCVRDCEKYKPGVL LGFNMKELNKVKHEMDFJAEGLFRNHDEKDGRVNASKCTADKKLN LGKEDDSSSDSFENLEBSSNESGSPPDPVPEVBFKISNDNPEEH VLKVIPBDASESBEKLDQKEDGSKYRTHHLTEEPTKLMHINASDS EVDQDDVVERWGGAJPSESGFGSQQVSDFEDNTCENKFGTWSDS SQSEDARSKPAAKKRATMGGDRRQLKWKNSSYGKVEGFWSKD QSOWKNASENDBERLSNPQIEMQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA  6009 4272 1534 CHGLQHLTPFRELNISLQG*BPH*AA*QAVRSEEKSIC*GGFSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EATTLCHQHHMMPFJQRPPLVMKGRASVYFTGNPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCEHHVUDAVC*SSHH*DHFLAAAFLENSTIIS*VAPCSWODHA VLQKEVQASVRCRGFBSVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGBGVPSVEGGUVTVLGLVVPQSIRRTFVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSPNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRPSITISSIHVDTKLQQELHDVMVAGADGVVQMG DPFFVGLAGJTHLJDDPLHQIELSFQRRV*BCCQGSVKPDSQFVP RPLKVGLLQVGPLVRGGGRRVAGRGKCWRDLLFPNRWGLSHRT			-	SNAREBSSIHCKRCLFMPKSYRALVQHVIEDHERIGYQVTAMIG
GQSMRLGLGGNAPVSIPQQSQSVKQLLPSGNGRSYGLGSEQRSQ APARYSLQSANASISSGQLKSPSLSQGQSKVLGQSSSKPAAA ATGPPPGNTSSTQKKLCTICNKLPPRNVYSVHPKEKEKEABKVP AVANYIMKINFTSKCLYCNRYLPTDTLLNHMLHGLSCPYCRS TFNDVEKMAAHMRNVHIDEBMGPKTDSTLFDLTLQQGSHTNIH LLVTTYNLRDAPABSVAYHAQNNPPVPPKPQPKVQBKADIPVKS SPQAAVPYKKDVGKTLCPLCPSILKGFISDALAHHLRRRHQVIQ TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP SPFBEKEEPVVLALDPKGH\EDGSYEARKSFLKYFT\KQPVP TRREIEKLAASLWVWK\SDIASHFSNKRKCVRDCEKYKPGVL LGRNMKBLNKVKHENDFDABGLFENHEDKDSRVAASK"ADKKLN LGKEDDSSSDSFENLEBSSNRSGSPFDPVFPVERKISNDNPEEH VLKUIPBDASESBERLDQKEGGSKYFTIHLTEBFTKLMHINASDS EVDQDDVVEWKDGASPSESGPGQQVSDFEDNTCEMKPGTWSDE SSQSEDARSSRPAAKKKATMQGBRRQLKWXNSSYGKVEGFMSKD QSQKXNASENDBRLSNPQIEMQNSTIDSEDGBQFDNMTDGVAEP MHGSLAGVKLSSQQA HLVLGVLVPVARQSSHSAGPAGSAFF*TGTGSGTPKAAEQSGYW EAYTLGHQHWMPPIQRPPLVMKGRRIMCGKCRKG*VSDSVTGG RAVAGEQASQRRTVFTRAGGGCLGAKSVRSVFTGNOPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLBAKVPLPVWGGTGBRASPG NCEIHIVDAVC*SBHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKKVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPDDGBGVPFVGGLVTVLGLVVPQSIRHTVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSRNAYG*GKNGGTTLHQLFASVN AVTRGSAVQRRSPSTIISSIHVTKLQQELHDVMVAGADOVVQMG DPFVVGLAGIFHLDDPLHQIELSFQRV*EQCGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKKCWRDLLFPRWRGLSHRT	•	•		HTNVVVPRSKPLMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLP
APARYSLQSANASLSSQLKSPSLSQSQASRVLCQSSSKPAAA ATGPPPGMTSSTQKMKICTI CONKLPPRMYYSVHFKKEHKABKUP AVANYIMKINHTESKCLYCNRYLPPTDTLINHMLIGUSCPYCRS TFNDVEKMAAHMRNVHIDEBMGPKTDSTLSFDLTLQQGSHTNIH LLUTTYMIRDAPAESVAYHAQNNPPVPPRQPRVQBKADIPVKS SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ TVHPVERKLITYKCIHCLGVYTSMMTASTITLHLUHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEPPLLKKRKLDDGSDSP SFFREKPEEPVULALDPKGH; EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFNMKBLNKVKHEMDFJABGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEESSNEGSSFDPUVEVERKISNDNPEEH VLKVIPEDASESBEKLDQKRDGSKYBTIHLTEEPTKLMHNASDS EVQDDVVENKDGASPSEGGFGQVSDFEDNTCENKPGTWSDB SSQSEDARSSRPAAKKATMQGDREQLKWKNSSYGKVEGFNSKD QSQWKNASENDERLSNPQIEMQNSTIDSEDGRQFDNNTDGVAEP MHGSLAGVKLSSOQA  6009 4272 1534 CHGLQHLTPFRELNLSLQG*BPH*AA*QAVRSEEKSIC*GSPSC HLVUGVLVPVARQSSHSAGFAQSAFR*TOTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCKG*VSDSVTGG RAVAGEQASQRRTVPTAGGGGCLGAKSVRASVFTGNQPGVMGLL NGKRGCFESGYLFGFIVIGKIQSLBAKVPLPVNGQTGERASPG NCRIHIUDAVC*SEHH*DHH*LAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGGGVFPVEGQLVTVLGLVVPQSIRHTPVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFABVN AVTRGSAVQRRPSITISSIHVDTKIQGLEHDWWAGAADGVVQNG DPFVVGLAGJIFHLLTUTKIQGLEHDWWAGAADGVVQNG DPFVGLAGJIFHLUTDTKIQGLEHDWWAGAADGVVQNG DPFVGLAGJIFHLUTDTKIQGLEHDWWAGAADGVVQNG DPFVGLAGJIFHLUTDTKIQGLEHDWWAGAADGVVQNG DPFVGLAGJIFHLUTDTKIQGLEHDWWAGAADGVVQNG DPFVGLAGJIFHLUTDTKIQGLEHDWWAGAADGVVQNG DPFVGLAGJIFHLUTDTKIQGLEHDWWAGAADGVVQNG DPFVGLAGJIFHLUTDTKIQGLEHDWWAGAADGVVQNG DPFVGLAGJIFHLUTDTKIQGLEHDWWAGAADGVVQNG DPFVGLAGJIFHLUTDTKIQGLEHDWWAGAADGVVQNG DPFVGLAGJIFHLUTDTKIQGLEHDWWAGAADGVVQNG DPFVGLAGJIFHLUTDTKIQGLEHDWWAGAADGVVQNG DPFVGLAGJIFHLIDDFLHQIELSFQRRV*EQCQGVKPDSGPVP	1			100
ATGPPPGNTSSTQKWKICTICNRIPPENVYSVHFREHKAEKVP AVANYINKIHNFTSKCIYCRRYLPTDTILINHMILHGISCPYCRS TFROVEKMAAHMRWHIDEMGPKTDSTISFDLTLQQGSHTNIH LLUTTYMLRDAPAESVAYHAQNNPPVPPRQPRVQEKADIPVKS SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ TVHPVEKKLITYKCIHCLGVYTSMTASTITLHLUHCKGVGKTQN GQDKTNAPSRINQSPSIAPVKRTYSQMEPPLLKKRKLDDESDSP SFFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASIMV\WK\SDIASHSSNRKKCVRDCCKKYKPGVL LGFNMKBLNKVKHEMDFJABGLFBNHDEKDSRVNASKTADKKLN LGKENDSSDSFENLESSNRSGSPFDLYFEVRENISNDNPBEH VLKVIPBDASESBEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVOQDDVVENKDGASPSESGFGQQVSDFEDNTCENKPGTWSDB SSQSEDARSSKPAAKKATMQGDREQLKWKNSSYGKVEGFWSKD QSOWNASENDERLSSNPQIEMQNSTIDSEDGROFDNMTDGVAEP MHGSLAGVKLSSQQA  6009 4272 1534 CHGIQHLTPFFREINISLQG*BPH*AA*QAVRSEEKSIC*GSPSC HLVIGVLVPVARQSSHSAPQASAF*TGTGSGTPKAAEQSGYW EATTLGHQHWMMPJQRPDLVMKGRRIMGXKCKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFBSGVLFGFIVIGKIQSLBAVVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFMAHSPPGLQGEPTTTSVSL FVLAPQDGBGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFHAP I*KLGALDVAFHHLLTLVCSSFNVAYG*6KNGGTTLHQLFAAFUN AVTRGSAVQRPPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHILDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPNRWGLSHRT	Ì			
AVANYIMKIHNFTSKCLYCNRYLPTDTLLNHMLIHGLSCPYCRS TFNDVEKNAAHMRNVHIDEBMGPKTDSTLSFDLITLQGGSHTNIH LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQPKVQBKADLPVKS SPQAAVPYKKDVCKTLCPLCPSILKGPISDALAHHLIRERHGVIQ GQDKTNAPSRINGSPSLAPVKRTYEQMEFPLLKKRKIDDDSDSP SFFEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLW\W\\\SQLASHFSNKRKCVRDCEKYKRGVL LGFNMKELNKVKHEMDFDAEGLFENHDEKDERVNASKTADKKLN LGKEDDSSSDSFENLEESSNRSGSPFDDVFEVERKISNDNPERH VLKVIPEDASESEEKLDQKEDGSKYFTIHLTEEPTKLMHINASDS EVVQDDVVENKDGASPSESGPGSQQVSDFEDNTCENKFGTWSDE SSQSEDARSSKPAAKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWXNASENDERLSNPQIEMONSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTFFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHEAGPAQSAFR*TGTGSGTFKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCKKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGARSVRASVFTGNQFGWGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEBH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPGLQGEPTTTSVSL FVLAPQDGBGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAG*GKRGGTTLHQLFAEVN AVTRGSAVQREPSITISSIHVDTKLQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDFLHQIELISFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				,
TFNDVEKMAAHMRNVHIDEBMGPKTDSTLSPDLTLQQGSHTNIH  LLUTTYNIRDAPAESVAYHAQNNPPVPP KPQPKVOEKADIPVKS  SPQAAVPYKKDVGKTLCPLCPSILKGPISDALAHHLRERHQVIQ  TVHPVEKKLITYKCIHCLGVYTSMMTASTITLHLVHCRGVGKTQN  GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP  SPFEEKEEEPVVLALDPKGH\EDDSYEARKSFLIKKYFT\KQPYP  TRREIEKLAASLWV\WK\SDIASHFSNKKKKCVRDCEKYKPGVL  LGFMKELNKVKHEMDFJAEGLFENHDEKDSRVNASKTADKKLN  LGKEDDSSSDSFENLEESSNESGSPFDVPVEVERKISNDNPEEH  VLKVIPEDASESERKLDQKEDGSKYFTIHLTEEPTKLMHNASDS  EVDQDDVVEWKDGASPSESGFGQVCSDFEDNTCEMKPGTWSDE  SSQSEDARSSKPAAKKKATMQGDREQLKMKNSSYGKVEGFWSKD  QSQWKNASENDERLSNPQIEMQNSTIDSEDGEQFDNMTDGVAEP  MHGSLAGVKLSSQQA  6009  4272  1534  CHGLQHLTPFRELNISLQG*EPH*AA*QAVRSEEKSIC*GSPSC  HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW  EAYTLGHQHWNMFPIQRPPLVWKGRRIMCGKCKGK*VSDSVTGG  RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQFGWGLL  NGRKGGCFESGYLFGFIVIGKIQSLERKVPLPVNGGTGERASPG  NCRIHIVDAVC*SBHH*DHFLAAFLENSTIIS*VAPGSWQDHA  VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQCEPTTTSVSL  FVLAPQDGBGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP  I*KLGALDVAPLHLLTLVCSSFNVAYG*GKKGKTLHQLFAEVN  AVTRGSAVQRRPSITISSIHVDTKLQQELHDVMVAGADGVVQWG  DPFVVGLAGIPHLDDFLHQIELISFQRRV*EQCQGVKPDSQPVP  RPLRVGLLQVGPLVRGGGRRVAGRGKCWRDLLFPWRWGLSHRT	1			
LLUTTYNLRDAPAESVAYHAQNNPPVPPRPQPKVQEKADIPVKS SPQAAVPYKKDVEKTLCPLCPSILKGPISDALAHHIREREQVIQ TVHPVEKKLTYKCHCLGVYTSNMTASTITLHLVHCKGVGKTQN GQDKTNAPSRIANGSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP SPFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHPSNKRKKCVRDCEKYKPGVL LGFNMKELNKVKHEMDFJABGLFRNHDEKDSRVKASKTADKKLN LGKEDDSSSDSFENLEESSNRSGSPFDPVFEVRPKISNDNPEEH VLKVIPEDASESERKLDQKRDGSKYFTIHITEPTKLMINASDS EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDE SSQSEDARSSKPAAKKATMQGDRRQLKMXNSSTGKVEGFWSKD QSGWKNASENDERLSNPQIEMQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSOQA CHGLQHLTFPFREINISLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EATTLGHQHWNMFPIQRPPLVMKGRRIMCGKCKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGWGLL NGKRGGCFBSGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SBHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGGGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAPLHILLTUCSSFNAYGY*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHILDDDPLHQIELSFQRRV*EQCGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWDLLFPWRWGLSHRT	ł '			
SPQAAVPYKKDVGKTLCPLCPSILKGPISDALAHHLRERHQVIQ TVHPVEKKLTYKCIHCLGVYTSMMTASTITLHLUHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYBQMEFPLLKKRKLDDDSDSP SFFREKPEEPDVLALDPKGH\BDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHPSNKRKKCVRDCEKYKPGVL LGFMMKELNKVKHEMDFJABGLFRNHDEKDSRVNASK"ADKKLN LGKEDDSSSDSFENLEESSBNESSPFDDVFVERKISNDNPERH VLKVIPEDASESERKLDQKRDGSKYPTIHLTEEPTKLMHNASDS EVVQDDVVENKDGASPSESGFGSQQVSDFEDNTCEMKPGTWSDR SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSOWKNASENDERLSNPQIEWQNSTIDSEDGEQFUNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFRELNISLQG*BPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMGGKCKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQFGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCEHHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPPVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQDFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVWVAGADGVVQWG DPFVVGLAGIFHLIDDPLHOIELSFQRVV*EQQQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	1			
TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVRRTYBQMEFPLLKKRKLDDDSDSP SFFEEKPEEPVVLALDPKSHI BDDSYEARKSFLTKKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFMMRELNKVKHEMDFJAEGLFFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEESSNESGSPFDPVFVEVERKISNDNPEEH VLKVIPEDASESERKLDQKRDGSKYFTTHLTEEPTKLMINASDS EVVQDDVVUENKDGASPSESGFGSQVSDFEDNTCEMKPGTWSDE SSQSEDARSSKPAAKKKATMQGDREQLKWNNSSYGKVEGFWSKD QSOWKNASENDBRLSNPQIEMONSTIDSEDGEQFUNMTDGVAEP MHGSLAGVKLSSOQA  6009 4272 1534 CHGLQHLTPFREINLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVIGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWMMPPIQRPPLVMKGRRIMGKEKGK*VSDSVTGG RAVAGEQASQRRTVPTAGGGECLGAKSVRASVPTGNQPGVMGLL NGRRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQQQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	i			
SPFEEKPEEPVULALDPKGH\BDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFMMKELMKVKHEMDFJAEGLFENHDEKDSRVNASK"ADKKLN LGKEDDSSSDSFENLEESSNESGSFFDPVFEVERKISNDNPEEH VLKVIPEDASESERKLDQKRDGSKYFTIHLTEEPTKLMHNASDS EVDQDDVVENKDGASPSESGFGSQQVSDFEDNTCEMKPGTWSDR SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEMQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA  CHGLQHLTPFRELNISLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGEKCLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGBGVPFVEGQLVTVLGLUVPQSIRHTFVHTTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHGIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				1
TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFNMKELNKVKHEMDFJAEGLFENHDEKDSRVNASK"ADKKLN LGKEDDSSSDSFENLEBESBNESGSPFDPVFEVERKISINNPERH VLKVIPEDASESBEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVVDQDVVENKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDR SSQSEDARSSKPAAKKATMGGDRRQLKWKNSFYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA  CHGLQHLTFFRELNISLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHAAPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMGGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHGIELSFQRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP
LGFNMKELNKVKHEMDFJAEGLFENHIDEKDSRVNASK"ADKKLN LGKEDDSSSDSFENLBESSNRSGSPPDPVFEVERKISNDNPERH VLKVIPEDASESERKLDQKEDGSKYETIHLTEEPTKLMINASDS EVDQDDVVEWKDGASPSESGPGSQVSDFEDNTCEMKPGTWSDE SSQSEDARSSKPAAKKATMQGDREQLKNWNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEMQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA  6009 4272 1534 CHGLQHLTPFRELNISLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMPPIQPPLVMKGRRIMGGKCEKG*VSDSVTGG RAVAGEQASQRRTVPTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFSGYLFGFIVIGKIQSLERKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVYRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	Į			
LGKEDDSSSDSFENLBESSNESGSPFDPVFEVERKISNDNPEEH VLKVIPEDASESERKLDQKEDGSKYFTIHLTEEPTKLMINASDS EVDQDDVVENKDGASPSEGGGSQQVSDFEDNTCEMKPGTWSDE SSQSEDARSKPAAKKKATMQGDREQLKNKNSSYGKVEGFWSKD QSQWKNASENDBRLSNPQIEMQNSTIDSEDGEQFUNMTDGVAEP MHGSLAGVKLSSQQA  6009 4272 1534 CHGLQHLTPFREINLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCKG*VSDSVTOG RAVAGEQASQRRTVPTAGGGECLGAKSVRASVPTGNQPGVMGLL NGRRGGCFESGYLFGFIVIGKIQSLBAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFFLIDDPLHQIELSFQRV*EQQQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				
VLKVIPEDASESERKLDQKRDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVENKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDR SSQSEDARSSKPAAKKATMGGDREQLKWKNSSYGKVEEFWSKD QSQWKNASENDERLSNPQIEMQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA  6009 4272 1534 CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EATTLGHQHWNMPFIQRPLVMKGRRIMCGKCKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGCLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLBAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPYVEGQLVTVLGLVVPQSIRHTPVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRV*EQQQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				
EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDE SSQSEDARSSKPAAKKKATMQGDREQLKNKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEMONSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA  6009 4272 1534 CHGLQHLTPFRELNLSLQG*EPH*AA*QAVREEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EATTLGHQHWNMPPIQRPPLVMKGRITMCGKCKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVPTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGPWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPYVEGQLVTVLGLVVPQSIRHTPVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHOIELSFQRRV*EQQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT			,	,
SSQSEDARSSKPAAKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEMQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQWMMPPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCPESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPPVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIPHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	i			
QSQWKNASENDERLSNPQIEWQNSTIDSEDGBQFDNMTDGVAEP MHGSLAGVKLSSQQA  CHGLQHLTPFRELNISLQG*EPH*AA*QAVREEKSIC*GSPSC HLVLGVLVPVARQSSHAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMPPIQRPPLVMKGRRIMGKCEKG*VSDSVTGG RAVAGEQASQRRTVPTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHGIELSFQRVX*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				
MHGSLAGVKLSSQQA  6009  4272  1534  CHGLQHLTPFREINLSLQG*BPH*AA*QAVRSEEKSIC*GSPSC  HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW  EAYTLGHQHWMMPPIQRPPLVMKGRRIMCGKCEKG*VSDSVTOG  RAVAGEQASQRRTVPTAGGGECLGAKSVRASVPTGNQPGVMGLL  NGKRGGCFBSGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG  NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA  VLQKEVQASVRCRGFBSVDTAPAGFWAHSPPGLQGEPTTTSVSL  FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP  I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN  AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG  DPFVVGLAGIFHLIDDPLHGIELSFQRV*EQCQGVKPDSQPVP  RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT			!	
6009 4272 1534 CHGLQHLTPFREINLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EATTLGHQHWNMFPIQRPLVMKGRRIMCGKCKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGRRGGCFBSGYLFGFIVIGKIQSLBAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKBVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPYVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLTDDFLHOIELSFQRV*EQQQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				1
HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCKKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGRRGGCFBSGYLFGFIVIGKIQSLBAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFILAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFBSVDTAPAGPWAHSPPGLQGEPTTTSVSL FVLAPQDGBGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSTTISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLJDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	6009	4272	1524	, I
EAYTLGHQHWNMPPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVPTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFBSGYLFGFIVIGKIQSLBAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFILAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFBSVDTAPAGPWAHSPPGLQGEPTTTSVSL FVLAPQDGBGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSTTISSIHVDTKIQQELHDWNAGADGVVQWG DPFVVGLAGIFHLJDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	""	36/4	2003	1
RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPEGWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGBGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSTTISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIPHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	f			
NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGBGVPFVESQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHGIKLSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				
NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGESVPFVESQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVWVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRVV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				·
VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGBGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIKLSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				
FVLAPQDGBGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIPHLIDDPLHQIKLSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	1			1
AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				
DPFVVGLAGIPHLIDDPLHQIRLSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				I+KLGALDVAPLHILITLVCSSPNVAYG+GKNGGTTLHQLFAEVN
RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	[			
)	]			,
RDLLRGGDRGHVVVIVLCRLGSLVGGLGTDKLLWFGGR*LIIIG	1	· .		
	L			RDLLKGGDRGHVVVIVLCRLGSLVGGLGTDKLLWFGGR*LIIIG

	and the state of t	on the participant of the second	선거 역사 이 기업에서 가는 역사 범위하다면 가지했다.
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, P-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		Ĭ	
1	amino acid	sedneuce	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1	1		I * * RGRLSGEWGCGLGRGELFQVSIGIGVSIVHIGQGDHEVLCG
]	J .	J	AGLVERGALHATGQGVEALVQQLLDVGPAGALGLCDGAALFQGP
1		l	GRVGQLPAEGLQVCITLVAQWRMHDGRELGGAENPWQALHGAAI
1			CGVGGAILLKALSQYFLKGG*RLWCARGQ*PVKKRQRRWRG*TR
	1		R*NGLTIHCFN*LI*GAVCCRLVILRWCGLLEVHGVYGT*IHCL
1	l		GSFPGRLWP+PFISQERPNGHCQWEFRLAVPSWKCRWSRWRVRG
1			TWRYGNPLLNLL+GAWLGGAACGGQQGGPLSTNQACTGPGQAAF
I	1		LPPFQGACRPRTQRCRTWVCPIAWRQLLAYTRD
6010	1	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM
1 5520	,	]	AGISQNAKTGDLPAFGECVGIASKALCGLTRAAAQAAYLVGIFD
	ľ		PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA
{	j	·	TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL
i	1	* 1	VKTIKALDGDPSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS
ł			<i>t</i>
	<b>,</b>	,	IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP
1	j		PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC
			IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQBIGHLIDP
1	·		IATAARGEAAQIGHKGTQLASYFEPLILAAVGVASKILDHQQQM
1	]	· .	TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK
1			RAVDDIMVTINKAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG
ł	]		TFVDYQTTVVKYSKALAVTAQEMNTKSVTNPBELGGLASQMTSD
1			YGHLAFQGQMAAATAEPBEIGFQIRTRVQDLGHGCIFLVQKAG\
1	· ·		ALQVCPTDSYTKRKLIECARAVTEKVSLVLSALQAGNKGTQACI
			TAATAVSGIIADLDTTIMFATAGTLNAENSBTFADHRENILKTA
			KALVEDTKLIVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA
1	· .		SIGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM
1			YQLKGAAKVMVTNVTSLLKTVKAVEDKATRGTRALEATIECIKQ
1	,		ELTVFQSKDVPEKTSSPRESIRMTKGITMATAKAVAAGNSCRQE
	· · · ·		DVIATANLSRKAVSDMLTACKQASFHPDVSDBVRTRALRFGTEC
1		,	TLGYLDLLEHVLVI:QKPTPELKQQLAAFSKRVAGAVTELIQAA
1			EAMKGTEWVDPEDPTVIABTELLGAAASIEAAAKKLEQLKPRAK
		•	PKQADETLDPEEQILEAAKSIAAATSALVKSASAAQRELVAQGK
		,	VGSIPANAADDGQWSQGLISAARMVAAATSSLCRAANASVQGHA
1		,	SERKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV
1	l i		
			KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM
		****	LKKERELEKARKKLAQIRQQQYKFLPTRLREDEG
6011	446	1835	LLQPAMRKSPGLSDCLWAWILLLSTLTGRSYGQPSLQDELKDNT
1	ĺ		TVFTRILDRLLDGYDNRLRPGLGERVTEVKTDIFVTSPGPVSDH
			DMEYTIDVFFRQSWKDERLKFKGPMTVLRLNNLMASKIWTPDTF
i	Ì		PHNGKKSVAHNMTMPNKLLRITEDGTLLYTMRLTVR\AECPMAF
1			GRDFPM\D\AHACPLKFGSYAYTRAEVVYEWTREPARSVVVAED
i l			GSRINQYDLLGQTVDSGIVQSSTGEYVVMTTHFHLKRKIGYFVI
			QTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLSIS
1			arnslpkvayatamdwfiavcyafvfsaliefatvnyftkrgya
1	l		wdgksvvpekpkkvkdplikknntyaptatsytpnlargdpgla
1			TIAKSATIEPKEVKPETKPPEPKKTFNSVSKIDRLSRIAFPLLP
1			GIFNLVYWATYLNRBPQLKAPTPHQ
6012	351	5013	PAELFOSFAIWHKELYDWRLGPWNQCQPVISKSLEKPLECIKGK
			EGIOVREIACIOKDEDIPAEDIICEYFEPEPLEQACLIPCOOD
			CIVSEPSAWSECSKTCGSGLQHRTRHVVAPPQFGGSGCPNLTEF
			QVCQSSPCEAEELRYSLHVGPWSTCSMPHSRQVRQARRRGKNKE
1			REKDRSKGVKDPEARELIKKKRNRNRONRQENKYWDIQIGYOTR
1	İ		
[			EVMCINKTGKAADLSFCQQEKLPMTFQSCVITKECQVSEWSBWS
1			PCSKTCHDMVSPAGTRVRTRTIRQFPIGSEKECPEFEEKEPCLS
			QGDGVVPCATYGWRTTEWTECRVDPLLSQQDKRRGNQ::ALCGGG
j		5	IQTREVYCVQANENLLSQLSTHKNKKASKPMDLKLCTGPIPNTT
			QLCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRKRRIT
			NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK
			<b>ECGPGTQVQEVVCINSDGBEVDRQLCRDAIPPIPVACDAPCPKD</b>
]			CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP
			NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW
<b>f</b> i			NGEASCSVGMQTRKVICVRVNVGQVGPKKCPRSLRPETVRPCLL
	<u></u>	L	HORDON AGUSTURATON VALADA AGE 1000 L 19 DESCRIPTANDESCRI

			<u> </u>
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
i			Totale, is about the, kshysine,
Į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	Dequence	\=possible nucleotide insertion)
<u> </u>	sequence		(-possible nucleocide insertion)
f			PCKKDCIVTPYSDWTSCPS\SCKEGDSSIRKQSRHRVIIQLPAN
i	1	1 .	GGRDCTDPLYEEKACEAPQACQSYRW\KTHKW\HRCQ\LVP\WS
ſ	1	í	VQQDSP\GAQEGCGPGRQARAITCRKQDGGQAGIHECLQYAGPV
1	)	1	PALTQACQIPCQDDCQLTSWSKFSSCNGDCGAVRTRKRTLVGKS
1	1		KKKEKCKNSHLYPLIETQYCPCDKYNAQPVGNWSDCILPEGKVE
1	ł	<u> </u>	
l .	1		VLLGMKVQGDIKECGQGYRYQAMACYDQNGRLVBTSRCNSHGYI
1	1	1	ERACII PCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLREKPYN
1	1		GGRPCPKLDHVNQAQVYEVVPCHSDCNQYLWVTEPWSICKVTFV
i	1		NMRENCGEGVQTRKVRCMQNTADGPSEHVEDYLCDPBEMPLGSR
	i	]	VCKLPCPEDCVISEWGPWTQCVLPCNQSSFRQRSADPIRQPADE
1	I	Ī	GRSCPNAVEKEPCNLNKNCYHYDYNVTDWSTCQLSEKAVCGNGI
1 .	1		
1	1	i	KTRMLDCVRSDGKSVDLKYCRALGLEKNWQMNTSCMVECPVNCQ
1	]	1	LSDWSPWSECSQTCGLTGKMIRRRTVTQPFQGDGRPCPSLMDQS
ŀ	j	1	KPCPVKPCYRWQYGQWSPCQVQRAQCGEGTRTRNISCVVSDGSA
	l	j	DDFSKVVDREFCADIBLIIDGNKNMVLKBSCSQPCPGDCYLKDW
ı	1	1	SSWSLCQLTCVNGEDLGFGGIQVRSRPVIIQELENQHLCPBQML
1	1		ETKSCYDGQCYEYKWMASAWKGSSRTVWCQRSDGINVTGGCLVM
	ľ		
1	1		SQPDADRSCNPPCSQPHSYCSBTKTCHCBEGYTEVMSSNSTLEQ
1	1		CTLI PVVVLPTMEDKRGDVKTSRAVHPTQPSSNPAGRGRTWFLQ
1		ļ	PFGPDGRLKTWVYGVAAGAFVLLIFIVSMIYLACKKPKKPQRRQ
			NNRLKPLTLAYDGDADM
6013	1161	710	GAFLAGVPVQPVLIRYPNSLDTTSWAWRGPGVLKVLWLTASOPC
1			SIVDVBFLPVYHPSPEBSRDPTLYANNVQRVMAQALGIPATECB
i			FVGSLPVIVVGRLKVALEPQL/WGTGKSASEGWAVRWLCGRWGR
ł			ARPESNDOPGRVCOAATAL
6014	2857	613	EAVAGGMEKSRMNLPKGPDTLCFDKDEFMKEDFDVDHFVSDCRK
į.			RVQLEELRDDLBLYYKLLKTAMVBLINKDYADF\VNLSTNLVGM
i	}		DKALNQLSVPLGQLREBVLSLRSSVSEGIRAVDERMSKQEDIRK
1	· ·		KKMCVLRLIQVIRSVEKIEKILNSQSSKETSALEASSPLLTGQI
	<u>!</u>		LERIATEFNQLQFHACQSK\GMPLLDKVRPRIAGITAMLQQSLE
	\$		
) .			
			GLLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI
1	•		GLLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DEVIIEQFVESHPNGLQVMYNKILEFVPHHCRLLREVTGGAISS
			GLLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DBVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLRBVTGGAISS KKGNTVPGYDFLVNSVWPQIVQGLBEKLPSLFNPGNPDAFHRKY
	·		GLLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DEVIIEQFVESHPNGLQVMYNKILEFVPHHCRLLREVTGGAISS
			GLLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DBVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLRBVTGGAISS KKGNTVPGYDFLVNSVWPQIVQGLBEKLPSLFNPGNPDAFHRKY
			GLLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLRBVTGGAISS BKGNTVPGYDFLVNSVWPQIVQGLBEKLPSLFNPGNPDAFHBKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYPQI RFRKIAGSLBAALTDVLEDAPABSPYCLLASHRTWSSLRRCWSD
			GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DBVIIEQFVBSHPNGLQVMYNKLLEFVPHHCRLLRBVTGGAISS EKGNTVPGYDFLVNSWPQIVQGLEEKLPSLFNPGRPDAPHRKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYPQI RFKEIAGSLEAALTDVLEDAPABSPYCLLASHRTWSSLRECWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKB
			GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DEVIIEQFVESHPNGLQVMYNKLLBFVPHHCRLLREVTGGAISS BKGNTVPGYDFLVNSVWPQIVQGLEKKLPSLFNPGGPPDAFHRKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI RFREIAGSLBAALTDVLEDAPABSPYCLLASHRTWSSLRRCWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\RLSLRPISNESPKB IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV
			GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS BKGNTVPGYDFLVNSVWPQIVQGLEKKLPSLFNPGRPDAFHEKY TISMDFVRRLERQCGSQASVKRIKAHPAYHSFNKKWNLPVYFQI RFREIAGSLEAALTDVLEDAPABSPYCLLASHRTWSSLRRCWSD EMTLPLLVHRLWRLHSGRFWARYSVFV\N\RLSLRPISNESPKE IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQEQLPELLEIIKPKLEMIGFKNPSSISAALEDSQSSPS
			GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS BKGNTVPGYDPIJVNSVMPQIVQGLBEKLPSLFNPGNPDAFHRKX TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKNNLPVYPQI RFREIAGSLBAALTDVLEDAPABSPYCLLASHRTWSSLRCWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\BLSLRPISNESPKB IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS
			GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DBVIIEQFVESHPNGLQVMYNKLLEFVPHHCKLLRBVTGGAISS EKGNTVPGYDFLVNSVWPQIVQGLEEKLPSLFNPGNPDAPHEKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI RFREIAGSLBAALTDVLEDAPABSPYCLLASHRTWSSLRRCWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE IKKPLVTGSKRPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDGSSFS ACVPSLSSKIIQDLEDSCFGFLKSALEVPRLYRTTKRVPTTAS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET
			GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS BKGNTVPGYDPIJVNSVMPQIVQGLBEKLPSLFNPGNPDAFHBKX TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKNNLPVYPQI RFREIAGSLBAALTDVLEDAPABSPYCLLASHRTWSSLRCWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\BLSLRPISNESPKB IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS
			GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DBVIIEQFVESHPNGLQVMYNKLLEFVPHHCKLLRBVTGGAISS EKGNTVPGYDFLVNSVWPQIVQGLEEKLPSLFNPGNPDAPHEKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI RFREIAGSLBAALTDVLEDAPABSPYCLLASHRTWSSLRRCWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE IKKPLVTGSKRPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDGSSFS ACVPSLSSKIIQDLEDSCFGFLKSALEVPRLYRTTKRVPTTAS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET
			GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DBVIIEQFVESHPNGLQWYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSVPQIVQGLEEKLPSLFNPGRPDAPHRKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYPQI RFREIAGSLEAALTDVLEDAPAESPYCLLASHRTWSSLRECWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE IKKPLVTGSKRPSITQGNTEDQGGGPSETREVVSISRTQLVYVV ADLDKLQEQLPELLEIIKPKLEMIGFKNFSISAALEDSQSSFS ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKRVPTTAS SYVDSALKPLFQLQSGHKKKLKQAIQQWLBGTLSESTHKYYET VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL
6015	13	2237	GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DRVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSWMPQIVQGLEKKLPSLFNPGMPDDAFHEKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI RPREIAGSLEAALITDVLEDAPABSPYCLLASHRTWSSLRRCWSD EMFLPLLVHRLWRLHSCRFWARYSVFV\N\ELSLRPISNESPKE IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET VSDVLNSVKKMESSLKRIKQARKTTPANPVGFSGGMSDDDKIRL QLALDVEYLGEQIQKLGLQASDIKSFSALAELVAAAKDQATAEQ
6015	13	2237	GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS BKGNTVPGYDFLVNSVMPQIVQGLEKKLPSLFNPGGPDAFHEKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKMNLPYYFQI RFREIAGSLBAALTDVLEDAPABSPYCLLASHRTWSSLRCWSD EMFLPLLVHRLWRLHSCRFMARYSVFV\N\BLSLRPISNESPKE IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQEQLPELLEIIKPKLEMIGPKNPSSISAALEDSQSSFS ACVPSLSSKIIQDLEDSCFGFLKSALEVPRLYRTTMKEVPTTAS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET VSDVLNSVKKMEESLKRLKQARKTTPANPUGPSGGMSDDDKIRL OLALDVEYLGBQIQKLGLQASDIKSFSALABLVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC
6015	13	2237	GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCKLLREVTGGAISS EKGNTVPGYDFLVNSVWPQIVQGLEEKLPSLFNPGNPDAPHEKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI RFREIAGSLEAALTDVLEDAPAESPYCLLASHRTMSSLRRCWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE IKKPLVTGSKRPSITQGNTEDQGSGPSETKRVVSISRTQLVYVV ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDQSSFS ACVPSLSSKIIQDLEDSCFGFLKSALEVPRLYRTTKKEVPTTAS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL QLALDVEYLGEQIQKLGLQASDIKSFSALAELVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN
6015	13	2237	GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSVPQILVQGLEEKLPSLFNPGRPDAPHRKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKMNLPVYPQI RFREIAGSLEAALTDVLEDAPAESPYCLLASHRTWSSLRECWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE IKKPLVTGSKRPSITQGNTEDQGGGPSETREVSISRALEDSQSSFS IKKPLVTGSKRPSITQGNTEDQGGGPSETREVSISRALEDSQSSFS ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKRVPFTTAS SYVDSALKPLFQLQSGHKDKLKQAIQQWLBGTLSESTHKYYET VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL OLALDVEYLGBQIQKLGLQASDIKSFSALAELVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEMDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
6015	13	2237	GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DRVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSWPQIVQGLEEKLPSLINPGRPDDAFHRKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKMNLPVYPQI RFREIAGSLEAALTDVLEDAPABSPYCLLASHRTWSSLRECWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\RLSLRPISNESPKB IKKPLVTGSKRPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQBQLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLBGTLSESTHKYYET VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL QLALDVEYLGBQIQKLGLQASDIKSFSALABLVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDBLRLLY GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT
6015	13	2237	GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSVPQILVQGLEEKLPSLFNPGRPDAPHRKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKMNLPVYPQI RFREIAGSLEAALTDVLEDAPAESPYCLLASHRTWSSLRECWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE IKKPLVTGSKRPSITQGNTEDQGGGPSETREVSISRALEDSQSSFS IKKPLVTGSKRPSITQGNTEDQGGGPSETREVSISRALEDSQSSFS ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKRVPFTTAS SYVDSALKPLFQLQSGHKDKLKQAIQQWLBGTLSESTHKYYET VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL OLALDVEYLGBQIQKLGLQASDIKSFSALAELVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEMDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
6015	13	2237	GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DRVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSWPQIVQGLEEKLPSLINPGRPDDAFHRKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKMNLPVYPQI RFREIAGSLEAALTDVLEDAPABSPYCLLASHRTWSSLRECWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\RLSLRPISNESPKB IKKPLVTGSKRPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQBQLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLBGTLSESTHKYYET VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL QLALDVEYLGBQIQKLGLQASDIKSFSALABLVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDBLRLLY GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT
6015	13	2237	GLLEGLQTSDVDITRHCLRTYATIDKTRDARALVGQVLVKPYI DRVITEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS BKGNTVPGYDFLVNSWPQIVQGLEKKLPSLFNPGRPDAFHRKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKMNLPYYFQI RPRETAGSLERALTDVLEDAPABSPYCLLASHRTWSSLRRCWSD EMFLPLLVHRLWRLHSCRFWARYSVFV\N\RLSLRPISNESPKE IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQEQLPELLETIKPKLEMTGFKNFSSISAALEDSQSSFS ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTMKEVPTTAS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET VSDVLNSVKKMESSLKRIKQARKTTPANPVGPSGGMSDDDKIRL QLALDVEYLGBQIQKLGLQASDIKSFSALABLVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEWDQVTYYLFCDDHKLQRYALM RITVWRSRSGMELPLAVASTADLIRCKLLDVTGGLGTDBLRLLY GMALVRFVNLISBRKTKFAKVPLKCLAQEVNIPDWIVDLRHELT HKMPHINDCRRGCYFVLDWLQKTYWCRQLENSBRETWBLEEFR EGIBEEDQEEDKNIVVDDITEQKPEPQDDGKSTBSDVKADGDSK
6015	13	2237	GLLEGLQTSDVDITRHCLRTYATIDKTRDARALVGQVLVKPYI DRVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSVMPQIVQGLEEKLPSLFNPGNDAPHEKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKNNLPVYFQI RFREIAGSLEAALTDVLEDAPAESPYCLLASHRTWSSLRRCWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE IKKPLVTGSKEPSITQGNTEDQGSGPSETKRVVSISRTQLVYVV ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS ACVPSLSSKIIQDLEDSCFGFLKSALEVPRLYRTTKKRVPTTAS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL QLALDVEYLGEQIQKLGLQASDIKSFSALAELVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDBLRLLY GMALVRFVNLISERKTKFAKVPLKCLAQENIPDWIVDLRHELT HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR EGIEEEDQEEDKNIVVDDITEQKPEPQDDGKSTESDVKADGDSK GSEEVDSHCKKALSHKELYERARELLVSYEEEQPTVLEKFPRYLP
6015	13	2237	GLLEGLQTSDVDITRHCLRTYATIDKTRDARALVGQVLVKPYI DEVITEQFVESHPNGLQWYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSVPQILVQGLEEKLPSLFNPGNPDAPHRKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKMNLPVYPQI RFRETAGSLEAALTDVLEDAPABSPYCLLASHRTWSSLRECWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE IKKPLVTGSKRPSITGGNTEDQGGGPSETKRVSISRALEDGQSSPS ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKRVPTTAS STVDSALKPLFQLQSGHKDKLKQATIQQWLBGTLSESTHKYYET VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL OLALDVEYLGBQIQKLGLQASDIKSFSALABLVAAAKDQATAEQ P AEGCAERRGTEPVVKLSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEMDQVTVYLFCDDHKLQRYALN RITVWRSRSGNKLPLAVASTADLIRCKLLDVTGGLGTDBLRLLY GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT HKKMPHINDCRGCYFVLDWLQKTYWCRQLENSLRETWBLEEFR EGIBEEDQEEDKNIVVDDITEQKPEPQDDGKSTESDVKADGDSK GSEEVDSHCKKALSHKRLYERARRLLVSYEEEQFTVLRKFRYLP KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT
6015	13	2237	GLLEGLQTSDVDITRHCLRTYATIDKTRDARALVGQVLVKPYI DBV1IEQFVBSHPNGLQVMYNKLLEFVPHHCRLLRBVTGGAISS EKGNTVPGYDFLVNSWPQIVQGLEEKLPSLINPGRPDAPHRKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKMNLPVYPQI RFREIAGSLBAALTDVLEDAPABSPYCLLASHRTWSSLRECWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKB IKKPLVTGSKRPSITQGNTEDQGGGPSETKPVSISRTQLVYVV ADLDKLQEQLPELLEIIKPKLENTGFKNFSSISAALEDSQSSFS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLBGTLSESTHKYYFT VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL OLALDVEYLGBQIQKLGLQASDIKSFSALABLVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEMDQVTVVLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT HKKMPHINDCRGCYFVLDWLOKTYWCRQLENSLBETWELBEFR GGIEEEDQEEDKNIVVDDITEQKPBPQDDGKSTESDVKADGDSK GSBEVDSHCKKALSHKBLYERARRLLVSYEEEQFTVLRKFRYLD KAIKAWNNESPRVECULAELKGVTCENREAVLDAFIDDGFLVPT PEQLAALQIEYERNVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ
6015	13	2237	GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DRVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSWPQIVQGLEKKLPSLINPGNPDAFHEKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYPQI RFREIAGSLEAALTDVLEDAPABSPYCLLASHRTWSSLRRCWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\RLSLRPISNESPKB IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS SYVDSALKPLFQLQSGHRKLKQAIIQQWLBGTLSESTHKYYET VSDVLNSVKKMEESLKRLKQARKTTPANFVGPSGGMSDDDKIRL QIALDVEYLGBQIQKLGLQASDIKSFSALAKLVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGS-PLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDBLRLLY GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR EGIEEDQEEDKNIVVDDITEQKPRPQDDGKSTESDVKADGDSK GSEEVDSHCKKALSHKELYERARELLVSYEEGFFVLEKFRYLD KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT FPQLAALQIEYERNVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF
6015	13	2237	GLLEGLQTSDVDITRHCLRTYATIDKTRDARALVGQVLVKPYI DBV1IEQFVBSHPNGLQVMYNKLLEFVPHHCRLLRBVTGGAISS EKGNTVPGYDFLVNSWPQIVQGLEEKLPSLINPGRPDAPHRKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKMNLPVYPQI RFREIAGSLBAALTDVLEDAPABSPYCLLASHRTWSSLRECWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKB IKKPLVTGSKRPSITQGNTEDQGGGPSETKPVSISRTQLVYVV ADLDKLQEQLPELLEIIKPKLENTGFKNFSSISAALEDSQSSFS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLBGTLSESTHKYYFT VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL OLALDVEYLGBQIQKLGLQASDIKSFSALABLVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEMDQVTVVLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT HKKMPHINDCRGCYFVLDWLOKTYWCRQLENSLBETWELBEFR GGIEEEDQEEDKNIVVDDITEQKPBPQDDGKSTESDVKADGDSK GSBEVDSHCKKALSHKBLYERARRLLVSYEEEQFTVLRKFRYLD KAIKAWNNESPRVECULAELKGVTCENREAVLDAFIDDGFLVPT PEQLAALQIEYERNVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ
6015	13	2237	GLLEGLQTSDVDIIRHCLRTYATIDKTRDARALVGQVLVKPYI DRVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSWMPQIVQGLEKKLPSLFNPGMPDAFHEKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI RFREIAGSLEAALTDVLEDAPABSPYCLLASHRTWSSLRRCWSD EMPLPLLVHRLWRLHSGRFWARYSVFV\N\RLSLRPISNESPKE IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLBGTLSESTHKYYET VSDVLNSVKKMEESLKRIKQARRTTPANPVGFSGGMDDDKIRL QLALDVEYLGBQIQKLGLQASDIKSFSALABLVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDBLRILLY GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR EGIBEEDQEEDKNIVVDDITEQKPBPQDDGKSTESDVKADGDSK GSEVDSHCKKALSHKELYERARELLVSYEEQFTVLRKFRYLP KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT PEQLAALQIEYERNVDLNDVLVPRPFSQFWQPLLRGLHSQNFTQ ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF SAGQWEARRGWRIFNCSASLDWPRWVESCLGSPCWASPQLLRII
6015	13	2237	GLLEGLQTSDVDITRHCLRTYATIDKTRDARALVGQVLVKPYI DEVITEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSVMPQIVQGLEEKLPSLFNPGNDAPHRKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKMNLPVYFQI RFREIAGSLBAALTDVLEDAPABSPYCLLASHRTMSSLRRCWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE IKKPLVTGSKRPSITQGNTEDQGSGPSETKRVVSISRTQLVYVV ADLDKLQEQLPELLETIKPKLEMIGFKNFSSISAALEDSQSSFS ACVPSLSSKIIQDLEDSCFGFLKSALEVPRLYRTTMKEVPTTAS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL OLALDVEYLGBQIQKLGLQASDIKSFSALABLVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY GMALVRFVMLISERKTKFAKVPLKCLAQEVNIPDMIVDLRHELT HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLETWELEEFR EGIBEEDGEBDKNIVVDDITEQKPBPQDDGKSTESDVKADGDSK GSEEVDSHCKKALSHKELYERARRLLVSYEEEQFTVLEKFRYLP KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT FPQLAALQIEYERNDLNDVLVPKPFSQFWQPLGCLASPGNLRIT FLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRP SAGGWEARRGWRLFNCSASLDWPRMVESCLASPCMASPQLLRII FKAMGQGLQDE\EQEKLLRICSIYTQSGENSLVQEGSEASPIG
6015	13	2237	GLLEGLQTSDVDITRHCLRTYATIDKTRDARALVGQVLVKPYI DEVITEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSVMPQIVQGLEEKLPSLFNPGNDAPHRKY TTSMDFVRRLERQCGSQASVKRLRAHPAYHSPNKKMNLPVYFQI RFRETAGSLEAALTDVLEDAPAESPYCLLASHRTMSSLRRCWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE IKKPLVTGSKEPSITGGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQEQLPELLETIKFKLEMIGFKNFSSISAALEDQSSFS SCVPSLSSKTIQDLSDSCFGFLKSALEVPRLYRTTMKEVPTTAS SYVDSALKPLFQLQSGHKDKLKQATIQQWLEGTLSESTHKYYET VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL OLALDVEYLGEQIQKLGLQASDIKSFSALAELVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY GMALVRFVMLISERKTKPAKVPLKCLAQEVNIPDMIVDLRHELT HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR EGIBEEDQEEDKNIVVDDITEQKPBPQDDGKSTESDVKADGDSK GSEEVDSHCKKALSHKELYERARRLLVSYEEGPFVLIRKFRYLP KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT FEQLAALOIEYERNVDLNDVLVPRPFSQFWQPLLRGLHSQNFTQ ALLERMLSELPALGISGIRPTYLIRWTVELJIVANTKTGRNARRF SAGQWEARRGWRLFNCSASLDWPRWVESCLGSPCWASPQLLRII F\RAMGQGLQDE\EGEKLLRIGSIYTYQSGENSLVQSGSSEASPIG KSPYTLDSLYWSVKPASSSFGSEAKAQQQEEQGSVNDVKEEKKE
6015	13	2237	GLLEGLQTSDVDITRHCLRTYATIDKTRDARALVGQVLVKPYI DEVITEQFVESHPNGLQWYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSVPPQIVQGLEEKLPSLFNPGNPDAPHRKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKMNLPVYPQI RFRETAGSLEAALTDVLEDAPABSPYCLLASHRTWSSLRECWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE IKKPLVTGSKRPSITQGNTEDQGGGPSETKRVSISRALEDGQSSPS IKKPLVTGSKRPSITQGNTEDQGGGPSETKRVSISRALEDGQSSPS SVDSALKPLPQLQSGHKDKLKQAILQQWLBGTLSESTHKYYET VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL OLALDVEYLGBQIQKLGLQASDIKSFSALABLVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGS-PLSAHGIVVAWLSRAEMDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY GMALVRFVNLISERKTKPAKVPLKCLAQEVNIPDWIVDLRHELT HKKMPHINDCRGCYFVLDWLQKTYWCRQLENSLRETWBLEEFR EGIBEEDQEEDKNIVVDDITEQKPEPPQDDGKSTESDVKADGDSK GSEVDSHCKKALSHKRLYERARRLLVSYEERQPTVLRKFRYLP KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT PEQLAALQIEYERNVDLNDVLVPRPFSQFWQPLLRGLHSQNFTQ ALLERMLSELPALGISGIRPTYILWTVELIVANTKTGRNARRP SAGQWEARRGWELFRCSASLDWPRWESCIESPCWASPQLLRII F\KAMGQGLQDE\EQGSKLRICSIYTQSGENSLVQEGSEASPIG KSPYTLDSLYWSVKPASSSFGSEAKAQQQKEQGSVMDVKEEBKE EKEVLPDQVEEEERNDDQBEEEEDEDDBDDEEEDRMEVGPPSTG
6015	13	2237	GLLEGLQTSDVDITRHCLRTYATIDKTRDARALVGQVLVKPYI DRVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSWPQIVQGLEEKLPSLINPGRPDJAFHEKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKMNLPVYPQI RFREIAGSLEAALTDVLEDAPARSPYCLLASHRTWSSLRECWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\RLSLRPISNESPKR IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQBQLPELLETIKPKLEMIGFKNFSSISAALEDSQSSFS ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS SYVDSALKPLFQLQSGHRKLKQAIQQWLBGTLSESTHKYYET VSDVLNSVKKMEESLKRLKQARKTTPANFVGPSGGMSDDDKIRL QLALDVEYLGBQIQKLGLQASDIKSFSALAKLVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDBLRLLY GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDMIVDLRHELT HKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR EGIEEEDQEEDKNIVVDDITEQKPRPQDDGKSTESDVKADGDSK GSEVDSHCKKALSHKELYERARRELLVSYEEEQFTVLRKFRYLD KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT FEQLAALQIEYERNVDLNDVLVPKPFSQFWQPLLRCLHSQMFTQ ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF SAGQWEARRGWRLFNCSASLDWPRWVESCLGSPCWASPQLLRII F\KRMGQGLODE\GEGKERDHDGGEGERDRMEVGPFSTG QESPTAKNARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR
	13	2237	GLLEGLQTSDVDITRHCLRTYATIDKTRDARALVGQVLVKPYI DRVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSWMPQIVQGLEKKLPSLFNPGMPDAFHEKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKMNLPVYFQI RFREIAGSLEAALTDVLEDAPABSPYCLLASHRTWSSLRRCWSD EMPLPLLVHRLWRLHSGRFWARYSVFV\N\RLSLRPISNESPKE IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQEQLPELLETIKPKLEMIGFKNFSSISAALEDSQSSFS ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLBGTLSESTHKYYET VSDVLNSVKKMEESLKRIKQARRTTPANPVGFSGCMSDDDKIZL QLALDVEYIGBQIQKLGLQASDIKSFSALAKLVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDBLRLLY GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR EGIEEEDQEEDKNIVVDDITEQKPBPQDDGKSTBSDVKADGDSK GSEEVDSHCKKALSHKELYERARELLVSYEEQFTVLEKFRYLP KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT FEQLAALQIEYERNUDLNDVLVPRFFSQFWQPLLRGLHSQNFTQ ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII F\RAMGQGLDDE\EGEKLLRICSIYTQSGENSLVQEGSEASPIG KSPYTLDSLYWSVKPASSSFGSEAKAQQQKEQGSVNDVKEEKKE EKEVLPDQVEEEERNDDQEEEEGDDBDDEREDRMEVGPFSTG OESPTARMARILLAOXRGALQGSAWQVSSEDVRWDTFP\LGRMPR SRPRTPARLMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL
6015	13	2237	GLLEGLQTSDVDITRHCLRTYATIDKTRDARALVGQVLVKPYI DRVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSWMPQIVQGLEKKLPSLFNPGMPDAFHEKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKMNLPVYFQI RFREIAGSLEAALTDVLEDAPABSPYCLLASHRTWSSLRRCWSD EMPLPLLVHRLWRLHSGRFWARYSVFV\N\RLSLRPISNESPKE IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQEQLPELLETIKPKLEMIGFKNFSSISAALEDSQSSFS ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLBGTLSESTHKYYET VSDVLNSVKKMEESLKRIKQARRTTPANPVGFSGCMSDDDKIZL QLALDVEYIGBQIQKLGLQASDIKSFSALAKLVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDBLRLLY GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR EGIEEEDQEEDKNIVVDDITEQKPBPQDDGKSTBSDVKADGDSK GSEEVDSHCKKALSHKELYERARELLVSYEEQFTVLEKFRYLP KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT FEQLAALQIEYERNUDLNDVLVPRFFSQFWQPLLRGLHSQNFTQ ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII F\RAMGQGLDDE\EGEKLLRICSIYTQSGENSLVQEGSEASPIG KSPYTLDSLYWSVKPASSSFGSEAKAQQQKEQGSVNDVKEEKKE EKEVLPDQVEEEERNDDQEEEEGDDBDDEREDRMEVGPFSTG OESPTARMARILLAOXRGALQGSAWQVSSEDVRWDTFP\LGRMPR SRPRTPARLMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL
	13	2237	GLLEGLQTSDVDITRHCLRTYATIDKTRDARALVGQVLVKPYI DRVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSWPQIVQGLEEKLPSLINPGRPDJAFHEKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKMNLPVYPQI RFREIAGSLEAALTDVLEDAPARSPYCLLASHRTWSSLRECWSD EMFLPLLVHRLWRLHSGRFWARYSVFV\N\RLSLRPISNESPKR IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQBQLPELLETIKPKLEMIGFKNFSSISAALEDSQSSFS ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS SYVDSALKPLFQLQSGHRKLKQAIQQWLBGTLSESTHKYYET VSDVLNSVKKMEESLKRLKQARKTTPANFVGPSGGMSDDDKIRL QLALDVEYLGBQIQKLGLQASDIKSFSALAKLVAAAKDQATAEQ P AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDBLRLLY GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDMIVDLRHELT HKMMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR EGIEEDQEEDKNIVVDDITEQKPRPQDDGKSTESDVKADGDSK GSEVDSHCKKALSHKELYERARRELLVSYEEEQFTVLRKFRYLD KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT FEQLAALQIEYERNVDLNDVLVPKPFSQFWQPLLRCLHSQMFTQ ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF SAGQWEARRGWRLFNCSASLDWPRWVESCLGSPCWASPQLLRII F\KRMGQGLODE\GEGKERDHDGGEGERDRMEVGPFSTG QESPTAKNARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR

CHO	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł .	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence	Dequence	\=possible nucleotide insertion)
<u> </u>	- Sequence	ļ_ <del></del>	VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN
į	· ·		RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
1	<u> </u>		GMALVREVNLISERKTKPAKVPLKCLAQEVNIPDWIVDLRHELT
l		•	HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR
}		1	EGIEEEDOEEDKNIVYDDITEOKPEPODDGKSTESDVKADGDSK
ļ	İ		GSEEVDSHCKKALSHKELYERARELLVSYBEEQFTVLEKFRYLP
1		}	KAIKAKNNPSPRVECVLABLKGVTCENREAVLDAFLDDGFLVPT
1			FEQLAALQIEYEENVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ
(	<b>[</b>	į	ALLERMLSELPALGISGIRPTYILRWTVBLIVANTKTGRNARRF
ł	ĺ		SAGOWEARRGWRLPNCSASLDWPRMVBSCLGSPCWASPOLLRII
l .	ļ	<u> </u>	F\KAMGQGLQDE\BQEKLLRICSIYTQSGENSLVQEGSEASPIG
	ì		KSPYTLDSLYNSVKPASSSFGSBAKAQQQEEQGSVNDVKBEEKB
ļ			BKEVLPDQVEEREKNDDQEEBEEDEDDBDDEBEDRMEVGPFSTG
İ	l .		QESPTAENARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR
1			SRPRTPARLMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL
	1	1	\SCCVGS\GNCSNSSSSNFRGAFLLBARGSLH\GL\KTGLQLF
6017	203	3469	SHQEIBQNSAMAPRKRGGRGISFIFCCFRNNDHPEITYRLRNDS
ł	}		NFALQTMEPALPMPPVEELDVMFSELVDRLDLTDKHREAMFALP
1	•	ļ	ARKKWQIYCSKKKDQEENKGATSWPEFYIDQLWSMAARKSLLAL
i		j	EKBEBERSKTIBSLKTALRTKPMRFVTRFIDLDGLSCILNFLK
,		ļ	TMDYBTSBSRIHTSLIGCIKALMNNSQGRAHVLAHSBSINVIAQ
Ì	ł		SLSTENIKTKVAVLBILGAVCLVPGGHKKVLQAMLHYQKYASER
Į.		į	TRFQTLINDLDKSTGRYRDEVSLKTAIMSFINAVLSQGAGVESL
ľ			DFRLHLRYE\FLMLGIHPVMDKLRKHENSTLDRHLDFFEMLRNE
	Į.		DELEFAKRPELVHIDTKSATOMPELTRKRLTHSEAYPHPMSILH
1	1	l	HCLOMPYKRSGNTVQYWLLLDRIIQQIVIQNDKGQDPDSTPLEN
į	l		FNIKNVVRMLVNENEVKQWKEQARKMRKEHNELQQKLBKKEREC
			DAKTQEKERMMQTLNKMKEKLEKETTEHKQVKQQVADLTAQLHE
1			LSRRAVCAS1PGGPSPGAPGGPFPSSVPGSLLPPPPPPPPLPGCM
1	1		LPPPPPPLPPGGPPPPPGPPPLGAIMPPPGAPMGLALKKKSIPQ
i	ţ	ł	PTNALKSFNWSKLPENKLEGTVWTEIDOTKVFKILDLEDLERTF
1			SAYQRQQDFFVNSNSKQKEADAIDDTLSSKLKVKELSVIDGRRA
1	l		QNCNILLSRLKLSNDEIKRAILTMDEQEDLPKDMLEQLLKFVPE
i		<b>[</b>	KSDIDLLEEHKHELDRMAKADRFLFEMSRINHYQQRLQSLYFKK
ł	Į.	ĺ	KPABRVAEVKPKVEAIRSGSEEVFRSGALKQLLEVVLAFGNYMN KGQRGNAYGFKISSINKIADTKSSIDKNITLLHYLITIVENKYP
	1		SVLNINEBLRDIPOAAKVNMTELDKEISTLRSGLKAVETELEYO
į	į	[	KSOPPOPGDKFVSVVSOFITVASFSFSDVEDLLARAKDLFTKAV
ł			KHFGERAGKIQPDEFFGIFDQFLQAVSEAKQENENMRKKKEEBE
l	l		RRARMEAQLKEQRERERKMRKAKENSEESGEFDDLVSALRSGEV
1	1	I	PDKDLSKLKRNRKRITNOMTDSSRERPITKLNF
6018	13	2510	TISQSGGIRRRRAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY
1 3320	1		ALSSSYSSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD
l	I		GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV
ĺ	1	ſ	TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD
Į.	Į.	1	GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT
[		1	AHPAAPGPVSRVYSRDRNOKCDDCKGKRHLDAHPGRAGTLWHIW
1	1	l	ACAGYPLLOILRRIGAYGOAVSRTAWSALWLAVVAPGKAASGVF
1	1		WWLGJGWYQFVTLJSWLNVFLLTRCLRNICKFLVLLIPLFLLLG
í	i		LSLRGQG\NFFSPLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ
Ì	1	Ì	PLOGDSRAFPWHWMSGVEOQVASLSGQCHHHGENLRELTTLLQK
1		[	LOARVDOMEGGAAGPSASVRDAVGOPPRETDFMAFHQEHEVRMS
1	1	ł	HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL
1	1	ļ	ELDOLKSELSSWRHVKTGCETVDAVQERVDVQVRENVKLLFSED
1	1	]	OOGGSLEQLLQRPSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV
1	1	İ	TKOLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG
1	]		MVDFALBSGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR
ł	1	l	VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL
1	ì	Ì	SPTGNISSAPKDFAVYGLENEYQKEGQLLGQFTYDQDGESLQMF
1	ĺ	l	OALKREDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK
6019	1 2	1066	TPNDREPPPORPPSSRRASHLAGEITSAASLGDQTQILGSLTTA
	<u> </u>	·	<u> </u>

				13(
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide	1
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=	160
NO:	nucleotide location	location corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Isysine,	1
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,	
	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,	[
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,	Ì
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop	ļ
	amino acid	aequence	Codon, /=possible nucleotide deletion,	ĺ
	sequence		\=possible nucleotide insertion\ PVITSAIRSMPGISSOILTNAGGOVIGTLPWVVNSASVAAPAPA	ļ.
	•		QSLQVQAVTPOLLLNAQGQVIATLASSPLPPPVAVRK\PSTPES	i
	j	j	LLKSEVQPIKPTPTVPQPAVVIASPAPAAKPSASAPIPITCSET	1
			PTVSQLVSKPHTPSLDEDGINLEEIRBFAKNFKIRRLSLGLTQT	1
	1	1	QVGQALTATEGPAYSQSAICRFEKLDITPKSAQKLKPVLEKWLN	Ì
	1		EABLRNQEGQQNLMEFVGGEPSKKRKRRTSFTPQAIEALNAYFE	
		]	KNPLPTGQBITEIAKBLNYDREVVRVWFCNRRQTLKNTSKLNVF	
6025	4052		QIP	Į
6020	4953	549	BAIQPBVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW AHTKPVVTLTSYWBDISHRLDAVNTLLAMAERLQTNIBALKSGI	
	1		QGKIPANQLAELWLKLIDEVIEDTRYTLPLTRGKANVTVLDTQI	{
			RKLRSRSLSQIHEAAVRMRSEATDVKSTLAETEDWLDKLMQLTB	
	j		EPON9MPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC	
			GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAB	f
		ì	GTPTVFAEMYRNQALMFGKWGTSGLVGRHKFSDVTGK1KLKREF	ł
	I	Í	FLP2KGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNBSRYP	
	Ì		GGDWKPARDYYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD	Ì
	}	i	LTOTASSTAGAMEBLODOEGNEYASLIGWKFHNKURSSDTFRRR	
	}		RWRRKMAPSETHGAAAIPKLEGALGADTTEDGDEKSLEKQKHSA	l
	Ļ		TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP	
		İ	YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ	į
		1	NPPKVIMELPDNDQVGKDEFLGR8IFSPVVKLNSEMDITPKLLW	
		ŀ	HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP	
	1	ſ	QGIRPVVQLTAIBILAWGLRNMKNFQWASITSPSLVVBCGGERV BSVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ	}
			FGRKPVVGQCTIERLDRFRCDFYAGKEDIVPQLKASLLSAPPCR	
		ì	DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEERIV	
	ĺ		DWWSKFYASSGEHRKCGQYIQKGYSKLKIYNCELBNVARFEGLT	İ
	}	1	DFSDTFKLYRGKSDKNEDPSVVGRFKGSFRIYPLPDDPSVPAPP	].
	ţ	Į.	ROFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG	
**	1	ł	KKVIK\DRDHYIPNTLNPVFGRMYBLSCYLPQBKDLKISVYDYD TFTRDBKVGBTIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW	ļ
			RDSLR/PTQ/LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE	ĺ
	l		FEANKILHOHLGAPEERLALHILRTQGLVPEHVETRTIHSTFQP	ļ
	· ·	1	NIS/RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE	}
	1	İ	NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW	
	İ	1	SIDQTEFRIPPR\LIIQIW\DNDKYS\LDDYLGFPRTLTCRHTI	Ì
			HPLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGNW PCYARKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP	
		ĺ	KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL	
	į	į	LPVAVLLYSLPNYLSMKIVKPNV	
6021	4953	549	EAIOFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW	
		1	A:TKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTN1EALKSGI	
			QGKIPANQLABLWLKLIDBVIBDTRYTLPLTEGKANVTVLDTQI	
	}		RKLRSRSLSQTHEAAVRMRSEATDVKSTLABIEDWLDKLMQLTB	Ĭ
	ł	1	EPONSMPDIIIWMIRGEKRLAYARIPAHOVLYSTSGENASGKYC	
	Ì	1	GKTQTIFLKYPQEKNNGPKVPVBLRVNIWLGLSAVEKKFNSFAE GTFTVFAEMYBNQALMFGKWGTSGLVGRHKPSDVTGKIKLKREP	
	1	1	FLPPKGWEWEGRWIVDPERSLITEADAGHTEFIDEVYQNESRYP	
	1		GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR	
	[	l	AVDEKGWEYGITIPPDHKPKSWVAABKMYHTHRRRRLVRKRKKD	
	ĺ		LTQTASSTAGAMBELQDQEGWEYASLIGWKFHWKQRSSDTFRRR	
		Į.	RNRRKMAPSETHGAAAI FKLEGALGADTTEDGDEKSLEKQKHSA	
	1		TIVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLAIJKDSFSDP	
	<b> </b>		YAHICFLHRSKTTBIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ	
			NPPKVIMELFDNDQVGKDEFLGESIFSPVVKLNSEMDITPKLLW	
	<b>\</b>		HPVMNGDKACGDVLVTAKLILRGKDGSNLPILPPQRAPNLYMVP QGIRPVVQLTAIKILAWGLRNMKNFQMASITSPSLVVECGGKRV	
			BSVVIKNLKKTPNYPSSVLFMKVFLPKEBLYMPPLVIKVIDHRQ	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l .	to first		P=Proline, Q=Glutamine, R=Arginine,
1	•	amino acid	
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
<b>\</b>	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, / possible nucleotide deletion,
	sequence	ł	\=possible nucleotide insertion)
			DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEREIV
Į.		į .	DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT
1			DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
ŀ			ROFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
1			KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
ŀ			TFTRDEKVGBTIIDLENPF\LSRFG\SHCG\IPEBYCVSGVNTW
}		ì	RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
ľ			PRANKILHOHLGAPEERLALHILRIQGLVPEHVETRILESTFQP
1		<b>\</b>	<b>,</b>
l	i	i	NIS/RYYLRVIIWNTKDVILDBKSITGEBMSDIYVKGWIPGNBE
1	1	<u>,</u>	NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPARQLCIVAKKEHFW
I	I	1	SIDOTRFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
Į.	l	l	HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
1	1	ĺ	PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
1	1	1	KLDLPNRPBTSFLWFTNPCKTMKPIVWRRFKUVIIGLLFLLILL
1	1	l	LPVAVLLYSLPNYLSMKIVKPNV
6022	4953	549	EAIQFEVSIGNYGNKFUTTCKPLASTTQYSRAVFDGNYYYYLPW
1	}	ì	AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIRALKSGI
			QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
	}	1	RKLRSRSLSQIHEAAVRMRSBATDVKSTLARIEDWLDKIMQLTB
			EPONSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
<b>[</b>	•	<b>\</b>	GKTOTIFLKYPOEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
!		l	GTFTVFARMYENOALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
l			PLPPKGWEWEGEWIVDPKRSLLTRADAGHTEFTDKVYQNESRYP
į .	1		GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
ì			AVDEKGWEYGITI PPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
1	1	**	LTOTASSTAGAMEELODQEGWEYASLIGWKPHWKQRSSDTFRRR
1	}		RWRRKMAPSRTHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
1	<b>}</b>		TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
1	1	}	YAHICPLHRSKTTBIIHSTLNPTWDQTIIFDEVBIYGEPQTVLQ
	İ		NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
ļ.		ł	HPVMNGDKACGDVLVTAKLILRGKDGSNLPILPPQRAPNLYMVP
i	1.		QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV
ļ	į.		ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
I	1	}	FGRKPVVGQCTIRRLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
	Ĩ	Ĭ	DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEBBIV
	1		DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT
	1	1	DFSDTFKLYRGKSDENEDPSVVGKFKGSFRIYPLPDDPSVPAPP
1	1	1	RQFRBLPDSVPQBCTVRIYIVRGLELQPQDNNGLCDPYIKITLG
	ĺ	1	KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
1	1	1	TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
1	1	1	RDSLR\PTO\LLONVARPKGPPOPILSEDGSRIRYGGRDYSLDE
}	}	<b>!</b>	FEANKILHOHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP
I	1	•	NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
ļ	<b>{</b>	<b>.</b>	NKOKTOVHYRSLOGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
İ	<b>!</b> .	1	SIDQTEFRIPPR\LIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
1 .	1	l	
	1	1	HPLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFRQKSMKGWW
1	1	1	PCYAEKDGARVMAGKVEMTUBILNEKEADERPAGKGRDEPNMNP
ì	Ī	1	KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
	<u></u>	L	LFVAVLLYSLPNYLSMKIVKPNV
6023	102	916	SQELGMFVELNNLLNTTPDRAEQGKLTLLCDAKTDGSFLVHHPL
1	ĺ	}	SFYLKANCKVCFVALIQSFSHYSIVGQKLGVSLTMARERGQLVF
1	<u> </u>	1	LEGL/IVCSGR\VFQAQKEPHPLQFLREANAGNLKPLFEFVREA
l	1	1	LKPVDSGEARWTYPVLLVDDLSVLLSLGMGAVAVLDFIHYCRAT
[	§	[	VCWELKGMMVVLVHDSGDAEDEENDILLINGLSHQSHLTLRAEGL
l	1	1	ATGFCRDVHGQLRILWRRPSQPAVHRDQSFTYQYKIQDKSVSFF
i	i	Į.	AKCMSPAVL
6074	<del> </del>		
6024	3	3260	FLSFLCYPRFRCLFCLQFAIPASRMEQLNELELLMEKSPWREAE
1	1	i	LPAELFOKKVVASFPRTVLSTGMDNRYLVLAVNTVONKEGNCEK
Ī	l	1	RLVITASQSLENKELCILRNDWCSVPVEPGDIIHLEGDCTSDTW
1	1	<b>\</b>	IIDKDFGYLILYPDMLISGTSIASSIRCMRRAVLSETFRSSDPA
l	1	1	TROMLIGTVLHEVFOKAINNSFAPEKLOELAFOTIOBIRHLKEM
•	<del></del>	<u> </u>	· · · · · · · · · · · · · · · · · · ·

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
ì	1		The state of the s
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	веquence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	<u> </u>		YRLNISQDEIKQEVEDYLPSFCKWAGDFMHKNTSTDFPQMQLSL
			PSDNSKDNSTCNIEVVXPMDIEESIWSPRFGLKGKIDVTVGVKI
Į.			HRGYKTKYKIMPLELKTGKESNSIEHRSQVVLYTLLSQERRADP
	<u> </u>	[	BAGLLLYLKTGQMYPVPANHLDKRELLKLRNQMAFSLFHRISKS
ļ	İ		ATROKTQLASLPQ1IEEEKTCKYCSQIGNCALYSRAVEQQMDCS
1	}	Ĭ	SVPIVMLPKIERETQHLKQTHLEYFSLWCLMLTLESQSKDNKKN
l	}	ļ.	HONIWLMPASEMEKSGSCIGNLIRMEHVKIVCDGOYLHNFOCKH
1	ļ	Į	GAIPVINLMAGDRVIVSGEERSLFALSRGYVKEINMTTVTCLLD
J	<b>{</b>		RNLSVLPESTLFRLDQKEKNCDIDTPLGNLSKLMENTFVSKKLR
1		ł	DLIIDPRBPQFISYLSSVLPHDAKDTVACILKGLNKPQRQAMKK
1	1	ì	VLLSKDYTLIVGMPGTGKTTTICTLVRILYACGFSVLLTSYTHS
1	1	l	AVDNILLKLAKFKIGFLRSR\QIQKVHPAIQQFTEHBICRSKSI
		l	KS\LALLERLYTSQLIDATTCMGINHPIP6RKIPDFCIVDEASQ
1	1	1	ISOPICLGPLFFSRRFVLVGDHQQLPPLVLNRBARALGMSESLF
ļ	[	1	
1	1	Ì	KRLEQNKSAVVQLTVQYRMNSKIMSLSNKLTYEGKLECGSDKVA
1			NAVINLRHFKDVKLELBFYADYSDNPWLMGVFBPNNPVCFLNTD
1	(	[	RVPAPEQVERGGVSNVTEAKI.IVFLTSIFVKAGCSPSDIGIIAP
1 .	1	1	YRQQLKIINDLLARSIGMVBVNTVDKYQD\RDKSIVLVSFVRSN
	,	i	KDGTVGELLKDWRRINVAITRAKHKLILLGCVPSLNCYPPLEKL
1			LNHLNSEKLIIDLPSREHESLCHILGDFQRE
6025	3977	89	GGFPAQSDHLPPVFPLRSDLLITMSTLYVSPHPDAFPSLRALIA
{ .	1	<b>]</b>	ARYGEAGEGPGWGGAHPRICLQPPPTSRTSPPPPRLPALEQGPG
	l		GLWVWGATAVAQLLWPAGLGGPGGSRAAVLVQQWVSYADTELIP
	•		AACGATLPALGLRSSAQDPQAVLGALGRALSPLEEWLRLHTYLA
ì		Ì	GRAPTLADLAAVTALLLPFRYVLDPPARRIWNNVTRWFVTCVRQ
	l	ł	PEFRAVLGEVVLYSGARPLSHQPGPRAPALPKTAAQLKKRAKKR
l l	ļ		EKTBKFQQKQK1QQQQPPPGEKKPKPEKREKRDPGV1TYDI.PTP
1		1	PGEKKDVSGPMPDSYSPRYVEAAWYPWWEQQGFFKPEYGRPNVS
	<u> </u>	İ	AANPRGVFMMCIPPPNVTGSLHLGHALTNAIQDSLTRWHRMRGE
1	1	}	TTLWNPGCDHAGIATQVVVEKKLWREQGLSRHQLGREAFLQEVW
	ì		KWKBEKGDRIYHOLKKLGSSLDWDRACFTMDPKLSAAVTRAFVR
1		ł	LHEEGIIYRSTRLVNWSCTLNSAISDIEVDKKELTGRTLLSVPG
1			YKEKVEFGVLVSFAYKVQGSDSDREVVVATTRIETMLGDVAVAV
Į.		i .	HPKDTRYOHLKGKNVIHPFLSRSLPIVPDEFVDMDFGTGAVKIT
j	1	i	PAHDONDYEVGORHGLEAISIMDSRGALINVPPPFLGLPRFEAR
i			KAVLVALKERGLPRGIEDNPMVVPLCNRSKDVVBPLLRPOWYVR
1	1	}	CGEMAQAASAAVTRGDLRILPERHQRTWHAWMDNIRE\WCMPPG
	1	ĺ	KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYNVSGRNEABARE
1	1	Į.	KAAKEYGVSPDKISLQQDEDVLDTWPSSGLPPLSILGWPNQSED
1	1	j	LSVFYPGTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYLHA
Į.	1	i	IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS
1		İ	EVEKAKEGOKADFPAGIPECGTDALRPGL-CAYMSQGRDINLDVN
1	1		RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSOPGGHESLVDR
1	1	1	WIRSRLTEAVRLSNOGFOAYDFPAVTTAQYSFWLYKLCDVYLEC
i	1		LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTERLFQ
1			RLPRRMPOAPPSLCVTPYPEPSECSWKDPEARAALELALSITRA
1			
1	1	[	VRP\LRADYNIHPESGPTCFLEVAD\EATGALASAVSGYVQGPG
1	1	}	QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP
1	Į.	1	ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E
L	ļ	<u></u>	VQEADEAKLQQTEABLRKVDRAIALFQKML
6026	2674	514	GPITFLKKKAKMKDMPLRIHVLIGLAITTLVQAVDKKVDCPRLC
1		l	TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ
1	}	1	TNNIAKIBYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV
1	]	ł	YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN
1	Į.	ł.	LLRLHLMSNRLOMINSKNFDALPNLEILMIGENPIIRIKDMNFK
		1	PLINLRSLVIAGINLTBIPDNALVGLENLESISFYDNRLIKVPH
1		1	VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL
1		Ì	ISIDSLAVDNLPDLRKIRATNNPRLSYIHPNAFFRLPKLESLML
1		j	NSNALSALYHGTIBSLPNLKBISIHSNPIRCDCVIRWMNMNKTN
1	Į.	l .	IRFMEPDSLPCVDPPBFQGQNVRQVHPRDMMEICLPLIAPESFP
í			
1			SNLNVEAGSYVSFHCRATA\BPQPBIYWITPSGQKLLPNT\LTD

F GPO	Predicted	Predicted end	I hains post
SEO			Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
I	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
i .		Begaciico	
<u></u>	sequence	<u> </u>	\=possible nucleotide insertion)
	l	i	KFYVHSEGTLDINGVTPKEGGLYTCIATNLVGADLKSVMIKVDG
ł	i	i	SPPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFVK
]	Ī	l .	TENSHAAQSARIPSDVKVYNLTHLNPSTBYKICIDIPTIYQKNR
1	ì	]	
1	1	1	KKCVNVTTKGLHPDQKEYEKNNTTTLMACLGGLLGIIGVICLIS
1	1	1	CLSPRMNCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKS
į.	1		TSLKVKATVIGLPTNMS
6027	5254	4148	GGRRAPGRPGRSIKDBEBBTVFRBVVSFSPDPLPVRYYDKDTTK
6027	3234	37.30	•
j	1	1	PISFYLSSLEELLAWKPRLEDGFNVALEPLACROPPLSSORPRT
(	(		LLCHCMMGGYLDDRFIQGSVVQTPYAFYHWQCIDVFVYFSHRTV
1		l	TIPPVGWTNTAHRHGVCVLGTFITEWNEGGRLCRAFLAGDBRSY
	1	1	QAVADRLVQIT\RFFRFDGWLINIENSLSLAAVGNMPPFLRYLT
1	Ī	}	1 = '
1	1		TQLHRQVPGGLVLWYDSVVQSGQLKWQDBLNQHNRVFFDSCDGF
į.	Į.	Į.	PTNYNWREEHLERMLGQAGERRADVYVGVDVFARGNVVGGRFDT
1	ŀ	1	DKVGGGFRPRASGPVPPLGPHFLMDLPFPSAPQRNDSSCSSQSG
I	1	1	DPVALRNRCPAPAKLCPH
	<u> </u>		I
6028	120	3432	NCLLLQAKGPHGE1EDLQQWLTDTERHLLASKPLGGLPETAKEQ
Į.	i		LNVHMEVCAAFEAKEETYKSLMQKGQQMLARCPKSARTNIDQDI
ļ	1		NNLKEKWESVETKLNER\KT\KLEEALNLA\MBFHNSL\QDFIN
į .	ì		WLTOAROTLNVASRPSLILDTVLFOIDEHXVPANEVNSHREQII
i	1	í	
1	1		BLDKTGTHLKYFSQKQDVVLIKNLLISVQSRWBKVVQRLVERGR
1	Į.	l	SLDDARKRAKQFHEANSKLMEWLEESEKSLDSELBIANDPDKIK
ı	l	ł	TQLAQHKEFQKSLGAKHSVYDTTNRTGRSLKEKTSLADDNLKLD
1			DMLSELRDKWDTICGKSVERQNKLERA\LLFSGQFTDALQALID
1	1	ł	WLYRVEPOLARDOPVHGDIDLVMNLIDNHKAFOKELGKRTSSVO
ł	1	<b>[</b>	
l	(		ALKRSARBLIEGSRDDSSWVKVQMQELSTRWETVCALSISKQTR
ı	i	ĺ	LEAALRQAEEFHSVVHALLEWLARAEQTLRFHGVLPDDEDALRT
J	1		LIDOHKEFMKKLEEKRAELNKATTMGDTVLAICHPDSITTIKHW
ì	i	j	ITIIRARFEEVLAWAKOHOORLASALAGLIAKOELLRALLAWLO
ı		ł	WABITLIDKDKEVIPQBIEEVKALIAEHQTFMBEMTRKQPDVDK
l .	į ·	Į.	
} `	}	Ļ	VTKTYKRRAADPSSLQSHIPVLDKGRAGRKRFPASSLYPSGSQT
i	i		QIBTKNPRVNLLVSKWQQVWLLALERRRKLNDALDRLBELREFA
l	) ·	j	NFDFDIWRKKYMRWMNHKKSRVMDFFRRIDKDQDGKITRQEFID
į	}		GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYRFVAALHPNKDA
l	ŧ	( -	YKPITDADKIEDEVTROVAKCKCAKRFOVRQIGDNKYRFFLGNO
1	1	1	
	l .	j	FGDSQQLRLVRILRSTVMVRVGGGWMALDEFLVKNDPCRAKGRT
1	į.	ì	NMBLREKFILADGASQGMAAFRPRGRRSRPSSRGASPNRSTSVS
I	1		SQAAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA
ł	ļ	l	ECSDFPVPSARGTPIQGSKLRLPGYLSGKGFHSGEDSGLITTAA
I	1		ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE
l	ŀ		
I	1	i	IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK
Ī	Ì	1	LDKSSKR
6029	1	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM
-	Ī		AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD
	]		PNSCAGHOGLVDPIOFARANOAIOMACONLVDPGSSPSOVLSAA
ì	]	]	
l		1	TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANI.
i	<u> </u>		VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS
I	1		IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP
1		]	PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC
1	1	]	
Ī	[		IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP
1	1		IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM
I			TVLDQTKTLABSALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK
ļ.	ļ		EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG
Ì	]		I I
1	}		TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEBLGGLASQMTSD
į.	[		YGHLAFQGQMAAATAEPEBIGFQIRTRVQDLGHGCIFLVQKAG\
l .	l		ALOVCPTDSYTKRRLIBCARAVTBKVSLVLSALQAGNKGTQACI
I	}		TAATAVSGI LADLUTTIMFATAGTLNABNSETFADHRENILKTA
ì	1	}	
1	1	Î	KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA
ţ	ł		SIGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM
l	ł		YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALBATIECIKQ
1	Ī		BLTVFQSKDVPBKTSSPBBSIRMTKGITMATAKAVAAGNSCRQB
1	}		· ·
L	L	<u></u>	DVIATANLSRKAVSDMLTACKQASFHPDVSDBVRTRALRPGTEC

SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence		\=possible nucleotide insertion)
			TLGYLDLLERVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA
1			EAMKGTEWVDPRDPTVIAETBLLGAAASIEAAAKKLEOLKPRAK
	1	ļ	PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK
			VGSIPANAADDGOWSOGLISAARMVAAATSSLCEAANASVOGHA
I			SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV
1	İ		KRASDNLVRAADKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM
l	i		LKKERELERARKKLAQIRQQQYKVLPTRLREDEG
6030	3	1777	FPGRGSPALQLEVLICLGLMGLERALNVLAPIFYRNIVNLLTEN
1	<u> </u>		APWNSLAWTYTSYYPLKFLQGGGTGSTGFYSNLRTFLWIRVQQF
	Į.		TSRRVELLIFSHLHBLSLRWHLGRRTGEVLRIADRGTSSVTGLL
ł	ľ		SYLVENVIPTLADIIIGIIYFSMFFNAWFGLIVFLCMSLYLTLT
	1		IVVTEWRTKFRRAMNTQENATRARAVDSLLNFETVKYYNAESYB
1	1		VERYREALIKYQGLEWKSSASLVLLNQTQNLVIGLGLLAGSLLC
	I		AYFVTEQKLQVGDYVLFGTYIIQLYMPLNWFGTYYRMIQTNFID
	1		MENMFDLLKK\ZTEVKDLPGAGPFRFQKGRIEFENVHFSYADGR
			BTLQDVSFTVMPGQTLALVGPSGAGKSTILRLLFRFYDISSGCI
	l	'	RIDGQDISQVTQALFRFSHWELCPKDTVLFNDTIADNIRYGRVT
}	Ì		agndevraaaqaagihdaimafpegyrtqvgerglkisggekqr
Í			VAIARTILKAPGIILLDEATSALDTSNERAIQASLAKVCANRTT
		i	IVVAHRLSTVVNADQILVIKDGCIVERGRHEALLSRGGVYADMW
			OLOGGETSEDTKPOTMER
6031	160	1694	LRMSENLDKSNVNEAGKSKSNDSEEGLEDAVEGADRALQKAIKS
	[		DSSSPQRVQRPHSSPPRFVTVEELLETARGVTNMALAHEIVVNG
1	Í		DFQIKPVELPENSLKKRVKBIVHKAFNDCLSVQLSBDPPAYDHA
1			IKLVGEIKETLLSFLLPGHTRLRNQITEVLDLDLIKQBAENGAL
1	i i		DISKLAEFIIGMMGTLCAPARDEBVKKLKDIKEIVPLFREIFSV
İ			LDLMKVDMANFAISSIRPHLMQQSVEYERKKFQBILERQPNSLD
ļ	'		FVTQWLERASEDLMTQKYKHALPVGGMAAGSGDMPRLSPVAVQN
1			YAYLKULKWDHLQRPFPETVLMDQSRFHBLQLQ\REQLTILGAV
			LLVTFSMAAPGISSQADFAEKLKMIVKILLTDMHLPSFHLKDVL
			TTIGEKVCLEVSSCLSLCGSSPFTTDKETVLKGQIQAVASPDDP
ł			IRRIMESRILTFLETYLASGHQKPLPTVPCGLSPVQRELEEVAI
6032	39	2415	KFARLVNYNKMVFCPYYDAILSKILVRS
6032	33	2413	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE SCDRIKEEFQFLQAQYHSLKLECEKKLASEKTEMQRHYVMYYRMS
1			YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK
			OVIMAELNAIIGOOOLOAQHLSHGHGLPVPLTPHPSGLQPPAIP
			PIGSSAGLLALSSALGGOSHLPIKDEKKHHDNDHORDRDSIKSS
1.			SVSPSASFRGAEKHRNSADYSSESKKOKTEKKEIAARYDSDGEK
J	]		SDDNLVVDVSNKDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
1			ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
1			NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG
			MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAAYGRSPVVGPD
1			PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGOMQPVPPPPDAL
1			IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
l		!	DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL
<u> </u>			SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
			AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS
[			W\DLREGRQLQQHD/FFTSPVFSLGYCP\TBEWLAVGMBNSN\V
i			EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
			w/RTPYG/ASIP/QSKESSS/VLSCDI/SVDDKYIVTGS/GDK/
			RATVYEVIY
6033	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
1			SCDRIKERFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
			YGINIEMHKQAEIVERLNAICAQVIPFLSQEHQQQVVQAVERAK
			QVTMABLNAIIGOQOLQAQHLSHGHGLPVPLTPHPSGLQPPAIP
1			PIGSSAGLLALSSALGGQSHLPIKDRKKHHDNDHQRDRDSIKSS
			SVSPSASFRGAEKHRNSADYSSESKKQKTERKZIAARYDSDGEK
1			SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
			ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
			NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG

SEQ	Predicted	Predicted end	Amino paid coment contain
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidinc, I=Isoleucine, K=Lysine,
i	corresponding	to first	La Leucine, Mamethionine, Nasparagine,
ļ	to first	amino acid	Debugine, Memethionine, Neasparagine,
F	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			MNGBLTSPGAAYAGLHNISPQMSAAAAAAAAAAAYGRSPVVGFD
i		1	PHHIMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL
		1	IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
		}	DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGRASTL
1	Ì	Ì	SIWDLAAPTPRIKARLTSSAPACYALAISPDSKVCFSCCSDGNI
į.		f	AVWDLHNQTLVRQFQGHIDGASCIDISNDGTKLWTGGLDNTVRS
1			W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEBWLAVGMENSN\V
			EVLHVTKPDKYQLHLHESCVLSLKPAHCGKWF\VSTGKDNLLNA
1			W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\
			RATVYKVIY
6034	2683	714	ESGRRRLKRRRSPCPGTAGGPGETNPGPGACPRGPREEAAAAM
ì			EIAPQEAPPVPGADGDIEEAPARAGSPSPASPPADGRLKAAAKR
1			VTPPSDEDIVSGAVEPKDPWRHAQNVTVDEVIGAYKQACQKLNC
1		-	RQIPKLLRQLQEFTDLGHRLDCLDLKGEKLDYKTCRALBEVFKR
1			LQFKVVDLEQTNLDEDGASALFDMIEYYESATHLNISFNKHIGT
l .	·		RGWQAAAHMMRKTSCLQYL\DARNTPLLDHSAPFVARALRIRSS
1			LAVIHLENASISGRPIMLIATALKMNMNLRE:YL\ADNKLNGLO
			DSAQLGNLLKFNCSLQILDLRNNHVLDSGLAYICEGLKEORKGL
1			VTL\VLWNNQLTHTGMAFLGMTLPHTQSLETLNLGHNPIGNEGV
1			RHLKNGLISNRSVLRLGLASTKLTCEGAVAVAEFIAESPRLLRL
			DLRENEIKTGGLMALSLALKVNHSLLRLDLDREPKKRAVKSFIE
İ			TOKALLAEIQNGCKRNLVLAREREBKEQPPQLSASMPETTATEP
			QPDDEPAAGVQNGAPSPAPSPDSDSDSDSDGEEBEBEBEGERDET
			PSGAIDTRDTGSSEPQPPPRPPRSGPPLPNGLKPRFALALPPRP
			PPGPEVKGGSCGLEHELSCSKNEKELEELLLEASOBSGOBTL
6035	19	404	SVTYLGIILHKNTGALPADPVQLISQTPTPSTKQQLLSFLGMVG
			YFYLNIPGFAILTKPLCKLTKENLADAIDPKSFSHSSFRSLKTA
1	,		LENASTLALPDSSQPF\SLHTARVQGCVVEILTQGLGPLPV
6036	1745	356	LPDVEKLGRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLORN
[ ]			SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW
			VLRAALDSGAFQSVWVSTDHDEIBNVAKQFGAQVHRRSSEVSKD
1 -			SSTSLDAILEFLNYHNEVDIVGNIQATSPCLHPTDLOKVAEMIR
1			EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRROD
			WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV
			DIDWPIAEORVLRYGYFGKBKLKBIKLLVCNIDGCLTNGHIYVS
1 ' 1			GDQKBIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK
1 1			LDCKMEVSVSDKLAVVDBWRKEMGLCWKBVAYLGNEVSDEECLK
] [			RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IRBFAEHIC\LL
1 1			MBKGLINFMPKNRNLAVNIGEKK
6037	2936	1919	WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA
1			GGGPPRRHSVTLPSSKFRONQLLSSLKGEPAPALSSRDSRFRDR
1 1	ł		SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG
1 1			DKCQPAHGIHKLRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI
	1		HNARERRALAGARDLSADRPRLQHSPSFAGFPSAAATAAATGLL
1 1	i		DSPTSITPPPILSADDLLGSPTLPDGTNNPP\AFSSQELASLFA
]	l		PSMOLPGGGSPTTFLFRPMSBSPHMFDSPPSPQDSLSDQEGYLS
			SSSSHSGSDSPTIDNSRRLPIFSRLSISDD
6038	1450	426	
"""	7470	340	SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH
[		1	YKGTKHAKKLKALRAMKNKQKSVTAKDSAKTTFTSITTNTINTS
[ ]	1		SDKTDGTAGTPAISTTTTVBIRKSSVMTTEITSKVBKSPTTATG
1 !	1	ł	NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLBAHNSGTKHK
1	!		TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLQNKTFHCBICD
	1		VHVNSBTQLKQHISSRRHKDRAAGKPPKPKYSPYNKLQKTAHPL
	Ì		GVKLVFSKBPSKPLAPRILPNPLAAAAAAAAVAVSSPPSLRTAP
<u> </u>			AATLFQTSALPPALLKPAPGPIRTAHTPVLFAPY
6039	4073	1000	LDEYEARLTLANLDDFREDNEDDDENRVNOREKAAKITELINKL
	,	•	NFLDEAEKDLATVNSNPFDDPDAAELNPFGDPDSEEPITETASP
[		ì	RKTEDSFYNNSYNPFKEVQTPQYLNPFDEPEAFVTIKDSPPQST
		ļ	KKKNIRPVDMSKYLYADSSKTEBEELDESNPPYBPKSTPPPNNL
L		i	VNPVQBLETERRVKRKAPAPPVLSPKTGVLNENTVSAGKDLSTS

C	T	Predicted end	
SEQ	Predicted		Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\-possible nucleotide insertion)
			PKPSPIPSPVLGRKPNASQSLLVWCKEVTKNYRGVKI1WFTTSW
)	1	1	RNGLSFCAILHHFRPDLIDYKSLNPODIKENNKKAYDGFASIGI
I	i e	]	SRLDEPSDMVLLAIPDKLTVMTYLYQIRAHFSGQBLNVVQIEEN
(	ł .	{ ·	
i	!		SSKSTYKVGNYETDTNSSVDQEKFYAELSDLKREPELQQPISGA
i	1 .	i	VDFLSQDDSVFVNDSGVGESESEHQTPDDHLSPSTASPYCRRTK
1	i	<b>\$</b>	SDTEPQKSQQSSGRTSGSDDPGICSNTDSTQAQVLLGKKRLLKA
i .	ŀ	1	BTLELSDLYVSDKKKDMSPPFICEETDEQKLQTLDIGSNLEKEK
<b>!</b> .			LENSRSLECRSDPESPIKKTSLSPTSKLGYSYSRDLDLAKKKHA
1	}	}	SLROTESDPDADRTTLNHADHSSKIVOHRLLSROKELKERARVL
1	1	Ī	LBOARRDAALKAGNKHNTNTAAPFCNRQLSDQQDEBRRRQLRER
1	l	į	
i	1	ŀ	ARQLIAEARSGGKMSBLPSYGERAAKKLKBRSKASGDENDNIBI
j :	1	ſ	DINEEIPEGFVVGGGDELTNLENDLDTPRQNSKLVDLKLKKLLE
1	l	į.	VQPQVANSPSSAAQKAVTESSEQDMKSGTEDLRTERLQKTTERF
1	1	l	RNPVVFSKDSTVRKTQLQSFSQYIENRPEMKRQRSIQEDTKKGN
1	1	Í	EEKAAITETORKPSEDEVLNKGPKDS\SOYVVGELAALENEOKO
1	}	}	IDTRAALVEKRLRYLMDTGRNTEEBEAMMOEWFMLVNKKNALIR
1		1	RYNOLSILEKEHDLERRYELLNRELRAMLATEDWOKTRAOKRRE
Į.	l	,	l "
ł	}		QLLLDE_VALVNKRDALVRDI DAQEKQAEEEDEHLERTLEQNKG
			KMAKKBEKCVLQ
6040	475	1052	PTALMTAPSCAFPVQFRQPSVSGLSQITKSLYISNGVAANNKLM
1	İ		LSSNQITMVINVSVEVVNTLYEDIQYMQVPVADSPNSRLCDFFD
1	<u> </u>	į	PIADHIHSVEMKQGR\TLLHCAAGVSRSAALCLAYLMKYHAMSL
1	1		LDAHTWTKSCRPIIRPNSGFWEQLTHYEFQLFGKNTVHMVSSPV
1	j		GMIPDIYEKEVRLMIPL
6041	2	3886	TEKDEKTAHNLENVLIHFWERLSEICVAKISEPEADVESVLGVS
8041	1 2	3000	· · · · · · · · · · · · · · · · · · ·
1	i	1	NLICVLQKPKGSLKSSKKKNGKVRFADEILESNKENEKCVSSEG
	1	}	BKIECWELTTEPSLTHNSSGLLSPLRKKPLEDLVCKLADISINY
		ļ	VNERKSEQHIRFLSTLLDSFSSSRVFKMLLGDEKQSIVQAKPLE
	<b>!</b>	:	IAKLVQKNPAVQFLYQKLIGWLNEDQRKDFGFLVDILYSALRCC
ı	1		
		l	DNDMERKKVLDDLTKVDLKWNSLLKIIEKACPSSDKHALVTPWL
			1
			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ
			KGDIIGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEABSSDSSVSFIC
			KGDIIGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEAESSDSSVSFIC DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAQSKEKTHLPDFLI
·			KGDIIGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEAESSDSSVSFIC DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAQSKEKTHLPDFLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL
			KGDIIGEKLVNIADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEAESSDSSVSFIC DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAQSKEKTHLPDFLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWEK
·			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDYYVERIIVRLHETLEKTKKLSEABSSDSSVSFIC DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAQSKEKTHLPDFLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDYKEQDIRTLPSHLCT
			KGDIIGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEABSSDSSVSFIC DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAGSKEKTHLPDFLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPMDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIKTLPSHLCT SALLSKMVLIALRKETVLKNNELEKTIAELLYSLQWCEKIDNPP
			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDYYVERIIVRLHETLEKTKKLSEABSSDSSVSFIC DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAQSKEKTHLPDFLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDYKEQDIRTLPSHLCT
			KGDIIGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEABSSDSSVSFIC DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAGSKEKTHLPDFLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPMDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIKTLPSHLCT SALLSKMVLIALRKETVLKNNELEKTIAELLYSLQWCEKIDNPP
			KGDIIGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEABSSDSSVSFIC DVAXNYFSSAKGCLLMPSSEDLLLTLFQLCAGSKEKTHLPDFLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGELSLNYBCFKTDFKEDDIKTLPSHLCT SALLSKMVLIALRKETVLKNNELBKTIAELLYSLQWCEBLDNPP IFLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW
			KGDIIGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEARSSDSSVSFIC DVAINYFSSAKGCLIMPSSEDLLLTLFQLCAQSKEKTHLPDFLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIKTLPSHLCT SALLSKMVLIALRKETVLKNNELBKIIAELLYSLQWCEBLIDNPP IFLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ
			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDYYVERIIVRLHETLFKTKKLSEABSSDSSVSFIC DVAYNYFSSAKGCLLMPSSEDLLTLFQLCAQSKEKTHLPDFLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIRTLPSHLCT SALLSKMVLTALRKETVLKNNELBKTIAELLYSLQWCEBLDNPP IFLIGFCEILQKMNITYDNLRVLGMMSGLLLLFNRSEHGTLW SLIIAKLLSRSISSDEVKPHYKRKESFPPLTEGNLHTIQSLCP FLSKEKKBFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGRLLHGILKTIISWKKEHRDIFLFSCNLSEASPBVLGV
			KGDIIGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRLHETLEKTKKLSEABSSDSSVSFIC DVAYNYPSSAKGCLLMPSSEDLLLTLEGLCAGSKEKTHLPDPLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDYKEQDIKTLPSHLCT SALLSKMVLIALRKETVLKNNELEKTIAELLYSLQWCEBLDNPP IFLIGFCEILOKMNITYDNLRVLGMMSGLLGLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEKKBFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGRLLHGILKIISWKKEREDIFLFSCNLSBASPEVLCV NIBIIRFLSLFLKYCSSPLABSENDFIMCSMLAWLETTSENQAL
			KGDIIGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEARSSDSVSFIC DVAXNYFSSAKGCLLMBSSEDLLLTLFQLCAQSKEKTHLPDFLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWEK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEDDIRTLPSHLCT SALLSKMVLIALRKETVLENNELEKTIAELLYSLQWCEBLDNPP IFLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRRESFFPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTMSGFGHLAIFNSCLQ TKSIDDGRLLHGILKIIISWKKEHRDIFLFSCNLSRASPEVLGV NIBIIRFLSLFIKYCSSPLABSEWDFMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFPDSTTLDTIGNLPVNLISEWK
			KGDIIGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEARSSDSSVSFIC DVAYNYFSSAKGCLIMPSSEDLLLTLFQLCAQSKEKTHLPDFLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEDDIKTLPSHLCT SALLSKMVLIALRKETVLENNELEKTIAELLYSLQWCEBLDNPP IFLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRRESFFPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTMGGFGHLAIFNSCLQ TKSIDDGBLLHGILKTIISNKKEHRDIFLFSCNLSRASFBVLGV NIBIIRFLSLFIKYCSSPLABSEWDFTMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCETLTY
			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDYYVERIIVRIHETLFKTKKLSEABSSDSSVSFIC DVAYNYFSAKGCLLMPSSEDLLTLFQLCAQSKEKTHLPDFLI CKLKNTWLSGVMLLVHQTDSSYKESTPLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIRTLPSHLCT SALLSKMVLIALRKETVLENNELERIIAELLYSLQWCEBIDNPP IFLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRRESFFPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGELLHGILKIIISWKKEHRDIFLFSCNLSRASPEVLGV NIBIIRFLSLFLKYCSSFLABSEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFPDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKFMCSTLTY ISKEQLLSHKLPARLVADQKTNLPEYLQTILNTLAPLLLFRARP
			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDYYVERIIVRLHETLFKTKKLSEABSSDSSVSFIC DVAYNYFSSAKGCLLMPSSEDLLTLFQLCAQSKEKTHLPDFLI CKLKNTWLSGVWLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIRTLPSHLCT SALLSKMVLIALRKETVLKNNELBKTIAELLYSLQWCEBLDNPP IFLIGFCEILQKMNITYDNLRVLGMMSGLLLFNRSEHGTLW SLIIAKLLSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGBLLHGILKTIISWKKEHRDIFLFSCNLSEASPEVLGV NIBIIRFLSLFLKYCSSPLABSENDFTMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLLPILVTVTGENKDVSBTSFQNAMLKPMCSTLTY ISBEQLLSHKLPARLVADQKTNLPEYLQTTLINTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDBEEEPALSPPAALMS
			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDYYVERIIVRIHETLFKTKKLSEABSSDSSVSFIC DVAYNYFSAKGCLLMPSSEDLLTLFQLCAQSKEKTHLPDFLI CKLKNTWLSGVMLLVHQTDSSYKESTPLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIRTLPSHLCT SALLSKMVLIALRKETVLENNELERIIAELLYSLQWCEBIDNPP IFLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRRESFFPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGELLHGILKIIISWKKEHRDIFLFSCNLSRASPEVLGV NIBIIRFLSLFLKYCSSFLABSEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFPDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKFMCSTLTY ISKEQLLSHKLPARLVADQKTNLPEYLQTILNTLAPLLLFRARP
			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDYYVERIIVRLHETLFKTKKLSEABSSDSSVSFIC DVAYNYFSSAKGCLLMPSSEDLLTLFQLCAQSKEKTHLPDFLI CKLKNTWLSGVWLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIRTLPSHLCT SALLSKMVLIALRKETVLKNNELBKTIAELLYSLQWCEBLDNPP IFLIGFCEILQKMNITYDNLRVLGMMSGLLLFNRSEHGTLW SLIIAKLLSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGBLLHGILKTIISWKKEHRDIFLFSCNLSEASPEVLGV NIBIIRFLSLFLKYCSSPLABSENDFTMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLLPILVTVTGENKDVSBTSFQNAMLKPMCSTLTY ISBEQLLSHKLPARLVADQKTNLPEYLQTTLINTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDBEEEPALSPPAALMS
			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRIHETLEKTKKLSEABSSDSSVSFIC DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAGSKEKTHLPDPLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDYKEQDIKTLPSHLCT SALLSKMVLIALRKETVLKNNELEKTIAELLYSLQWCEBLDNPP IFLIGFCEILOKMNITYDNLRVLGMMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEKKBFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGRLLHGHIKIIISWKKENEDIFLFSCNLSBASPEVLGV NIBIIRFLSLFLKYCSSPLABSENDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVMLISEWK EFFSQGIHSLLIPILVTVTGENKDVSETSFQNAMLKPMCETLTY ISKEQLLSHKLPARLVADQKTNLPEYLQTILNTLAPLLLFRARP VQIAVYHMLYKLMPELPQVDQDNLKSYGDEBEBPALSFPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI
			KGDIIGEKLVNIADCLCNEDLESRVSSESHFSERWTILSLVLSQ HVKNDYLIGDVYVERIIVRIHETLFKTKKLSEARSSDSSVSFIC DVAYNYFSAKGCLIMPSSEDLLITLFQLCAGSKEKTHLPDFLI CKLKNTWLSGVNILLVHQTDSSYKESTFIHLSALWLKNQVQASSL DINSLQVILSAVDDILNTILESEDSYLMGVYIGSVMPMDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIKTLPSHLCT SALLSKMVLIALRKETVLENNELEKTIAELLYSLQWCEBIDNPP IFLIGFCEILQKMNITYDNLRVIGMMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRESFFPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTMSGFGHLAIFNSCLQ TKSIDDGRLLHGILKTITSWKKEHRDIFLFSCNLSRASPEVLGV NIBIIRFLSLFLKYCSSPLABSEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFPDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCSTLTY ISKEQLLSHKLPARLVADQKTNLPEYLGTLLNTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDBEEEPALSPPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGVILTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAK TAVEVPNKDPKTPFTEBLQLSIRETTMLPYHIPHLACSVYHMTL
		•	KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDYYVERIIVRIHETLFKTKKLSEABSSDSSVSFIC DVAYNYFSAKGCLLMPSSEDLLTLFQLCAQSKEKTHLPDFLI CKLKNTWLSGVMLLVHQTDSSYKESTPLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIRTLPSHLCT SALLSKMVLIALRKBTVLENNBLERTIAELLYSLQWCEBLDNPP IFLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGRLLHGILKTITSWKKEHRDIFLFSCNLSRASPEVLGV NIBIIRFLSLFLKYCSSPLABSBWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK BFFSQGIHSLLIPILVTVTGENKDVSETSFQNAMLKEMCETLTY ISKEQLLSHKLPARLVADQKTNLPEYLQTILNTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDBEBEPALSFPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLL LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAK TAVEVPNKDPRTPFTBELQLSIRBTTMLPYHIPHLACSVYHMTL KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSPQBISSVQT
			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDYYVERIIVRIHETLFKTKKLSEABSSDSSVSFIC DVAYNYFSAKGCLLMPSSEDLLTLFQLCAGSKEKTHLPDFLI CKLKNTWLSGVWLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDYKEQDIKTLPSHLCT SALLSKMVLIALRKETVLKNNELBKIIAELLYSLQWCEBLDNPP IFLIGFCEILQKMNITYDNLRVLGMMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTMGGFGHLAIFNSCLQ TKSIDDGELLHGILKIIISWKKEHRDIFLFSCNLSEASPEVLGV NIBIIRFLSLFLKYCSSPLABSENDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK BFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCETLTY ISKEQLLSHKLPARLVADQKTNLPFYLQTILNTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDBEEEPALSPPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAR TAVEVPNKDPKTPFTBELQLSIRBTTWLPYHIPHLACSVYHMTL KDLPAMVRLWWNSSEKRVNIVDRFTSKYVSSVLSFQBISSVQT STQLFNGMTVKARATTREVMATYTIRDIVIBLIIQLPSNYPLGS
			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDYYVERIIVRIHETLFKTKKLSEABSSDSSVSFIC DVAYNYFSAKGCLLMPSSEDLLLTLFQLCAGSKEKTHLPDFLI CKLKNTWLSGVWLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIRTLPSHLCT SALLSKMVLIALRKETVLKNNELEKTIAELLYSLQWCERLDNPP IFLIGFCEILQKMNITYDNLRVLGMMSGLJLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGELLHGILKIIISWKKEHRDIFLFSCNLSEASPEVLGV NIBIIRFLSLFLKYCSSPLABSBNDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLFWNLISEWK EFFSQGIHSLLIPILVTVTGENKDVSETSFQNAMLKPMCETLTY ISKEQLLSHKLPARLVADQKTNLPSYLQTILINTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDBEEEPALSPPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSOLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAR TAVEVPNKDPKTPFTBELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWMNSSEKRVWNIVDRFTSKYVSSVLSFQBISSVQT STOLFNGMTVKARATTREVMATYTTRDIVIKLIIQLPSNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN
			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRIHETLEKTKKLSEABSSDSSVSFIC DVAYNYPSSAKGCLLMPSSEDLLLTLEGLCAGSKEKTHLPDPLI CKLKNTWLSGVWLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDYKEQDIKTLPSHLCT SALLSKMVLTALRKETVLKNNELEKTIAELLYSLQWCEBLDNPP IFLIGFCEILQKMNITYDNLRVLGKMSGLIQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFPPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALIGWTKKDLCSTNGGFGHLATFNSCLQ TKSIDDGRLLHGILKTIISWKKEHRDIFLFSCNLSBASPEVLGV NIBIIRFLSLFLKYCSSPLABSEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLIPILVTVTGENKDVSETSFQNAMLKPMCETLTY USLAYHMLYKLMPELPQTQDQDNLKSYGDBEEEPALSFPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAR TAVEVPNKDPKTFPTBELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWMNSSEKRVFNIVDRFTSKYVSSVLSFQBISSVQT STQLFNGMTVKARATTREVWATYTTRDIVIBLIQLPSNYPLGS ITVESGKRVGVAVQQWRNWMLQLSTYLTHQMGSIMEGLALWKNN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY
			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDYYVERIIVRIHETLFKTKKLSEABSSDSSVSFIC DVAYNYFSAKGCLLMPSSEDLLLTLFQLCAGSKEKTHLPDFLI CKLKNTWLSGVWLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIRTLPSHLCT SALLSKMVLIALRKETVLKNNELEKTIAELLYSLQWCERLDNPP IFLIGFCEILQKMNITYDNLRVLGMMSGLJLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGELLHGILKIIISWKKEHRDIFLFSCNLSEASPEVLGV NIBIIRFLSLFLKYCSSPLABSBNDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLFWNLISEWK EFFSQGIHSLLIPILVTVTGENKDVSETSFQNAMLKPMCETLTY ISKEQLLSHKLPARLVADQKTNLPSYLQTILINTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDBEEEPALSPPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSOLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAR TAVEVPNKDPKTPFTBELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWMNSSEKRVWNIVDRFTSKYVSSVLSFQBISSVQT STOLFNGMTVKARATTREVMATYTTRDIVIKLIIQLPSNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN
6042	1306	253	KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRIHETLFKTKKLSEABSSDSSVSFIC DVAYNYFSAKGCLLMPSSBDLLLTLFQLCAGSKEKTHLPDFLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKBQDIKTLPSHLCT SALLSKMVLIALRKETVLKNNELEKTIAELLYSLQWCEBLDNPP IFLIGFCEILOKMNITYDNLRVLGMMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDBVKPHYKRKESFFPLTEGNLFTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGRLLHGHILKIIISWKKENEDIFLFSCNLSBASPBVLGV NIBIIRFLSLFLKYCSSPLABSENDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVMLISEWK EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCETLTY ISKEQLLSHKLPARLVADQKTNLPBYLGTLLNTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDEBEBPALSFPAALMS LLSIQBDLENVLGCIPYGGIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAB TAVEVPNKDPKTPFTEBLQLSIRETTMLPYHIPHLACSVYHMTL KOLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQBISSVQT STQLFNGMTVKARATTREVMATYTIRDIVIBLIIQLPSNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQMGSIMEGLALWKNN VDKRFEGVEDCMICFSVLHGFNYSLPKKACRTCKKKFHSA\CLY
6042	1306	253	KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDYYVERIIVRIHETLFKTKKLSEARSSDSSVSFIC DVAYNYFSAKGCLLMPSSEDLLTLFQLCAQSKEKTHLPDFLI CKLKNTWLSGVMLLVHQTDSSYKESTPLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGYYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIRTLPSHLCT SALLSKMVLIALRKETVLENNELERIIAELLYSLQWCEBLDNPP IFLIGFCEILQKMNITYDNLRVLGMMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRRESFFPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTMGGFGHLAIFNSCLQ TKSIDDGRLLHGILKIIISWKEHRDIFLFSCNLSRASPEVLGV NIBIIRFLSLFLKYCSSPLABSEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK BFFSQGIHSLLIPILVTVTGENKDVSETSFQNAMLKFMCETLTY ISKEQLLSHKLPARLVADQKTNLPEYLQTILNTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDBEEPPALSPPAALMS LLSIQEDLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAK TAVEVPNKDPKTFFTBELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSPQBISSVQT STOLFNGMTVKARATTREVMATYTIRDIVIBLIIQLESNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSSNKSTCSLCRETFF MARLAPASSPDIKASVSNGDTTLLCSKRQSCGMNEVRQVSLTYP
6042	1306	253	KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDYYVERIIVRIHETLFKTKKLSEABSSDSSVSFIC DVAYNYFSAKGCLLMPSSEDLLTLFQLCAQSKEKTHLPDFLI CKLKNTWLSGVMLLVHQTDSSYKESTPLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGYVIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIRTLPSHLCT SALLSKMVLIALRKETVLENNELBRITAELLYSLQWCEBLDNPP IFLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW SLIIKKLILSRSISSDEVKPHYKRRESFFPLREGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTMGGFGHLAIFNSCLQ TKSIDDGBLLHGILKIIISWKKEHRDIFLFSCNLSRASPBVLGV NIBIIRFLSLFLKYCSSPLABSBWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAPFDSTTLDTIGNLPVNLISEWK EFFSGGIHSLLLPILVTVTGENKDVSETSFQNAMLXPMCSTLTY ISKEQLLSHKLPARLVADQKTNLPEYLQTTLNTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDEEEPALSPPAALMS LLSIQBDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFPRLMPENPTYAB TAVEVPNKDPKTPFTBELQLSIRBTTMLPYHIPHLACSVYHMTL KDLPAMVRLWWNSSEKRVNIVDRPTSKYVSSVLSFQBISSVQT STQLFNGMTVKARATTREVMATYTIRDIVIBLIIQLPSNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQMGSIMEGLALWKNN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSSNKSTCSLCRETFF MARLAPASPSDIKASVENGDTTLLCSKRQSCGMNEVRQVSLTYP GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY
6042	1306	253	KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDYYVERIIVRIHETLFKTKKLSEABSSDSSVSFIC DVAYNYFSAKGCLLMPSSEDLLTLFQLCAGSKEKTHLPDFLI CKLKNTWLSGVWLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIRTLPSHLCT SALLSKMVLTALRKETVLKNNELBKIIAELLYSLQWCEBLDNPP IFLIGFCEILQKMNITYDNLRVLGMMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFPPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGRLLHGILKIIISWKKEHRDIFLPSCNLSEASPEVLGV NIBIIRFLSLFLKYCSSPLABSENDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFPDSTTLDTIGNLPVULISEWK BFFSQGLISLLLPILVTVTGENKDVSETSFQNAMLKPMCSTLTY ISBEQLLSHKLPARLVADQKTNLPEYLQTILINTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDBEEEPALSPPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAL KDLPAMVRLWWNSSEKRVWNIVDRFTSKYVSSVLSFDGISSVQT STQLFNGMTVKARATTREVMATYTIRDIVIBLIIQLPSNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQMGSIMEGLALWKNN VDKRPEGVEDCMICFSVLHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSSNKSTCSLCRETFF MARLAPASPSDIKASVSNGDTTLLCSKRQSCGMNEVRQVSLTYP GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKB
6042	1306	253	KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDYYVERIIVRIHETLFKTKKLSEABSSDSSVSFIC DVAYNYPSSAKGCLLMPSSEDLLLTLFQLCAGSKEKTHLPDPLI CKLKNTWLSGVWLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDYKEQDIKTLPSHLCT SALLSKMVLIALRKETVLKNNELEKTIAELLYSLQWCSELDNPP IFLIGFCEILQKMNITYDNLRVLGMMSGLLQLLFNRSEHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGELLHGILKIIISWKKEHRDIFLPSCNLSEASPEVLGV NIBIIRFLSLFLKYCSSPLABSBNDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLIPILVTVTGENKDVSETSFQNAMLKPMCETLTY ISKEQLLSHKLPARLVADQKTNLPSYLQTILINTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDBEEEPALSPPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSOLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAR TAVEVPNKDPKTPFTBELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWMNSSEKRVFNIVDRFTSKYVSSVLSFQBISSVQT STQLFNGMTVKARATTREVMATYTTRDIVIKLIIQLPSNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSSNKSTCSLCRETFF MAELAPASPSDIKASVSNGDTTLLCSERQSCGMNEVRQVSLTYP GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTTSAQSRGY GARAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKB LVDKNIDRPIPITKLKYYFAVDTMYVGRKLGLLFPPYLHQDWEV
6042	1306	253	KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRIHETLEKTKKLSEABSSDSSVFIC DVAYNYPSARGCLLMPSSEDLLLTLEGLGAGKEKHHLPDPLI CKLKNTWLSGVWLLVHQTDSSYKESTPLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDYKEQDIKTLPSHLCT SALLSKMVLTALRKETVLKNNELEKTIAELLYSLQWCEBLDNPP IFLIGFCEILQKMNITYDNLRVLGMMSGLIQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFPPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALIGWTKKDLCSTNGGFGHLATFNSCLQ TKSIDDGRLLHGILKTIISWKKEHRDIFLFSCNLSBASPEVLGV NIBIIRFLSLFLKYCSSPLABSEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLIPILVTVTGENKDVSETSFQNAMLKPMCETLTY USLAYHMLYKLMPELPQTQDQDNLKSYGDBEEEPALSFPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAK TAVEVPNKDPKTPFTBELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQBISSVQT STQLFNGMTVKARATTREVWATYTTRDIVIBLIQLPSNYPLGS ITVESGKRVGVAVQOWRNWMLQLSTYLTHQMGSIMEGLALWKNN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSNKSTCSLCRETFF MARIAPASPSDIKASVSNGDTTLLCSKRQSCGMNEVRQVSLTYP GSPAPSHSLPLQPRSGGSLCPSRAM/PDPHQLFDDTSSAQSRGY GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKB LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV QYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQDRFS
6042	1306	253	KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDYYVERIIVRIHETLFKTKKLSEABSSDSSVSFIC DVAYNYPSSAKGCLLMPSSEDLLLTLFQLCAGSKEKTHLPDPLI CKLKNTWLSGVWLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDYKEQDIKTLPSHLCT SALLSKMVLIALRKETVLKNNELEKTIAELLYSLQWCSELDNPP IFLIGFCEILQKMNITYDNLRVLGMMSGLLQLLFNRSEHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGELLHGILKIIISWKKEHRDIFLPSCNLSEASPEVLGV NIBIIRFLSLFLKYCSSPLABSBNDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLIPILVTVTGENKDVSETSFQNAMLKPMCETLTY ISKEQLLSHKLPARLVADQKTNLPSYLQTILINTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDBEEEPALSPPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSOLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAR TAVEVPNKDPKTPFTBELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWMNSSEKRVFNIVDRFTSKYVSSVLSFQBISSVQT STQLFNGMTVKARATTREVMATYTTRDIVIKLIIQLPSNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSSNKSTCSLCRETFF MAELAPASPSDIKASVSNGDTTLLCSERQSCGMNEVRQVSLTYP GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTTSAQSRGY GARAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKB LVDKNIDRPIPITKLKYYFAVDTMYVGRKLGLLFPPYLHQDWEV
6042	1306	253	KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRIHETLEKTKKLSEABSSDSSVFIC DVAYNYPSARGCLLMPSSEDLLLTLEGLGAGKEKHHLPDPLI CKLKNTWLSGVWLLVHQTDSSYKESTPLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWBK MRQSLPMQWLHRPLLEGRLSLNYECFKTDYKEQDIKTLPSHLCT SALLSKMVLTALRKETVLKNNELEKTIAELLYSLQWCEBLDNPP IFLIGFCEILQKMNITYDNLRVLGMMSGLIQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFPPLTEGNLHTIQSLCP FLSKEEKKBFSAQCIPALIGWTKKDLCSTNGGFGHLATFNSCLQ TKSIDDGRLLHGILKTIISWKKEHRDIFLFSCNLSBASPEVLGV NIBIIRFLSLFLKYCSSPLABSEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLIPILVTVTGENKDVSETSFQNAMLKPMCETLTY USLAYHMLYKLMPELPQTQDQDNLKSYGDBEEEPALSFPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAK TAVEVPNKDPKTPFTBELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQBISSVQT STQLFNGMTVKARATTREVWATYTTRDIVIBLIQLPSNYPLGS ITVESGKRVGVAVQOWRNWMLQLSTYLTHQMGSIMEGLALWKNN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSNKSTCSLCRETFF MARIAPASPSDIKASVSNGDTTLLCSKRQSCGMNEVRQVSLTYP GSPAPSHSLPLQPRSGGSLCPSRAM/PDPHQLFDDTSSAQSRGY GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKB LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV QYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQDRFS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
{	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	amino acid	sequence	Codon, /-possible nucleotide deletion,
ł	sequence	ocquence	\=possible nucleotide insertion)
<b></b>	Sequence		ILADAAAEGVPVRGARNQLRMYLTMAVAAAQPMLMYWLTFHLVR
6043	403	599	LCLFFFFPCATPVLPLPSLISAL/CLSHLSVSSWFCPCOPPLPC
0043	403	333	PLPPLONKTAKGSLSTEQSRRG
6044	793	412	KLEMWNFTLISKVKISREVTMIASKFGIGQOVRHSLLGYLGVVV
6044	/33	412	DIDPVYSLSEPSPDELAVNDELRAAPWYHVVMEDDNGLPVHTYL
Į		į	AEAOLSSELODEHP\BOPSMDELAOTIRKOLOAPRLRN
L-5045	L	2299	SPLPOVAAMNYLRRRLSDSNFMANLPNGYMTDLORPOPPPPPPPG
6045	155	2299	1
1			AHSPGATPGPGTATAKKSSGVAPAASPAAPSPGSSGGGGFFSSL
1			SNAVKQTTAAAAATFSEQVGGGSGGAGRGGAASRVLLVIDEPHT
{	ł.	ł	DWAKYFKCKKIHGBIDIKVRQABFSDLNLVAHANGGFSVDMEVL
ì		İ	RNGVKVVRSLKPDFVLIRQHAFSMARNGDYRSLVIGLQYAGIPS
I	Į.		VNSLHSVYNPCDKPWVFAQMVRLHKKLGTEEFPLIDQTFYPNHK
1	1		EMLSS\TTYPVVVKMGHGTLMGWGKVKVDNQHDFQDIASVVALT
1	!	}	KTYATAEPFIDAKYDVRVQKIGQNYKAYMRTSVSGNWKTNTGSA
1	1	[	MLEQIAMSDRYKLMVDTCSRIFGGLDICAVEALHGKDGRDHIIE
l	1	l	VVGSSMPLIGDHQDEDKQLIVELVVNKMAQALPRQRQRDASPGR
	4		GSHGQTPSPGALPLGRQTSQQPAGPPAQQRPPPQGGPPQPGPGP QRQGPPLOORPPPQGOOHLSGLGPPAGSPLPORLPSPTSAPQOP
l			
İ	i		ASQAAPPTQGQGRQSRPVAGGPGAPPAARPPASPSPQRQAGPPQ
l		ļ	ATROTSVSGPAPPKASGAPPGGQQRQGPPQKPPGPAGPTRQASQ
Į.		ŀ	AGPVPRTGPPTTQQPRPSGPGPAGRPKPQLAQKPSQDVPPPATA
j	1	}	AAGGPPHPQLNKSQSLTNAPNLPEPAPPRPSLSQDEVKAETIRS
			LRKSFASLFSD
6046	212	1075	EGLTGPCERVPFLLGRGPPHGATRAGHRRAVRWAGPBSLPPLPR
ļ			SLIMDSPRAGTHQGPLDAETEVGADRCTSTAYQEQRPQVEQVGK
	<b>†</b>		QAPLS 2GLPAMGGPGPGPCEDPAGAGGAGGGBEPLVTVTVQCA
}	1		PTVALRARGADLSSLRALLGQALPHQ\AQLGQLSYLAPGEDGH
1 .			WVPIPEEESLQRAWQDAAACPRGLQLQCRGAGGRPVLYQVVAQH
1		ì	SYSAQGPEDLGFRQGDTVDVLCEVDQAWLEGHCDGRIGIFPKCF
		1405	VVPAGPRMSGAPGRLPRSQQGDQP PVLVTSLRMREADTLRPPQLMEVSADIISTVEFNHTGELLATGD
6047	49	1405	KGGRVVIFOREPESKNAPHSOGKYDVYSTFOSHEPEFDYLKSLE
		ļ	IERKINKIKWLPQQNAAHSLLSTNDKTIKLWKITERDKRPEGYN
<b>.</b>	· .		LKDREGKLKDLSTVTSLQVPVLKPMDLMVEVSPRRIFANGHTYH
1			<u> </u>
1	1		INSISVNSDCETYMSADDLRINLWHLAITDRSFTP\NIVDIKPA
1	}		MMEDLTEVITASEFHPHHCNLFVYSSSKGSLRLCDMRAAALCDK     HSKLFEEPEDPSNRSFFSEIIS\SVSDVKPSHSDRYMLTR\DYL
1	ĺ		TVKVWDL\NMEARPIETYQVHDYLRSKLCSLYENDCIFDKFECA
١.	<b>!</b>	•	
1			WNGSDSVIMTGA\YNNFFRMFDRNTKRDVTL\EASRESSKPRAV LKPRRVCVGGKRRDDISVDSLDFTKKILHTAWHPAENIIAIAA
[	· ,		TNNLYIFODKVNSDMH
(010	<del>                                     </del>	3104	
6048	1	3194	GIRTPKFCDSPTSDLEMRNGRGRGKRMRPNSNTPVNETATASDS
1	}		KGTSNSSKTRAGANSKGRRGSQNSSBHRPPASSTSEDVKASPSS ANKRKNKPLSDMRLNSSSEDSKGSKRVRTNSMGSATGPLPGTKV
1			
1	Į į		RPTVLDRNCPSPVLIDCPHPNCNKKYKHINGLKYHQAHAHTDDD
1	[		SKPEADGDSEYGEEPILHADLGSCNG\ASVSQK\GSLSPARSAT
1			PKVRLVEPHSPSPSSKFSTKGLCKKKLSGEGDTDLGALSNDGSD
1	[		DGPSVMDETSNDAFDSLERKCMEKEKCKKPSSLKPEKIPSKSLK
1			SARPI/APLAIPPQQIYTFQTATFTAASPGSSSGLTATVAQAMP
}	}		NSPQLKPIQPKPTVMGEPFTVNPALTPAKDKKKKDKKKKRSSKE
	]		LESPLTPGKVCRAEEGKSPFRESSGNGMKMEGLLNGSSDPHQSR
	Į.		LASIKAEADKIYSFTDNAPSPSIGGSSRLENTTPTQPLTPLHVV
1	ļ.	Ī	TONGARASSVKTNSPAYSDISDAGEDGEGKVDSVKSKDAEQLVK
1			EGAKKTLFPPQPQSKDSPYYQGPESYYSPSYAQESPGALNPSSQ
1	]		AGVESQALKTKRDEEPESIEGKVKNDICEEKKPELSSSSQQPSV
1			IQQRPNMYMQSLYYNQYAYVPPYGYSDQSYHTHLLSTNTAYRQQ
	[		YEEQQKRQSLEQQQRGVDKKAEMGLKEREAALKEKWKQKPSIPP
)	1		TLTKAPSLTDLVKSGPGKAKEPGADPAKSVIIPKLDDSSKLPGQ
1			APEGLKVKLSDASHLSKEASEAKTGAECGRQAEMDPILWYRQBA
			EPRMWTYVYPAKYSDIKSEDERWKEERDRKLKBERSRSKDSVPK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Į.	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine.
	corresponding	to first	Labeucine, Mamethionine, NaAsparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
]	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
i i	sequence	bequence	\=possible nucleotide insertion)
<del> </del>	111111111111111111111111111111111111111		EDGKESTSSDCKLPTSEESRLGSKEPRPSVHVPVSSPLTQHQSY
1		i	IPYMHGYSYSQSYDPNHPSYRSMPAVMMQNYPGSYLPSSYSFSP
	İ	ì	YG9KVSGGEDADKARASPSVTCKSSSESKALDILQOHASHYKSK
1			
•			SPTISDKTSQERDRGGCGVVGGGGSCSSVGGASGGERSVDRPRT
1	}		SPSQRLMSTHHHHHHLGYSLLPAQYNLPYAAGLSSTAIVASQQG
6049	215	1089	STPSLYPPPRR
0049	1 415	1089	AMTGVFDRRVPSIRSGDFQAPFQTSAAMHHPSQESPTLPESSAT
1	ļ.		DSDYYSPTGGAPHGYCSPTSASYG\KALNPYQYQYHGVNGSAGS
J			YPAKAYADYSYASSYHQYGGAYNRVPSATNQPEKEVTEPEVRMV
i			NGKPKKVRKPRTIYSSFQLAALQRRFQKTQYLALPERABLAASL
1			GLTQTQVKTWFQNKRSKIKKIMKNGEMPPEHSPSSSDPMACNSP
1	1		QSPAVWBPQGSSRSLSHHPHAHPPTSNQSPASSYLENSASWYTS
-			AASSINSHLPPPGSLQHPLALASGTLY
6050	566	1718	KGLERTCCAMBESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL
			PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD
i i			RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW
ł			DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRBLEKDMHY
			YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKRREEDLR
i			RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN
			FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
1			FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI
			PSAATLINIRNARKHFEKLERVDGPKOCLLMR
6051	566	1718	KGLERTCCAMRESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL
	i i		PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD
			RIHSLQINSSLSTYSLVDSVGNTKTFDVBHSHVRFLGNLVLNLW
		-	DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY
1			YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDLR
.1		•	RLSRPLBCSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN
i			FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
1			FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI
			PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6052	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL
1			PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD
i l			RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW
			DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRBLEKDMHY
1	,		YQSCLEAILQNSPDAKIPCLVHXMDLVQEDQRDLIFKBRREDLR
			RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN
			FABIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
1			FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI
			PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6053	201	1704	KGTEMNKSRWQSRRRHGRRSHQQNPWFRLRDSEDRSDSRAAQPA
1			HDSGHGDDBSPSTSSGTAGTSSVPELPGFYFDPEKKRYFRLLPG
[			HNNCNPLTKESIRQKEMESKRLRLLQEEDRRKKIARMGFNASSM
1	1		LRKSQLGFLNVTNYCHLAHELRLSCMERKKVQIRSMDPSALASD
1		•	RFNLILADTNSDRLFTVNDVTVGGSKYGIINLQSLKTPTLKVFM
1	]		HENLYFTNRKV\NSVCWASLNHLDSHILLCLMGLARTPGCATLL
	1		PASLFVNSHPAGIDRPG\MLCSFRIPGANSCAWSLNIQANNCFS
]	1		TGLSRRVLLTNVVTGHRQSFGTNSDVLAQQFALMAPLLFNGCRS
			GRIFAIDLROGNOGKGWKATRLFHDSAVTSVRILQDBQYLMASD
]	ľ		MAGKIKLWDLRTTKCVRQYBGHVNEYAYLPLHVHBEEGILVAVG
1	. [		QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG
1 !			APGLLMAVGQDLYCYSYS
6054	1	1054	PPIARLQEPGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH
1 1	' I		KOSSSQQRRWFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY
<u> </u>	}		VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV
j l	į		DMTTEEIDALVHREIISHNAYPSPLGYGGPPKSVCTSVNNVLCH
]	<b>\</b>		GI?DSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK
1 1	ł		LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF
] ]			VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPE
j i	İ	ŀ	FKVLEDAWTVVSLD/TSKVSAQFEHTVLITSRGAQILTKLPHEA
	L		TATALOGRAFIA TODON TOWNSHIP KHITVII TSKGAQI DIKIDHKA

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1 10.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arqinine,
1		residue of	
1	amino acid		S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6055	421	2364	PPYFLLSFLAWWLYGQSDRTBTD15QSAGPPPGTLQCSALHHDP
1			GCANCSRFCRDCSPPACQCHTHVFPGNALWGVQPPELSRTLALI
1	1	1	SSRBPPRKKKKSQTETGKERBRTSFLTQGGKRFELQHGLAGICM
i	j		TLLITGDSIVSAEAVWDHVTMANRELAFKAGDVIKVLDASNKDW
	'		WWGQIDDEEGNFPASFVRLWVNHEDEVEEGPSDVQNGHLDPNSD
1	ļ		CLCLGRPLQNRDQMRANVINBIMSTERHYIKHLKDICEGYLKQC
	1		RKRRDMFSDEQLKVIFGNIEDIYRFQMGFVRDLEKQYNNDDFHL
1	1		SEIGPCFLBHQDGFWIYSBYCNNHLDACMELSKLMKDSRYQHFF
f		1	RACRILQQMIDIA\IDGFLLTPVQKICKYPLQLAELLKYTAQDH
İ	[		SDYRYVAAALAVMRNVTQQINERKRRLENIDKIAQWQASVLDWE
1		ì	GEDILDRSSELIYTGEMAWIYQP\YGRNQQRVFFLFDHQMVLCK
Į.			KOLIRRDILYYKGRIDADKYEVVDIEDGRDDDFNVSMKNAFKLH
1	ł	1	NKETEBIHLFFAKKLEEKIRWLRAFRBERKMVQEDEKIGFEISE
i	1	1	NOKROAAMTVRKVPKOKGVNSARSVPPSYPPPODPLNHGQYLVP
1	<b>!</b>	l	\DGIAQSQVFBFTKPKRSQSPFWQNFSRLTPFKK
6056	43	3358	SGGRGPVRVRSEOLSPSAEQVSQISQISLGRRPLSSLPPPPSRA
""	"	1 225	LAPTRAPDTALTIMEVAEVESPLNPSCKIMTFRPSMEEFREFNK
			YLAYMESKGAHRAGLAKVIPPKEWKPROCYDDIDNLLIPAPIOO
1	1		MVTGOSGLETOYNIOKKAMTVKREROLANSGKYCTERYLDYBDL
1			ERKYWKNLTFVAPIYGADINGSIYDBGVDBWNIARLNTVLDVVE
	ł		RECGISIEGVNTPYLYFGMNKTTFAWHTEDMDLYSINYLHFGEP
1		•	KSWYAIPPEHGKRLERLAOGFFPSSSOGCDAFLRHKMTLISPSV
	i	-	LKKYGI?FDKITORAGEFMITFPYGYHAGFNHGFNCAESTNFAT
1	i	ŧ	VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQGKD
	1		IYTIDHTKPTPASTPEVKAWLORRRKVRKASRSFQCARSTSKRP
1	ŀ		KADREEEVSDEVDGABVPNPDSVTDDLKVSEKSEAAVKLRNTEA
	[	ł	SSERESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDDKA
ł	1		YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSKLSWPKSPESCS
			SVARSNGVLTEGERSDVESHGNGLEPGEIPAVPSGERNSFKVPS
1 1	1	1	IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVLSI
		1	EERVEBTESWAKPLIHLWQTKPPNFAABQEYNATVARMKPHCAI
1	į ·	[	CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEMCF
			IYSEENIEYSPPNAFLEEDGTSLLISCAKCCVRVHASCYGIPSH
1		į	BICDGWLCARCKRNAWTAECCLCNLRGGALKOTKNNKWAHVMCA
		İ	VAVPBVRFTNVPERTQIDVGRIPLQRLKLKCIFCRHRVKRVSGA
1	}		CIOCSYGRCPASFHVTCAHAAGVI\MEPDDWPYVVNITCFRHKV
1	i	1	NPNVKSKACEKVISVGQTVITKHRNTRYYSCRVMAVTSQTFYEV
1			MFDDGSFSRDTFPRDIVSRDCLKLGPPAEGEVVQVKNPDGKLYG
1	1		AKYPGSNIAHMYOVEFEDGSQIAMKREDIYTLDEELPKRVKARF
1			VSAGRCHLGTCOVNSLSSPHVSQAQQETYLGFWINSKXSQCNIF
1	I		LSGTY
6057	1	853	FVARLKEQEGEGGLGPRKEKGRARGRERRRKMQLTRCCFVFLVQ
"""	,	555	GSLYLVICGODDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKS
1		l	RPMANSTLICILAPPGRAWGIIGOPPNRPNHSPPPSAKVKKIFG
1		1	WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNIS
1		ļ	ISLVPPSKAVEFHQEQQIFIRAKASKIFNC\RMBWBKVB\RGRR
j.	1	]	TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR
			7
COES	ļ		LVQKVCPDYNYHSDTPYYPSG
6058	1	986	HPLPSASLGLPSVSTGVSLCVRSALLEAVVPMLPKRRARVGSP
	1		SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR
	1	}	VLDACSSEATHVVMEETSAERAVSWQERRMAAAPPGCTPPALLD
]	}		ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR
1	ì		PTPLTHHNTGLSEALBILAEAAGFEGSBGRLLTFCRAASVLKAL
1	1		PSPVTTLSQLQGLPHFGBHSSRVVQELLEHGVCEEVERVRSB/
1			RLFTQIFGVGVKTADRWYRBGLRTLDDLREQPQKLTQQQKAGBP
			SREAGPWASLNCTLDPSASTP
6059	2	3650	QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT
1			QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH
			SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS
] .			RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK
1			EHLAKSEKBAKKDDFMCDYCRDTFSQTEELEKHVLTRHPQLSEK
			· · · · · · · · · · · · · · · · · · ·

PCT/US00/34263

и**.**,. .

		1	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	Bequence	}	ADLQCIHCPEVFVDENTLLAHIHQAHANQKHXCPMCPB\QFSSV
	•		\EGVYCHLDSHRQPDSSNHSVSPDPVLGSVASMSSATPDSSASV
		Ì	RRGSTPDSTLKPLRGQKKMRDDGQGWTKVVYSCPYCSKRDFNSL
	1	[	
		ļ	AVLEIHLKTIHADKPQQSHTCQICLDSMPTLYNLNRHVRKLHKN
			HAYPVMQFGNISAFHCNYCPEMFADINSLQEHIRVSHCGPNANP
	l		SDGNNAFFCNQCSMGFLTESSLTEHIQ\Q\AHCSVGSAKLESPV
	1		VQPTQSFMEVYSCPYCTNSPIFGSILKLTKHIKENHKNIPLAHS
			KKSKARQSPVSSDVEVSSPKRQRLSASANSISNGEYPCNQCDLK
		ļ	FSNFESPQTHLXLHLELLLRKQACPQCKEDFDSQESLLQHLTVH
	l		YMTTSTHYVCESCDKQPSSVDD\LQKH\LLDMPHPLCCTHCT\L
		1	CQEVFDS\KVSI\QVHLAVKHSNEKKMYRCTACNWDFRKEADLQ
	1		VHVKHSHLGNPAKAHKCIPCGETFSTEVELQCHITTHSKKYNCK
		l	FCSKAPHAIILLEKHLREKHCVFDAATENGTANGVPPMATKKAB
	l .	}	PADLQGMLLKNPRAPNSHEASEDDVDASEPMYGCDICGAAYTME
	1	}	VLLQNHRLRDHNIRPGEDDGSRKKABFIKGSHKCNVCSRTFFSE
	1	1	NGLREHLQTHRGPAKHYMCPICGERFPSLLTLTEHKVTHSKSLD
		1	TGTCRICKMPLQSKEEPIEHCCMHPDLRNSLTGFRCVVCMQTVT
ŀ		İ	STLELKIHGTFHMOKLAGSSAASSPNGOGLQKLYKCALCLKEFR
Į.	1		SKODLVKLDVNGLPYGLCAGCMARSANGQVGGLAPPEPADRPCA
i	1		OF DODGOGUUZEGAEDT BOLMOUNUEDI TEETSGERKOTOTSEV
			GLRCPECSVKFESAEDLESHMQVDHRDLTFETSGPRKGTQTSPV
1		i	PRKKTYQCIKCQMTFENBREIQIHVANHMIBEGINHECKLCNQM
ł			FDSPAKLLCHLIEHSFRGMGGTFKCPVCFTVFVQANKLQQHIFA
			VHGQEDKIYDCSQCPQKFFPQTELQNHTMSQHAQ
6060	2145	202	SYETVGKNKLEVNHSQLKALCKCSLPSRLLPLGENLPLLDRGFR
			KEPRSRGSRERDNMLHLHHSCLCFRSWLPAMLAVLLSLAPSASS
•	ļ	i	DISASRPNILLLMADDLGIGDIGCYGNNTMRTPNIDRLAEDGVK
			LTQHISAASLCTPSRAAFLTGRYPVRSGMVSSIGYRVLQWTGAS
			GGLPTNETTFAKILEBKGYATGLIGKWHLGLNCESASDHCHHPL
l ·			HHGPDHFYGMPFSLMGDCARNELSEKRVNLEQKLNFLFQVLALV
			ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA
		ł	DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPPLLFV
2		ł	SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV
		f .	EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW
	i ·		EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP
1		1	ODRVIDGODLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR
1	1		GTMNKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD
l	Į.	1	LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ
l	I	1	LDRIGHTWRPWLQPCCGPFFLCWCLREDDPQ
	ļ	1330	MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTRLLESBQGSPN
6061	110	1.330	VHNYPDMEAVPLLLNNVKGEPPEDGLSVDHFQTQTEPVDLSINK
1	1		ARTEPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS
1	1	1	
1		1	VSSASSSTVLTPGPLVASASGVGGQQFLHIHPVPPSSPMNLQ
1	i		SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG
ļ	I	1	HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNRTGSTALSIA
1		Į.	RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN
ł	1	i	PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY
1		1	KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH
]		1	LALHRRRHMLV
6062	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT
1	1	1	LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR
[	1		TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
1	1	1	EFSEPEEEIDENBEITTTFFEQSVIWVPAEKPIENRDFLKNSKI
	1	1	LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE
[		1	EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP
1		1	INDYTENGISFDPMLDERGYCCIYCRGNRYCRRVCBPLLGYYP
1	1	1	YPYCYQGGRVICRVIMPCNWWVARMLGRV
L	ļ	<u> </u>	INICIAOUS ICRATUS CHANASCALOROS ALCOSTABATI VITA
6063	71	1079	BTMAKNGPENCEDCHILNAEAPKSKKICKSLKICGLVFGILALT
1			LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMBIDPVTR
1	ł		TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
		1	EFSEPKERIDENEKITTTFFKQSVIWVPAKPIENRDFLKNSKI
i		I	LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE

650	December 2	[ n 31 at = 3 -= 3	
SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
) NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding to first	to first	L-Leucine, M-Methionine, N-Asparagine,
i		amino acid	P=Proline, Q=Glutamine, R=Arginine,
ĺ	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1	1	<u> </u>	EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASKKKLP
1			INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCLPLLGYYP
			YPYCYQGGRVICRVIMPCNWWVARMLGRV
6064	913	311	NLPQSLPRPTEHSPPYSLEKMTDLVAVWDVALSDGVHKIEFEHG
1	Ì		TTSGKRVVYVDGKEEIRKEWMFKLVGKETFYVGAAKTKATINID
1			AISGFAYEYTLEINGKSLKKYMEDRSKTINTWVLHMDGENFRIV
Į.	ł		LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYIKAV\
ŀ			SSG\KRKEGIIHTLIVDNREIPEIAS
6065	1153	641	MSVRVARVAWVRGLGASYRRGASSFPVPPPGAQGVAELLRDATG
			AEERAPWAATERRMPGQCSVLLFPGQGSQVVGMGRGLLNYPRVR
1			RLYAAARRVLGYDLLELSLHGPORTLDRTVHCOPATFVASLAAV
1			EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG
6066	68	3470	VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGDVRIW
			BDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHTFPEG
1			VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDVMDSS
İ	<b>}</b>		QQKT?RGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISDOTCA
			ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVKLYRR
1	<b>}</b>		ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLIIVWNV
			ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGLLENV
}			CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNAVEIP
1		·	SFSKGIINDDEDDEDLMMASGRPRORSHILEDDENSVDISMLKT
1			GSSLLKEBREDGQEGSIHNLPLVTSORPFYDGPMPTPROKPFOS
			GSTPLHLTHRFMVWNSIGLIRCYNDEQDNAIDVEFHDTSIHHAT
			HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSWDSSK
1			EWIIDLPONEDIRAICLGOGWAAAATSALLLRLFTIGGVOKEVF
1		•	SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELGKKKK
			QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLNRGLG
İ			NTWTPICNTREHCKGKSDHYWVVGIHENPOOLRCIPCKGSRFPP
l i			TLPRPAVAILSFKLPYCQ1ATEKGQMEEQFWRSV1FHNHLDYLA
1			KNGYEYEBSTKNQATKEQQELLMKMLALSCKLEREFRCVELADL
	·		MTQNAVNLAIKYASRSRKLILAQKLSELAVEKAABLTATQVEBE
1	•		EEEEDFRKKLNAGYSNTATENSQPRFRNQVEEDAEDSGRADDEE
1			KPBIHKPGONSFSKSTNSSDVSAKSGAVTFSSQGRVNPFKVSAS
1	i		SKEPAMSMNSARSTNILDNMGKSSKKSTALSRTTNNEKSPIIKP
1			Lipkpkpxqasaasypqkrnsqtnktbevkeenlknvlsetpai
1			CPPCNTENQRPKTGPQMWLEENRSNILSDNPDFSDEADIIKEGM
1			IRPRVLSTBERKVWANKAKGETASEGTBAKKRKRVVDESDETEN
		İ	QBBKAKKNLNLSKRQKPLDFSTNQKLSAFAFKQB
6067	858	321	LPWQRLGVLLSRGEMAVTGWLESLRTAQKTALLQDGRRKVHYLF
1	ſ	İ	PDGKEMABEYDEKTSELLVRKWRVKSALGAMGQWQLEVGDPAPL
			GAGNLGPELIKESNANPIFMRKDTKMSFQWRIRNLPYPKDVYSV
			SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T
		İ	PTAP
6068	13	1730	GSKMADLANEEKPATAPPVFVFQKDKGQESPABQKNLSDSGERP
			RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL
			PPPPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRERTSSLTQ
j l		j	FPPSQSEERSSGFRLKPPTLIHGQAPSAGLPSQKPKEQQRSVLR
] [	j	j	PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW
į l	Ì		RSPSEAADEVCALEEKEPQKNESSNASEBRACEKKDPATQQAFV
1 1			FGQNLRDRVKLINESVDRADMENAGHPSADTPTATNYFLQYISS
Į		į	SLENSTNSADASSNKFVFGQNMSKRVLSPPKLNEVSSDANRENA
(			AAESGSESSOEATPEKESLABSAAAYTKATARKCLLEKVEVIT
			GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG
}	1	ļ	TIQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM
j	]	j	
[ [	(		DNEDQGVKVFI-ISASSKDTGQVYAALHHRILALRSRVEQEQEAK
	İ		MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDBGDGQTTGS
6069	583		T PURPOSE CONTRACTOR OF THE PURPOSE PROPERTY OF THE PURPOSE PURPOSE PROPERTY OF THE PURPOSE PURPOSE PURPOSE PURPOSE PURPOSE PU
0007	265	27	PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK
	į	!	RHARVTVKYDRRELQRRLDVEKWIDGRLERLYRGMEADMPDEIN
Щ			IDELLELESEERSRKIQGLLKSCGKPVEDFIQELLAKLQGLHR

	T	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i .	location	to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding		P=Proline, Q=Glutamine, R=Arginine,
i	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	
l .	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			Q\PGLRQPSPSP\DGQPSAPFQGPGARTASPLTLLALFPGPPER
ļ			RPALLCVLSCI
6070	478	858	IRVTVDGEFLHYIFPLQFLDSPEW/RFTETHRGRHF\QVTLTAE
i	1	1	TDCRYVSWRRKKLYLLFAQHRYISRLFSVLIGSDIADKLYALND
ļ			RVYIGKRYEYDIRLPNFYQMSTPBIRRSPLTQHFQNSRRYW
6071	2	1654	HEARTKGNMALARP\VRLFSLVTRLLLAPRRGLTVRSPDBPLPV
1	_	İ	VRIPVALQRQLEQRQSRRRNLPRPVLVRPGPLLVSARRPELNQP
			ARLTLGRWERAPLASQGWKSRRARRDHFSIBRAQQBAPAVRKLS
ļ .		İ	SKGSFADLGAWKPRVLHALQB\AAPEVVQ\PTTVQSSTIPSLLR
Ì		ļ	GRHVVCAAETGSGKTLSYLLPLLQRLLG\HPSLDSLPIPAPRGL
į.	1	İ	VLVPSRELAQQVRAVAQPLGRSLGLLVRDLRGGHGMRRIRLQLS
l l	i		ROPSADVLVATPGALWKALKSRLISLEQLSFLVLDRADTLLDES
			FLRLVDYILEKSHIAEGPADLEDPFNPKAQLVLVGATFPEGVGQ
ļ	ļ	}	LLNKVASPDAVTTITSSKLHCIMPHVKQTFLRLKGADKVABLVH
į		1	ILKHRDRAERTGPSGTVLVFCNSSSTVNWLGYILDDHKIQHLRL
ŀ			QCOMPALMRVGIFQSFQKSSRDILLCTDIASRGLDSTGVBLVVN
i			YDFPPTLQDY IHRAGRYGRYGSEVPGTVISFVTHPWDVSLVQKI
	-	1	I " =
L			BLAARRRRSLPGLASSVKEPLPQAT  KMERTEMMPTINSQLEFKSKPFPLVSSSRWLVKRGELTAYVEDT
6072	1	742	
1		l .	VLFSRRTSKQQVYFFLFNDVLIITKKKSEESYNVNDYSLRDQLL
		1	VESCONRELNSSPGKNSSTMLYSRQSSASHLFTLTVLSNHANBK
ļ.			VEMLIGAETQSERARWITALGHSSGKPPADRTSLTQVEIVRSPT
ł	ļ		AKQPDELSLQVADVVLI\YQRVSDGWYEGER\LRDGERGWFPME
ł			CAKBITCOATIDENVERMGRLLGLETNV
6073	620	860	PCRRGLARPLSRRPG/SILVHCAVGVSRSATLVLAYLMLYHHLT
1		1	LVBAIKKVKDHRGIIPNKGFLRQLLALDRRLRQGLEA
6074	168	1110	PGARCMATELQCPDSMPCHNQQVNSASTPSPEQLRPGDLILDHA
	1		GCNRASRAKVILLTGYAHSSLPAELDSGACGGSSLNSEGNSGSG
1		1	DSSSYDAPAGNSFLEDCELSRQIGAQLKLLPMNDQIRELQTIIR
ì			DKTASRGDFMFSADRLIRLVVEEGLNQLPYKECMVTTPTGYKYE
1			GVKFEKGNCGVSIMRSGEAMEQGLRDCCRSIRIGKILIQSDEET
1		1	QRAKVYYAKFPPDIYRRKVLLMYPILQTG\NTVIRAVKVLIKHG
1	1		VQPSVIILLSLFSTPHGAKSIIQEFPRITILTTEVHPVAPTHFG
1 .	1		QKYFGTD
6075	320	1091	PPTCQPQEVEHH\YGYVPILGNKTLPSRCHQCVIVSSSHLLGT
"""			KLGPEIERABCTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV
}	1	1	LRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFP
1	1		NMEAYAVSPGRMRQPDDLFRGETGKDREKSHSWLSTGWFTMVIA
1			VELCOHVHYYGMVPPNYCSQRPRLQRMPYHYYEPKGPDECVTYI
1		•	ONEHSRKGNHHRFITEKRVPSSWAQLYGITFSHPSWT
6076	1721	107	HPSPTEAPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGAEV
0076	1 1/21	1	KKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGAFDPBD
i			GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD
1			HGDYAFDIWGQGTMVTVSSAPTKAPDVFPIISGCRHPKDNSPVV
1	}		LACLITGYHPTSV\TVTWYMGTQSQA\QRTFPBIQRRDSYYMTS
1			SOLSTPLOOWROGEYKCVVOHTASKSKKEIFRWPESPKAQASSV
1	1		PTAQPQAEGSLAKATTAPATTRNTGRGGEEKKKEKEKEKERQEERE
ĺ			TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD
1			AHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWNA
1	1		WITH ADAPPARATION STOCK
1	}	1	GTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSLNLLASSDPPE
	1	1	A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\
		j .	RSTTPWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL
1		1	BVSYVTDHGPMK
6077	3687	1268	LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLXANAKSCGECIQ
		1	AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPR
1		1	GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGBP
I		1	OTPTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN
1	1		EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS
1		1	PESYKNVLSLTNKGEVENELVGKQRISGNLDSPEGGFDAIMQVA
1		1	VCGSLIGWRNVTRLLVFSTDAGFHFAGDGKLGGIVLPNDGQCHL
			TOO WATER TANDER OF THE PARTY O

SEO	Predicted	Predicted end	Tamino agid coment contains signal -cutide
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
NO:	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	
ł	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
I	sequence	sequence	
L	sequence		\=possible nucleotide insertion)
1			ENNMYTMSHYYDYPSIAHLVQKLSENNIQTIPAVTREFQPVYKE
			LKNLIPKSAVGTLSANSSNVIQLIIDAYNSLSSEVILENGKLSE
i	ł		GVT19YQSY\CKNGVNGTGBNGRKCSN1S1GDEVQFB1S1TSNK
1	1		CPKKDSDSFKIRPLGFTBEVEVILQYICECECQSEGIPESPKCH
		}	EGNGTFECGACRCNEGRVGRHCECSTDEVNSEDIGCFTARKENQ
Į	ļ	}	FQKSASNHGRVPSAGQCVCRKRDNTNEIYSGKFCECDNFNCDRS NGLICGGNGVCKCRVCECNPNYTGSACDCSLDTSTCEASNGOIC
ł		i	MGRGICECGVCKCTDPKFQGQTCEMCQTCLGVCABHKECVOCRA
1		<b> </b>	
Į			FNKGEKKDTCTQECSYFNITKVESRDKLPQPVQPDPVSHCKEKD VDDCWFYFTYSVNGNNEVMVHVVENPECPTGPDIIPIYAGVVAG
1			· ·
j .		j	IVLIGLALLLIWKLLMIIHDRREPAKFEKEKMNAKWDTGENPIY KSAVTTVVNPKYEGK
6078	1426	180	BTEDVMKLLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILE
30/8	1440	100	GSVRNSLWRPVPFKCPTCRKKTFSYWELIPLOVNYSLKGIVEKY
	i	1	NKIKISPKMPVCKGH\LGQPLNIF\CL\TDMOLDL/CGIC\ATR
{	ĺ		GEHTKHVFCSIEDAYAOERDAFESLFOSFETWRGDALSRLDTL
İ	Ì	1	ETSKRKSLQLLTKDSDKVKEFFEKLQHTLDQKKNEILSDFETMK
ł			LAVMQAYDPKINKLNTILQEQRMAPNIARAFKDVSEPIVFLQOM
1	ļ		QEFREKIKVIKETPLPPSNLPASPLMKNFDTSQWEDIKLVDVDK
J	Ì	}	LSLPQDTGTFISKIPWSFYKLFLLILLGLVIVFGPTMFLEWSL
l			FDDLATWKGCLSNFSSYLTKTADFIEQSVFYWEQVTDGFFIFNE
i			RFKNFTLVVLNNVAEPVCKYKLL
6079	1586	141	ATARDLGCARRIDRVVMESTPSRGLNRVHLQCRNLQEFLGGLSP
1	}	1	GVLDRLYGHPATCLAVFRELPSLAKNWVMRNLFLEQPLPQAAVA
	}		LWVKKBFSKAQEESTGLLSGLRIWHTQLLPGGLQGLILNPIPRO
1	ļ		NLRIALLGGGKAWSDDTSQLGPDKHARDVPSLDKYAEERWEVVL
		,	HFNVGSPSAAVSQDLAQLLSQAGLMKSTEPGEPPCITSAGFOFL
i	i ·		LLDTPAQLWYFMLQYLQTAQSRGMDLVEILSFLFQLSPSTLGKD
	· ·		YSVEGMSDSLLNFLQHLREFGLVPQRKRKSRRYYPT/RALAINL
	ļ	Í	SSGVSGAGGTVHQPGFIV\VETNYRLYAYTESELQIALIALFSE
	]		MLYPFP\NMVV\ARVIR\ESVQQAIASGITAQQIIHFLRTRAHP
i .			VMLKQTPVLPPTITDQIRLWELERDRLRFTEGVLYNQFLSQVDF
}		İ	ELL\LAHAPKLGVLVFB/NTPAKRIMVVTPAGHSDVKRFWKRQK
1			HSS
6080	1	1199	TETIDHVGEFAMAAQAAGVSRQRAATQGLGSNQNALKYLGQDFK
			TLRQQCLDSGVLFKDPBFPACPSALGYKDLGPG8PQTQGIIWKR
1		l	PTELCPSPOFIVGGATRTDICQGGLGDCWLLAAIASLTLNEELL
	1	ļ	YRVVPRDQDFQENYAGIFHFQPLCPPSP\FWQYGEWVEVVIDDR
	1	[	LPTKNGQLLFLHSEQGNEFWSALLEKAYAKLNGCYBALAGGSTV
	1		EGFEDFTGGISEFYDLKKPPANLYQIIRKALCAGSLLGCSIDVY
			SAAEAEAITSQKLVKSHAYSVIGVEEVNFQGHPEKLIRLRNPWG
			EVENSGAMSDDAPEWNHIDPRRKBELDKKVEDGEFWMSLSDFVR
			QFSRLEICNLSPDSLSSBEVHKWNLVLFNGHWTRGSTAGGCQNY
	•		PGSS
6081	3	865	BMLPLLLPLPLLWA/GALAQDARFRLEMPESVTVQEGLCIFVHC
			SVFYLEYGWKDSTPAYGHWFREGVSVDQBTPVATNNSTQKVQKB
			TOGRPHLLGDPSRNNCSLSIRDARRRDNGSYFFWVARGRTKFSY
	ļ		KYSPLSVYVTALTHRPDILIPEPLKSGHPSNLTCSVPWVCRQGT
			PPIFSWMSAAPTSLGPRTLHSSVLTIIPRPQDHGTNLICQVTFP
			GAGVTTERTIQLSVSWKSGTVREVVVLAVGVVAVKILLLCLCLI
			ILSFHKKKAVRAVEVEENVYAVMG
6082	283	1288	RARSPGPTQTRTAPGLAAPGLAQPAALRLLLSRPPSAAMDGDGD
		ļ ,	PESVGQPREASPEEQPEEASAEEERPEDQQEREAAAAA\Y\LDB
			LPEPLLA/LRVLAALPRHE/LVQACR/LVCLRWKELVDGAPLWL
	]		LKCQQEGLVPEGGVEEERDHWQQFYFLSKRRRNLLRNPCGEEDL
			egwcdvehggdgwrveelpgdsgvefthdesvkkyfassfewcr
			KAQVIDLQAPGYWEKLLDTTQPAIVVKDWYSGRSDAGCLYBLTV
			KLLSEHENVLAEFSSGQVAVPQDSDGGGWMBISHTFTDYGPGVR
			FVRFEHGGQDSVYWKGWPGARVTNSSVWVEP
6083	1865	309	KOWCAERRGLGMSLADELLADLEEAABBEBEGGSYGEEBEEPAIE

PCT/US00/34263

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ľ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
•	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bequence	\=possible nucleotide insertion)
<del></del>	cequonoc		DVQEETQLDLSGDSVKTIAKLWDSKMFAEIMMKIEBYISKOAKA
l .		ì	SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR
1			FPBLESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM
1			VVSVTASTTQGQQLSEEELERLEEACDMALKLNASKHRIYEYVE
1	i		SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG
ļ	Į		AQRKTLSGPSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL
	İ		RKAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
1		j	QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ
] .			ANRMSFGEIEEDAYQEDLGPSLGHLGKSGSGRVRQTQVNEATKA
l	i	ľ	RISKTLORTLOKOSVVYGGKSTIRDRSSGTASSVAFTPLOGLEI
J	j		VNPQAAEKKVAEANQKYPSSMAEFLKVKGEKSGLMST
6084	1865	309	KOWCAERRGLGMSLADELLADLEBAAREEEGGSYGEREEKPATE
3307	-303	""	DVQKBTQLDLSGDSVKTIAKLWDSKMFARIMMKIEEYISKQAKA
1	1		SEVMGPVEAAPEYEVIVDANNLTVEIENELNIIHKFIRDKYSKE
1	1		FPELESLVPNALDYIRTVKELGNSLDKCKNNENLOOILTNATIM
ļ			VVSVTASTTQQQQLSEELERLEEACDMALKLNASKHRIYEYVE
			SRMSFIAPNLSIIIGASTAAKINGVAGGLTNLSKMPACNIMLIG
1			AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL
i			RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
ł	ì		QBPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTBIR\KQ
1	}		ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA
	ļ.		RISKTLORTLOKOSVVYGGKSTIRDRSSGTASSVAFTPLOGLBI
ł	}		VNPQAAEKKVAKANQKYFSSMAEFLKVKGEKSGLMST
6085	2	1456	SGPRSFQGNRAVGRISLGGKRNPEVTLLPGVSSERVRRWRRARV
		•	GVARVKPGNPWKPSPATQVPR/VPAQVYLPGRGPPLREGEELVM
İ			DEBAYVLYHRAQTGAPCLSFDIVRDHLGDNRTELPLTLYLCAGT
			QAESAQSNRLMMLRMHNLHGTKPPPSEGSDEEEEBEDBEDBEBR
			KPQLELAMVPHYGGINRVRVSWLGERPVAGVWSEKGQVEVFALR
1			RLLQVVEBPQALAAFLRDEQAQMKPIFSFAGHMGEGFALDWSPR
'			VTGRLLTGDCQKNIHLWTPTDGGSWHVDQRPFVGHTRSVEDLQW
)			SPTENTVFASCSADASIRIWDIRAAPSKACMLTTATAHDGDVNV
			ISWSRREPFLLSGGDDGALKIWDLRQFKSGSPVATFKQHVAPVT
			SVEWHPQDSGVFAASGADHQITQWDLG/IVERDPEAGDVEADPG
1		,	LADLPQQLLFVHQGETELKELHWHPQCPGLLVSTALSGFTIFRT
i			ISV
6086	2419	1357	GAATQHGGAMNLLPCNPHGNGLLYAGFNQDHGCFACGMRNGFRV
1		,	YNTDPLKEKEKQEFLEGGVGHVEMLFRCNYLALVGGGKKPKYPP
[ .	:		NKVMIWDDLKKKTVIBIEFSTEVKAVKLRR\DKIVVVLDSMIKV
			FTFTHNP\HQLHVFE\TCYNPKGLCVLCPNSNNSLLAPPGTHTG
			HVQLVDLASTEKPPVDIPAHEGVLSCIALNLQGTRIATASEKGT
			LIRIFDTSSGHLIQELRRGSQAANIYCINFNQDASLICVSSDHG
			TVHIPAARDPKRNKQSSLASASFLPKYFSSKWSFSKFQVPSGSP
	1		CICAFGTEPNAVIAICADGSYYKPLFNPKGECIRDVYAQFLEMT
			DDKL
6087	476	1877	QNSQRTGLPITIPSRSFPLLTGSDLCKNMPCTCTWRNWRQWIRP
]		!	LVAVIYLVSIVVAVPLCVWBLQKLEVGIHTKAWFIAGIFLLLTI
j			biermaiföhfahladdefökbiikirmmabiaerdemiyfkab
j !	ì		GIAIYVDTCRECYBAYVIYNFMGFLTNYLTNRYPNLVLILBAKD
]			QQKHFPPLCCCPPWAMGEVLLFRCKLGVLQYTVVRPFTTIVALI
1			CELLGIYDEGNFSFSNAWTYLVIINNMSQLFAMYCLLLFYKVLK
			EKLSPIOPVGKFLCVKLVVFVSFWQAVVIALLVKVGVISKHTW
]		1	EWQTVEAVATGLQDFIICIEMFLAAIA\HHYTFSYKPYVQEABE
			GSCFDSFLAMWDVSDIRDDISEQVRHVGRTVRGHPRKKLFPEDQ
	·		DQNEHTSLLSSSSQDAISIASSMPPSPMGHYQGFGHTVTPQTTP
<u> </u>			TTAKISDEILSDTIGEKKEPSDKSVDS
6088	1684	689	GASGLVRLLQQGHRCLLAPVAPKLVPPVRGVKKGFRAAFRFQKE
۱ ۰			LERGRLLRCPPPPVRRSEKPNWDYHAEIQAFGHRLQENFSLDLL
] .			KTAFVNSCYIKSEEAKROOLGIEKEAVLLNLKSNOELSEOGTSF
	J		SOTCLTOFLEDRYPDMPTEGIKNLVDFLTGERVVCHVARNLAVE
			QLTLSEEPPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI
j 1	J		TOMTCKELFEMWKIINPMCLLVEELKKRNVSAPESRLTROSG\A

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nuclectide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ľ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	J	\=possible nucleotide insertion)
			PTALPLYFVGLYCDKKLIAEGPGETVLVAEEEAARVALRKLYGF
1			TENRRPWNYSKPKETLRAEKSITAS
6089	3	3054	TRIGIPGSTISSRPRICALAAEGHFIGHSWTGSRAGAHTGAPAW
			PSRRLRDLPAGGMWRLRRAAVACEVCQSLVKHSSGIKGSLPLQK
1			LHLVSRSIYHSHHPTLKLQRPQLRTSFQQFSSLTNLPLRKLKFS
			PIKYGYQPRRNFWPARLATRLLKLRYLILGSAVGGGYTAKKTFD
			QWKDMIPDLSEYKWIVPDIVWEIDEYIDFEKIRKALPSSEDLVK
1			LAPDFDKIVESLSLLKDFFTSGSPEETAFRATDRGSESDKHFRK
	<b>!</b>		VSDKEKIDQLQEELLHTQLKYQRILERLBKENKKLRKLVLQKDD
1			KGIPFIESLRKSLIDMYSEVLDVLSDYDASYNTODHLPRVVVVG
			DQSAGKTSVLEMIAQARIFPRGSGEMMTRSPVKVTLSEGPHHVA
1			LPKDSSREFDLTKEEDLAALRHEIELRMRKNVKEGCTVSPETIS
1			LNVKGPGLQRMVLVDLPGVINTVTSGMAPDTKETIPSISKAYMQ
1			DPNAIILCIQDGSVDAERSIVTDLVSQMDPHGRRTIFVLTKVDL
1			AEKNVASPSRIQQIIEGKLFPMKALGYFAVVTGKGNSSESIEAI
			REYEEPPONSKILKTSMLKAHQVTTRNLSIAVSDCPWKMVRES
i			VEQQADSPKATRFNLETENKNNYPRLRELDRNELFEKAKNETLD
1			EVISLSQVTPRHWEBILQQSLWERVSTHVIENIYLPAAQTMNSG
1			TPNTTVDIKLKQWTDKQLPNKAVEVAWETLQKBFSRFMTEPKGK KHDDIFDKLKEAVKEBSIKRHKWNDFAKDSLRVIOHNALKDRSI
1		i	
			SDKQQWDAAIYFMEEALQARLKDTENAIENMVGPD\WKKRWLYW KNRTQBQCVHNETKNBLBKMLKCNEBHPAYLASDBITTVRKNLB
			SRGVEVDPSLIKDTWHQVYRRHFLKTALMHCNLCRRGFYYYQRH
l I			FVDSELECNDVVLFWRIQRMLAITANTLRQQLTNTEVRRLEKNV
		•	KEVLEDFAEDGEKKIKILTGKRVOLAEDLKKVREIOEKLDAFIE
1			ALHOBK
6090	194	1560	PVFVPAPGAVLEQAS/ASPPLATOTVVPLQHCKIPELPVQASIL
			FELOLFFCOLIALFVHYINIYKTVWWYPPSHPPSHTSLNFHLID
			FNLLMVTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTRFTV
1			LTATGWSLCRSLIHLFRTYSFLNLL/FPLLSVWDVHSVPAABLR
i			P\RKTSLFNHMASMGPRBAVSGLAKSRDYLLTLR\RRGSSTQDS
1			CMARTPCP/PHACCLSPSLIRSEVEFLKMDFNWRMKEVLVSSML
1			SAYYVAFVPVWFVKYTHYYDKRWSCELFLLVSISTSVILMQHLL
			PASYCDLLHKAAAHLGCWQKVDPALCSNVLQHPWTEECMWPQGV
1			
1		1	LVKESKNVYKAVGHYNVAIPSDVSHFRFHFFFSKPLRILNILLL
			LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL
			LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VLGKAYSYSASPQRDLDHRFS
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VLGKAYSYSASPQRDLDHRFS SSRTREMEEKBILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VLGKAYSYSASPQRDLDHRFS SSRTREMBEKBILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VLGKAYSYSASPQRDLDHRFS SSRTREMEEKBILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VLCKAYSYSASPQRDLDHRPS SSRTREMEERBILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVOLSQGQNVVIK VKPPSKSGSASASGAQRGSLEBFEDTPWSDQRPRBGEGEPPRGQ
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VLGKAYSYSASPQRDLDHRFS SSRTREMEBKRILRQJIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHEFPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLBRQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLBEFEDTPWSDQRPRBGEGEPPRGQ LQPSRPTRARGICSVEDPLLVCQKEPGKPRWVKSVGSVGDSPRE
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VLGKAYSYSASPQRDLDHRFS SSFTREMEBKRILRRQIRLLQGLIDDYKTLHGNAPAPGIPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASAGAQRGSLBEFEDIPWSDQRPREGGGEPPRGQ LQPSRPTRARGICSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRIVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VLGKAYSYSASPQRDLDHRFS SSFTREMEBKBILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLBRQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLBEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGICSVBDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VLGKAYSYSASPQRDLDHRFS SSRTREMEBKBILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYRPSRRGYSSHHGFSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLBRQVOLSQGQNVVIK VKPPSKSGSASASGAQRGSLEBFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGICSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VICKAYSYSASPQRDLDHRPS SSRTREMEEKBILRRQIRLLQGLIDDYKTLHGNAPAFGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVOLSQGQNVVIK VKPPSKSGSASASGAQRGSLEBFEDTPWSDQRPREGGEPPRGQ LQPSRPTRARGICSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRKTVSESVLAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGBRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TMKFRKNNYKNVASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VLGKAYSYSASPQRDLDHRFS SSTTREMEBKBILRQQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHEPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLBRQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLBEFEDTPWSDQRPRBGEGEPPRGQ LQPSRPTRARGICSVEDPLLVCQKEPGKPRWKSVGSVGDSPRE PRRTVSESVLAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVCHSGLKPLSGB
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VLGKAYSYSASPQRDLDHRFS SSTTREMEBKRILRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASAGAQRGSLBEFEDTPWSDQRPRBGEGEPPRGQ LQPSRPTRARGICSVEDPLLVCQKEPGKPRWKSVGSVGDSPRE PRRTVSESVLAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNYKWVAASSKSPRVARRALSPRVAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVCHSGLKPLSGK TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VLGKAYSYSASPQRDLDHRFS SSFTREMEBKRILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYYRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASAGAQRGSLBEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGICSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRIVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQARRASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKUHASQLSPVLSRSPSGD\RPAVCHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VLGKAYSYSASPQRDLDHRFS SSETREMEBKRILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYSPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASAGAQRGSLBEFEDTPWSDQRPREGGGEPPRGQ LQPSRPTRARGICSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRIVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDASHTDQPVPSGSVGGPARPASGPRQARRASLVVTCR TMKFRKMNYKNVAASSKSPRVARRALSPRVAAENVCKASACMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSFSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGB TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKRA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA
6091.	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VICKAYSYSASPQRDLDHRPS SSRTREMEBERBILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLBRQVOLSQGQNVVIK VKPPSKSGSASASGAQRGSLBEFEDTPWSDQRPRBGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKBPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TMKFRKNNYKNVASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKOHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGB TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKBA SSLHAVRTAPTSKVIKTRYRIVKKTPASFLSAPPPPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY
6091.	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VICKAYSYSASPQRDLDHRPS SSRTREMEBKRILRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLKRQVOLSGGONVVIK VKPPSKSGSASASGAQRGSLBEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGICSVEDPLLVCQKBPGKPRWKSVGSVGDSPRE PRRTVSESVLAVKASFPSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVCHSGLKPLSGB TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKRA RSLHGVRTAPTSKVIKTRYRIVKKTPASPLSAPPPPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSFWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VICKAYSYSASPQRDLDHRPS SSRTREMEBERBILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLBRQVOLSQGQNVVIK VKPPSKSGSASASGAQRGSLBEFEDTPWSDQRPRBGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKBPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TMKFRKNNYKNVASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKOHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGB TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKBA SSLHAVRTAPTSKVIKTRYRIVKKTPASFLSAPPPPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY
6091	<b>3279</b>	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VICKAYSYSASPQRDLDHRFS SSTREMEBKRILRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHEPSWKKYSLVNRPPG PSDFPADHAVAPLHGARGGQPPVPQQHVLKRQVOLSGGNVVIK VKPPSKSGSASASGAQRGSLBEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGICSVEDPLLVCQKBPGKPRWKSVGSVGDSPRE PRRTVSESVLAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGB TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKRA RSLSLSRSVULNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VIGKAYSYSASPQRDLDHRFS SSTTREMEBERETLRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLBEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGICSVEDPLLVCQKEPGKPRWKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPQARRASLVVTCR TNKFRKNNYKWAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVEHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKBA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFFLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCRRGERCPYIHDPBRV AVCTRPVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VIGKAYSYSASPQRDLDHRFS SSTTREMEBKRILRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASAGAQRGSLBEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRWKSVGSVGDSPRE PRRTVSESVLAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGPARPASGPRQARBASLVVTCR TNKFRKNNYKWAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKQQLIADPEPKPRFATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVCHSGLKPLSGB TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKRA SSLHAVRTAPTSKVIKTYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPBKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN
6091.	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VICKAYSYSASPQRDLDHRPS  SSRTREMEBERILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVOLSQGQNVVIK VKPPSKSGSASASGAQRGSLBEFEDTPWSDQRPRBGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKBPGKPRWKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TMKFRKNNYKWAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKOHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGB TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASFLSAPFPPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRRBKKREYCMYMRFGRCMGRCCPYHDPBKV AVCTRPVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFRARG ACPRGAQCQLLHRTQKRSRRAATSPAPGPSDATARSRVSASHG
6091.	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VICKAYSYSASPQRDLDHRPS  SSRTREMEBRITLRQITHLQQLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDF PADHAVRPLHGARGGQPPVPQQHVLERQVOLSQGQNVVIK VKPPSKSGSASASGAQRGSLBEFEDTPWSDQRPREGGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKBPGKPRWKSVGSVGDSPRE PRRTVSESVLAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGB TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRPPSRAHLPTKEA RSLHAVRTAPTSKVIKTPNKGLVQVTTHRLCRPPSRAHLPTKEA RSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSQQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCMRGERCPYIHDPRKV AVCTRPVRGTCKKTDGTCPFSHHVSKEKMPVCSYPLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKHTLLCPDFARRG ACPRGAQCQLLHRTOKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS
6091	3279	3190	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VICKAYSYSASPQRDLDHRFS  SSRTREMEBERILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLKRQVOLSGGONVVIK VKPPSKSGSASASGAQRGSLBEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGICSVEDPLLVCQKBPGKPRWKSVGSVGDSPRE PRRTVSESVIAVKASFPSALPPRTGVALGRKIGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGB TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKRA RSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPPPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSFWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRPVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPPFRARG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHS PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGGSASPSSSKAS SSSSSSSSPPASIDHEAPSLQRAALAAACSNRLCKLPSFISLQS
	·		LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAPFKLLRDRL VLGKAYSYSASPQRDLDHRFS SSTTREMEBKRILRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLBRQVQLSGGQNVVIK VKPPSKSGSASASGAQRGSLBEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKBPGKPRWKSVGSVGDSPRE PRRTVSESVLAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQARBASLVVTCR TNKFRKNNYKWAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSXPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVCHSGLKPLSGB TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKRA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPPPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRPVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGGYCPLGAKCKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDAATARSVASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGGSASPSSSKAS SSSSSSSSPPASLDHKAPRLQKAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL

		<del></del>	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1D	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sedneuce		\=possible nucleotide insertion)
			VIQLIKTNKKHIHSRSTLECAYRTHLVAGIGFYQHLLLYIQSHY
	j		QLBLQCCIDWTHVTDPLIGCKKPVSASGKEMDWAQMACHRCLVY
	ł	}	LGDLSRYQNELAGVDTBLLAERFYYQALSVAPQIGMPFNQLGTL
	<b>j</b>		AGSKYYNVEAMYCYLRCIQSEVSFEGAYGNLKRLYDKAAKMYHQ
			LKKCETRKLSPGKKRCKDIKRLLVNFMYLQSLLQPKSSSVDSBL
	İ	} .	TSLCQSVLEDFNLCLFYLPSSPNLSLASEDEREYESGYAFLPDL
	1		LIFOMVIICLMCVHSLBRAGSKQYSAAIAFTLALFSHLVNHVNI
!	1		RLQAELREGENPVPAFQSDGTDEPESKEPVEKEEEPDPEPPPVT
	1	į.	POVGEGRKSRKFSRLSCLRRRRHPPKVGDDSDLSEGFESDSSHD
	<b>!</b>	{	SARASEGSDSGSDKSLEGGGTAFDAETDSEMNSQRSRSDLEDME
		1	BEEGTRSPTLEPPRGRSEAPDSLNGPLGPSRASIASNLQAMSTQ
	į		MFQTKRCPRLAPTFSNLLLQPTTNPHTSASHRPCVNGDVDKPSB
,	1		PASKEGSESEGSESSGRSCRNERSIQEKLQVLMAEGLLPAVKVF
	1	}	LDWLRTNPDLIIVCAQSSQSLWNRLSVLLNLLPAAGELQESGLA
		ł	LCPEVQDLLEGCELPDLPSSLLLPEDMALRNLPPLRAAHRRFNF
		1	DTDRPLLSTLEESVVRICCIRSFGHFIARLQGSILQFNPEVGIF
i			VSIAQSEQESLLQQAQAQFRMAQEEARRNRLMRDMAQLRLQLEV
	Į.	<b>\</b>	SQLEGSLQQPKAQSAMSPYLVPDTQALCHHLPVIRQLATSGRFI
		}	VIIPRTVIDGLDLLKKRHPGARDGIRYLEAEFKKGNRYIRCQKB
		,	VGKSFERHKLKRQDADAWTLYKILDSCKQLT\LAQGAGEEDPSG
		ľ	MVTIITGLPLDNPSLLSGPMQAALQAAAHASVDIKNVLDFYKQW
	1		KEIG
6093	76	1002	ACGRRAMLALRVART/SRWGAL\RGAVWAPGTRPSKRRACWALL
}	1	}	PPVPCCLGCLAERWRLRPAALGLRLFGIGQRNHCSGAGKAAPR\
			PAAGAGAAARAPGGQWGPASTPSLYRNPWTIPNMLSMTRIGLAP
· .	}	ł	VLGYLIIEBDFNIALGVFALAGLTDLLDGFIARNWANQRSALGS
į	<b>i</b>		ALDPLADKILISILYVSLTYADLIPVPLTYMIISRDVMLIAAVF
}.	}		YVRYRTLPTPRTLAKYFNPCYATARLKPTFISKVNTAVQLILVA
ĺ	1	Ĭ	ASLAAPVPNYADSIYLQILWCFTAFTTAASAYSYYHYGRKTVQV
<b>[</b>	1		IKD
6094	23	1010	PFLRCLRGDQKAKMSERKVLNKYYPPDFDPSKIPKLKLPKDRQY
1 0034	1		VURLMAPFNMRCKTCGEYIYKGKKFNARKETVQNEVYLGLPIFR
}	1	1	FYTKCTRCLABITFKTDPENTDYTMEHGATRNFQAEKLLEEEEK
1	}		RVOKEREDBELNNPMKVLENRTKDSKLEMEVLKNLQELKDLNQR
ł	1	1	OAHVDFRAMLROHRLSBEERRRQQQBEDEQETAALLBEARKRRL
1			LEDSDSEDRAAPSPLOPALRPNPTAILDEAPKPKRKVEVWEQSV
ł	1	1	GSLGSRPPLSRLVVVKKAKADPDCSNGQPQA/APHPRSPAEQEG
ſ			COPYTPDAWRVLPEPTGCIPGO
6095	1	1599	TRGRAARRSRGRGHGFLGGGPA\SVVDYFPSEDFYRCGYCKNES
2005	1 4	1	GSRSNGMWAHSMTVODYODLIDRGWRRSGKYVYKPVMNQTCCPQ
1		<b>[</b>	VTTRCRPLOPOPSKSHKKVLKKMLKFLAKGEVPKGSCB\DEPMD
l		}	STMDDAVAGDFALINKLDIQCDLKTLSDDIKESLESEGKNSKKE
}		1	RPOELLOSODFVGEKLGSGEPSHS
)	1	1	DE KINDKOKOT AND MANAGED TO THE MANA

TRADOCS:1416257.1(%CSH011.DOC)

Mo: moleotide location corresponding to first amino acid acid amino acid acid amino acid amino acid amino acid acid amino acid amino acid acid acid acid acid acid acid acid	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Mo:			1	(A=Alanine C-Overeine D-Assautic Acid P.
location corresponding to first to first to first to first to first amino acid amino aci			1	Glutamic Acid F-Phenylalanina G-Glymina
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid aequence control of the control of	i			H-Histidine T-Teolegian W-Lymine
to first amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acquence    H-Tryptophan, Y-Tyrosine, X-Unknown, *=Stol Coden, /-possible nucleotide deletion,  -possible nucleotide deletion				
amino acid residue of amino acid amino acid amino acid amino acid sequence sequence sequence sequence (Codon, /=possible nucleotide deletion, /=possible nucle	i			D-Proling O-Clubaning D-Amining
residue of amino acid sequence				S-Carine T-Thronging W. Waling
amino acid sequence  Codon, /=possible nucleotide deletion, /=possible nucleotide insertion  VKVHTVPREPERGEADISKPPCRAKETERSERGEACHAQQNPAGE  BGRQAQGHPPSLFPPKAKSNQPKSLEBLIFESLEMAGENGP VVSSPPSSQPKATLLSSQVLYBYRQWIHDHPDTPTESGP PLCSSPLEAETPPNOPDCYGSPHQQWHDGKLIAWGVUDIC CVSSVLYLYDPDSYSLSLGVSYARIENTSTRQLIBERTSGLIS WGFYHISCPKMYKQYRSDLLCPETYWWPIRQCLSFRIGGY WGFYHISCPKMYKQYRSDLLCPETYWWPIRQCLSFRIGGY VCSPNOPEASVDERSTEPPDRIQWPHKRAIMPYGVYKKQOKDI BERAAVQYASLUGGKCSERMLLFRR  GRYAPALLSSAMEDSERLGFFRINGLDFRILQAVTDLGMSRFTI QRKATPLALBGKOLLARAKTSGGTTANYAIMPLQLLLIRKNYT VVSQAVRGLVIAPTKELAKQAGSHIQQLATICARDVRVAMS  BEDSYGRAVIMEKPDVVVOTFSRILSKLQOGESTRULLARAL LILMSPVTLLAGESGLGFPGHQLQPGVVCGFREFRILMYALL LILMSPVTLLAGESGLGFPGHQLQPGVVCGFREFRILMYALL LILMSPVTLLAGESGLGFPGHQLQPGVVCGFREFRILMYALL LILMSPVTLAGESGLGFPGHQCPQVVCGFREFRILMYALL LILMSPVTLAGESGLGFPGHQCPQVVCGFREFRILMYALL LILMSPVTLAGESGLGFPGHQCPQVVCGFREFRILMYALL LILMSPVTLAGESGLGFFGHGTLLAFFGREFAGNEDHAL LILMSPVTLAGHAGESGLGFPGHAGATTVAGREFAGNE CHIISOPMQCPFVCULTATAKETHLAISEKLXTYFFDDPR CHIPSGFKKESFDJTGCKGTPRINGSPPGAAPSTFYCHAGELDER LAVARGIAMTATVATYERBULEBISFTGLLES IRGASGGAGGEBLG LIVUFSKAKASKPPJSARSFQGRPPEPFTGSAGTSRAATPLEB RELABENAALGDRSCLIKASSPQGRPPEPTGSAGTSRAATPLEB RELABENAALGDRSCLIKASSPQGRPPEPTGSAGTSRAATPLEB RELABENAALGDRSCLIKASSPQGRPPEPTGSAGTSRAATPLEB RELABENAALGDRSCLIKASSPQGRPPEPTGSAGTSRAATPLEB RELABENAALGDRSCLIKASSPCGGAGGEBLGAGG SDDDSGGSGLWGIDNIKGMUNKIMHMAGHAGUVFKERVSULKR RELABENAALGDRSCLIKALASSPGGGRFTTGGQGAGPSGE QPPPSLOTEDO  168  168  1074  MYCLERIBSPLEKGSSPGSSSTSLLLIKGGESSTTPIMEALKIL RELABENAALGDRSCLIKASSPTKERGILLITVANSFRRISK NIJSGGFSHLISKNISSPTFFOILLDDLDTVVNTYLGNSRRISK NIJSGGFSHLISKNISSPTFFOILDDLDTVVNTYLGNSRRISK NIJSGGFSHLISKNISSPTFFOILDDLDTVVNTYLGNSRRISK NIJSGGFSHLISKNISSPTFFOILDDLDTVVNTYLGNSRRISK NIJSGGFSHLISKNISSPTFROILDDLDTVVNTYLGNSRRISK NIJSGGRSSSTPSMRKSSTPTKREIMITTVTANSFRRISK NIJSGGFSHLISKNISSPTFROILDDLDTVVNTYLGNSRRISK NIJSGGRSSSTPSMRKSSTPTKREIMITTVTANSFRRISK NIJSGGSSSTPSMRKSSSTPTKREIMITTVTANSFRRISK NIJSGGRSSSTPSMRKSSSTPTKREIMITTVTANSFRRISK NIJSGGSSSTLICHKORGGGRFTTGTGTGAGAGGEB CODARD AND AND		1		
Sequence   Sequence   Sequence   Sequence   Sequence   Sevent Se				Coden (
WANTTYPEREKGADISKPERTÄKE IRKERGEKENGONPEGE   GEPOAGCHPPSLEPPKAKESINPERSLELITESIJERASHKENG   VVESSPESSGYKATLLSSYGVYERYON-HIRMPOTPTEKSEP   VVESSPESSGYKATLLSSYGVYERYON-HIRMPOTPTEKSEP   FLCSSPLEARTPPNOPPCOYGEPTIQQYMIDGKILAWGYUDIG   CVSSYVLYYPPDYSTILGIGVYSALREIDATRIGUERYSGUSYY   MGFYIHSCPRINKYKGQYRSDLLCPBTYWYPIEQCLUBERYSGUSYY   MGFYIHSCPRINKYKGQYRSDLLCPBTYWYPIEQCLUBERYSGUSYY   MGFYIHSCPRINKYKGQYRSDLLCPBTYWYPIEQCLUBERYSGUSYY   MGFYIHSCPRINKYKGQYRSDLLCPBTYWYPIEQCLUBERYSGUSYY   WGRAPALLSSKMOESRAIGERICIPPHIQAVTOLGNSRPTI   ORKAPILALISKOLLARARTGSGKTANAYIPMLQLLIBERKYT   VVEGANGGLUPYTRELARQAGSHIQQLATYCARDYWANYSS   EBAAVQYASLUVQKCSERMLLPRI   VQRAPALLISKALLCHLPRIYQAFIASATYPROPQUANISS   EDSTOCK   DEBAAVLQYASLUVQKCSERMLLPRIYQAFIASATYPROPQUANISS   EDSTOCK   DEBAAVLQYASLUVQKCSERMLLPRIYQAFIASATYPROPQUANISS   EDSTOCK   DEBAAVLQYASLUVQKCSERMLLPRIYQAFIASATYPROPQUANISS   EDSTOCK   DEBAAVLQYASLUVQKCSERMLLPRIYQAFIASATYPROPQUANISS   EDSTOCK   DEBAAVLQYASLUVQKCSERMLLPRIYQAFIASATYPROPQUANISS   EDSTOCK   DEBAAVLQYASLUVQKCSERMLLPRIYQAFIASATYPROPQUANISS   EDSTOCK   DEBAAVLQYASLUVQKCSERMLLPRIYQAFIASATYPROPQUANISS   CHINSPOTE   DEBAAVLGATARAN   DEBAAVLGATYPROPQUANISS   CHINSPOTE   DEBAAVLGATARAN   DEBAAVLGATYPROPQUANISS   DEBAAVLGATY	1		seduence	
BGFOAGGHPPSLEPPSKARNOPESLEDLIFESLEENARKINE  VURSSPERSOKATLLESVOVYRRYMYMINDETTPESCEP  PLCSSPLRAFTPENGPCGYGSFHQCYMOCKTLAWGYDDIA  CVGSVYLYYDPDYSPLSLGVYSALRELAFTQUENCUSTI  MGFTHSCPKMYKKGYPSDLLCPSTTVWPPIEGCLESIENS  YCEPNDDPERVDEDRSTBPDRLQVFHKRAIMPYGYYRKQCKDI  SYCHNDDPERVDEDRSTBPDRLQVFHKRAIMPYGYYRKQCKDI  EBAANLQVASLVQKCGSERMLJPRM  GORAFIELALEKOLLARARNISGKTAATAJEMQLLLIHRKYKOKAT  VURGAVRGLULVFTKRLAROAGSHIOQLATYCARDVRYANYS  BDGYSGRAVLAREKDOVVGTSKLIGHGOLATYCARDVRYANYS  BDGYSGRAVLAREKDOVVGTSKLIGHGOLATYCARDVRYANYS  BDGYSGRAVLAREKDOVVGTSKLIGHLGOLATYCARDVRYANYS  BDGYSGRAVLAREKDOVVGTSKLIGHLGOLATYCARDVRYANYS  BDGYSGRAVLAREKDOVVGTSKLIGHLGOLATYCARDVRYANYS  BDGYSGRAVLAREKDOVVGTSKLIGHLGOLATYCARDVRYANYS  BDGYSGRAVLAREKDOVVGTSKLIGHLGOLATYCARDVRYANYS  BDGYSGRAVLAREKDOVVGTSKLIGHLGOLATYCARDVRYANYS  BDGYSGRAVLAREKDOVVGTSKLIGHLGOLATYCARDVRYANYS  BDGYSGRAVHEREDOVGGTSVSLIGHLGOLATYCARDVRYANYS  BDGYSGRAVINERDOVGTSKLIGHLGOLATYCARDVRYANYS  BDGYSGRAVINERDOVGTSKLIGHLGOLATYCARDVRYANYS  BDGYSGRAVINERDOVGTSKLIGHLGOLATYCARDVRYANYS  BCHARRAFICANIA BROWNERGERGERGOLASI  CHISSPPALLAFINGARIA BROWNERGERGOLASI  BCHARRAFICARIA  BCHARRAFICARIA  BCHARRAFICARIA  BCHARRAFICARIA  BCHARRAFICARIA  BCHARRAFICARIA BROWNERGERGERGOLASI  BCHARRAFICARIA SPECIALSGRASGAGGRISLIGHE  BCHARRAFICARIA SPECIALSGRASGAGGRISLIGH  BCHARRAFICARIA SPECIALSGRASGAGFORPEPE LIGHP  PROPPUSLICHSTIPUSLICHISTOPPERVARAGRYPEN LIGHP  PROPPUSLICHSTIPUSLICHISTOPPERVARAGRYPEN LIGHP  BCHARRAFICARIA SPECIALSGRAPPEN LIGHP  BCHARRAFICARIA SPECIALSGRAPPEN LIGHP  BCHARRAFICARIA SPECIALSGRAPPEN LIGHP  BCHARRAFICARIA SPECIALSGRAPPEN LIGHP  BCHARRAFICARIA SPECIALSGRAPPEN LIGHP  BCHARRAFICARIA SPECIALSGRAPPEN LIGHP  BCHARRAFICARIA SPECIALSGRAPPEN LIGHP  BCHARRAFICARIA SPECIALSGRAPPEN LIGHP  BCHARRAFICARIA SPECIALSGRAPPEN LIGHP  BCHARRAFICARIA SPECIALSGRAPPEN LIGHP  BCHARRAFICARIA SPECIALSGRAPPEN LIGHP  BCHARRAFICARIA SPECIALSGRAPPEN LIGHP  BCHARRAFICARIA SPECIALSGRAPPEN LIGHP  BCHARRAFICARIA SPECIALSGRAPPEN LIGHP  BCHARRAFICARIA SPECIALSGRAPPEN LIGHP  BCHARRAFICARIA  BCHARRAFICARIA  BCHARRAFICARIA  BCHARRAFI	ļ	bequence		
UVESSPESOCKATLLESTQUYERYQMUIRKNEPDTPESOCP FICSSPERAPPENDEDGOSTORSHQQYMUIRKNEPDTPESOCP FICSSPERAPPENDEDGOSTORSHQQYMRAIDKI JAWGUTILL CVSSVYLYTOPDYSPLSIGVYSALREIAFTRQLIEKTSQUSYY MGFYTHSCPKMCKKGQYRPSDLLCPBTYWWPIEGCLUSIAN YCHNODERADDENSTPENDLLQVPHRAIDFYWYKRQOKD ERAAVLQYASLVOQKCSERMLLPRM ORNAIDLASJAMDENSAIGPERLQDSKALDAVDLGNSRPTI ORNAIDLASJAMDENSAIGPERLQDSKALDAVDLGNSRPTI ORNAIDLASJAMDENSAIGPERLADAVDLANDAVIDLANDAVIDLANDAVIDLANDAVIDLANDAVIDLANDAVIDLANDAVISAI BERAULQYASLVOQUAYVYKRALDAVDLADAVIDLANDAV	Ī			
PLCSSPLEAPTPPNGPCGYGSTPIQQYMIGHKTIGUSTYDILG CVSSVLIVIPDPSYSHISLGYSALRELAPTQUIBERTSOLSYS MGFYIHSCPKMKYKGQYRPSDLLCPBTYWVPIEQCLPSLENE YCRFMQDPERAVEGURSTBPDRLQVPHKRAIMPYGYVKRQKDI BERAVLQTASILVQKCSERMLJERM GERAVLQTASILVQKCSERMLJERM GERAVLQTASILVQKCSERMLJERM GERAVLQTASILVQKCSERMLJERM UNGAVRGLULVPTKRSTATSGKTATAYJAPHQLLIAHRKATT VVBOAVRGLULVPTKRSTATSGKTATAYJAPHQLLIAHRKATT VVBOAVRGLULVPTKRSTATSGKTATAYJAPHQLIAHRKATT VVBOAVRGLULVPTKRSTRISGKTATAYJENGLELIA DERADLISPSGFERBIKSSLICHLPRIYQAFKASTRINDVQALI LIHMPVILKIQESQLPGPPQLQQPQVVCTERBKFLLIYALI LISJIRKGLLPAVTKRSTRIRLIPLEQPSTITCVLNGSLPJRA CHIISQPAQGFYDCVLATARAVLGAPVKGKRGGFKGKASI RAGVARGLDYBHVSAVLNFULPPTPAYTHATGATRANNEN LITVULPTEQPHIGKIBELLSGERRGP ILLPYQFRMERIEGFRY CRDAMRSVTKQAI REARLKSTRBRIAHSBKLKTYFRONDR\DI LITVULPTEQPHIGKIBELLSGERRGP ILLPYQFRMERIEGFRY CRDAMRSVTKQAI REARLKSTRBRIAHSBKLKTYFRONDR\DI LITVULPTEQPHIGKIBELLSGERRGP ILLPYQFRMERIEGFRY CRDAMRSVTKQAI REARLKSTRBRIAHSBKLKTYFRONDR\DI LITVULPTEQPHIGKIBELLSGERRGP ILLPYQFRMERIEGFRY CRDAMRSVTKQAI REARLKSTRBRIAHSBKLKTYFRONDR\DI LITVULPTEQPHIGKKEBELLSGERRGP ILLPYQFRMERIEGFRY CRDAMRSVTKQAI REARLKSTRBRIAHSBKLKTYFRONDR\DI LITVULPTEQPHIGKKEBELLSGERRGP ILLPYQFRMERIEGFRY CRDAMRSVTKQAI REARLKSTRBRIAHSBKLKTYFRONDR\DI LITVULPTEQPHIGKKEBELLSGERRGP ILLPYQFRMERITEGFRY CRDAMRSVTKQAI REARLKSTRBRIAHSBLWATHTKACHTART PROPERSILLSKRSSPIPTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOT	1			
CVSSVILYDDDYSTISLGVYSALREIAFTRQLIBRETSGLSYN MGFYTHISC PUNKKKGGYRESDLLCPBTYWWPTEQCLPBLENB YCRFNQDPEAVDEDRSTBPDRLQVFHKRAINPYGVYKKQGKDI ERAAVLQYASLWCQKCSERNILLPRN ORRAFLALSSAMDGSEALGFHRMGLDFFLLQAVTDLGWSRPTI ORRAFLALBGKDLLARARTSGGKTAAVIFMQLLLBRKAT VWRQAVRGLUVPTKELARAQOSINIOQATAAVIFMQLLLBRKAT VWRQAVRGLUVPTKELARAQOSINIOQATAAVIFMQLLLBRKAT VWRQAVRGLUVPTKELARAQOSINIOQATAAVIFMQLLLBRKAT DERADLLPSFGFEERKSLLCHLPRIYQAFIMASTPRBDVQALI LILBRPVTLKLGSSGLPODLQOQVCVCTEREDKRLLIDAL LILBRPVTLKLGSSGLPODLQOQVCVCTEREDKRLLIDAL LILBRYTLKLGSSGLPODLQOQVCVCTEREDKRLLIDAL LILBRYTLKLGSSGLPODLQOQVCVCTEREDKRLLIDAL LILBRYTLKLGSSGLPODLQOQVCVCTEREDKRLLIDAL LILBRYTLKLGSSGLPODLQOQVCVCTEREDKRLLIDAL LILBRYTLKLGSSGLPODLQOQVCVCTEREDKRLLIDAL LILBRYTLKLGSSGLPODLQOQVCVCTEREDKRLLIDAL LILBRYTLKLGSSGLPODLQOQVCTEREDKRLLIDAL LILBRYTLKLGSSGLPODLQOQVCTEREDKRLLIDAL LILBRYTLKLGSSGLPTBLARKGRAVAGRARGERGLDAS RAOVARGTDPHIVSAVLANICHPODLYPPALVIRRACKTARANNOGI LIVPLFTSGPILGKTERLSGERRGFLIDAGRACGAGGGGLDAS FLYGRPREGSPRTKVANALPPRENCYPPTEGATERANNOGI LILBRIDALPPAVVRHLCHUPDVLVPPALVEPHEKYGRS PLYGRPREGSPRTHCAASSTKERNSDPQRSPRPVVKLCHELGE FRLEMSGGKKSSSFDITSVTTDYEGGSSEASDPPTVVGLHCLG YRGRATCVDVVERDLERSSPFGGLEGGSLDAS ELASLGLABTPPSGLSGGTSSLPSGSSRFRVVKLCHELGE LVVPSKAKAKKPPLSASSPQQRPPRPETGSSAGTSRAATPLAS RVBARAGGGARTPPLSARRAVVMILRBGSPRGASSFTVDPFTQPTGFG RVBARAGGGARTPPLSARRAVVMILRBGSPRGWDVPRLLGP RPSSPALVFTIDASLVHKSPDPFCAVAAQKPSLAHSMLAISGH PRSSPALVFTIDASLVHKSPDPFCAVAAQKPSLAHSMLAISGH PRSSPALVFTIDASLVHKSPDPFCAVAAQKPSLAHSMLAISGH PRSSPALVFTIDASLVHKSPDPFCAVAAQKPSLAHSMLAISGH PRSSPALVFTIDASLVHKSPDPFCAVAAQKPSLAHSMLAISGH PRSSPALVFTIDASLVHKSPDPFCAVAAQKPSLAHSMLAISGH RVBARAGGGRSSSLPPSNKSSTTPKKSTTPTVATARTTAPTTVTVSPPGC QPPSLLGSTDQ VQALSNOGMSGGLUTILDSLGGGGFTGTRQCQAPFGES BGKI FKNWGYQTEKKBUTSNINPRQTETSVRASSSPEKCAQQRQ RLNASAGRSSSLPPSNKSSTTPKKSITIPTVTVATSPRSPK NLSGGSFBLISKNSSSPERPOLLLLDLIDTVPVSTLQCHTMPRG VQPLEDBSSFLISKNSSSPERPOLLLDLIDTVPVSTLQCHTMPRG LTKKRQQI RAALSRMSPCGGTTTLQTRLNQRAFGRSFGKD VGLEDHSSFLISKNSSSPERPOLLLDLIDTVPVSTLQCTRTHTQ VGPLEDBSSFLISKNSSSTPTKRITHITTSWLEDAGGRSGKD VGPLEDBSSFLISKNSSTTRATARTTAPTRAPTSVR VG	ŀ			
MGFYIHSCERMKYKGQYRSBLLCHETYWVPIEGLCSLESH.     YCRPNODPENDERNOTERSTERDRIQVPHKRA MPYGVYKKQQKD    REAAVLQYASLVGQKCSERMLLFRN    GRVARALLSSAMEDSRALGFRNHGLDPRILQAVTDLGWSRPTI    GRVARALLSSAMEDSRALGFRNHGLDPRILQAVTDLGWSRPTI    GRVARALLSGAMLARATGGGTRAYAJPMIQLLHRKAY     VVBQAVRGLVLVPYKKLARQAGSNIQQLAYTCARDVRVANVS    BUGSVGGANLHKERDVVVOTOSRILSHAJPMIQQLATYCARDVRVANVS    BUGSVGGANLHKERDVVVOTOSRILSHAJPMIQQLATYCARDVRVANVS    LILHINPVILKLQESQLPGPQULQCFUVVATTARVLGAPVKGRRGRGPKGDKAS    LILHINPVILKLQESQLPGPQULQCFUVVATTARVLGAPVKGRRGRGPKGDKAS    CHI ISQPNQGFYDCVLATDARVLGAPVKGRRGRGPKGDKAS    CHI ISQPNQGFYDCVLATDARVLGAPVKGRRGRGPKGDKAS    CHI ISQPNQGFYDCVLATDARVLGAPVKGRRGRGPKGDKAS    CHI ISQPNQGFYDCVLATDARVLGAPVKGRRGRGPKGDKAS    CHI ISQPNQGFYDCVLATDARVLGAPVKGRRGRGPKGDKAS    CHI ISQPNQGFYDCVLATDARVLGAPVKGRRGRGPKGDKAS    CHI ISQPNQGFYDCVLATDARVLGAPVKGRRGRGPKGDKAS    CHI ISQPNQGFYDCVLATDARVLGAPVKGRRGRGPKGDKAS    CHI ISQPNQGFYDCVLATDARVLGAPVKGRRGRGPKGDKAS    CHI ISQPNQGFYDCVLATDARVLGAPVKGRRGRGPKGDKAS    CHI ISQPNQGFYDCVLATDARVLGAPVKGRGRGRGRGPKGDKAS    CHI ISQPNQGFYDCVLATDARVLGAPVKGRRGRGRGRGPKGDKAS    CHI ISQPNQGFYDCVLATDARVLGAPVKGRRGRGRGRGPKGDKAS    CHI ISQPNQGFYDCVLATDARVLGAPVKGRRGRGPFKCNQCKAS    CHI ISQPNQGFYDGKGKTSHANGAPPRASTATILTARVLATARVLANALGAPTARVLANALGAPPRASTATILTARVLAN	İ			
CERANUL/DYSLIVOCKCSERMILEPRN	į.	i .		
BRANIQYASILVGKCSERMILIPEN	ŀ			
6096  2277  575  GRWARILSSAMEDSEALGFERNSLDERLIQAVTDLGNSRETT QBKAIPLALBGKOLLARARTSGKTAAYAIPMLQLLLHRIGAT VARGAVGGULVPYRKLLARQAGGMIQLATYCARDVRAWSS EDSVSQRAVLMKKPDVVVGTPSKILSHLQODSLKURDSLKURDSLKUL DEADLIJESGFERKIKSLICHURJOALHSATYRHDVQALI LILHNPYTLKLQESQLPQPDOLQQPQUVCETEEDKPILLVALI LSLIRGKSLLFVWTLERSYRLREPLEQFSIPTCVINGERLPLRE CHISQPRQGFYDCVIATDAEVLGAPVKKKRGKGRPKGDKASI EAGVARGIDPHRVSAVLNFDLPTPEAYTHRAGKTARANDPGIL LIFVLJTEGPHIGKIERLIGERGAPVKKKRGKGRPKGDKASI EAGVARGIDPHRVSAVLNFDLPTPEAYTHRAGKTARANDPGIL LIFVLJTEGPHIGKIERLIGERGAGTFTRANDPGIL LIFVLJTEGPHIGKIERLIGHVGFRWERE IEGFRY CRDAMBSVTKQAIREARLIKSIKRBLHJGKKLKTFEDNPR \ \DIL LLRHDLPLHPAVVKPHLGHVPDYLVPPALRGLVRPHKK\GRSC CRDAMBSVTKQAIREARLIKSIKRBLHJGKKLKTFFEDNPR \ \DIL LLRHDLPLHPAVVKPHLGHVPDYLVPPALRGLVRPHKK\GRSC PLUGRPREQSPRTHVCAASSTKRENSDPDSPPFVVVGLWS PROMPENSPPFVGGGKKKSSFQITSVTTDVEGGGSGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA				
QBKAIPLALEGKOLLARARTGSGKTAAVAIPMLQLLLHRKATT VVRQAVRGLUVPTKELARQAQSMIQQLATYCARDVERVANVS EDSVSQRAVLMKENDVVGTPSELELQODISLKINGSLELAL DEADLLPSSGFRERIKSILCHLERIYQDAIMASATENBOVQALI LILHNPVTLKLQESQLPGPDQLQOFQVVCTSTEEDKFILLYALI LSLIRGKSLLEVNTLERSYRLRIPLEQPSIPTCVLNGELPLRE CHIISQPNQGFYDCVIATDAEVLGAPVKGKREGPKODASI EAGVARGIDPHHVSAVLNFDLPPTPEYTHRAGRITARANPGI LTPVLPTEQPHIGKIEBLLSGERRGFILLPVQPRMERIEGFIRE CRDAMRSVTKQAIREARLKEIKBELLHSEKKTYFENNFEN LTPVLPTEQPHIGKIEBLLSGERRGFILLDPVQPRMERIEGFIRE CRDAMRSVTKQAIREARLKEIKBELLHSEKKTYFENNFEN LIMBLPLHDAVVRHLGHVDVLVDPPALRGLVEPHKK\GRS CRDAMRSVTKQAIREARLKSDPQSPSPVVGLMS  APGTNSGCKKKSSFOJTSVTTDVEDVEDGSSGASDPFTQPTGFIRE PROGRESSGKSSTOJTSVTTDVEDGSSGASDPFTQPTGFIRE PROGRESSGKSSTOJTSVTTDVEDGSSGASDPFTQPTGPTGPTQARSFTGGL VRGRRATCVDVERDLEPHSFGGLLEGIRGASGGAGGELDS BELASLGAPTPSGGLSGGFTSHLARPPTSPGQARSFTGGL VRGRRATCVDVERDLEPHSFGGLLEGIRGASGGAGGELDS BELASLGAPTPSGGLAGGGGTSLDSH RYSERAGGSGATFLFSTSTALVERREPTSPGQARSFTGGL LVVPSKAKARKPPLSASSQQRPPBPETGSSAGTSRAATPLES RYSERAGGSGATFLFSTSRAVVMRIRMSLGAPBERGGVPFL RPSSPALYFTHDASLVHKSPDPFGAVAQKPSLAHSMLAISGH RYSERAGGSGATFLFSTSRAVVMRIRMSLGAPBERGGVPFL RPSSPALYFTHDASLVHKSPDPFGAVAQKPSLAHSMLAISGH PNOPPVLSLPSLTIVDIGLEGLASAAWPPLMPALLVPVPFGAV VDALSMGWSFGPLEHLLITPSLDCGGGGFTTGQQCAPPGGES QPPPSLPGTPQQ  ***POSTPATA**********************************	5006	2222		
UVBOANGLULPTKELAROAGSMIQOLATYCARDVRANDS EDSUSGRAVLMEKPDUVUGTPSRILSHLQODSLKLRIDSLELAL DRADLIFSSGFEREILKSLLCHURTI YOAFLASATINBUQALI LILHINPYTIKLOESQLPSPDOLQOPQUVUGTEBORFILLIVALI LISLIRGEGLLFVINTERSYRIRJELBOPSIPPCUNGELPLRE CHIISQPNQGPYDCUIATDAEULGAPUKKKRGRGPKODKASI RAGVARGIDPHRUSAVLINFDLPPTPSAYIHRAGETARANDPGI LITVILPTEOPHIGKIERBLIGERINGETLLHPQFRWERIEGFT CRDAMBSUTKOALREALKSIKRELLHSEKUKTYFRONPR\DI LLRHDLPLIPAVVKPHILGHVPDYLVPPDAAYIHRAGETARANDPGI LLRHDLPLIPAVVKPHILGHVPDYLVPPDAAYIHRAGETARANDPG\DI LLRHDLPLIPAVVKPHILGHVPDYLVPPDAAYIHRAGETARANDPG\DI LLRHDLPLIPAVVKPHILGHVPDYLVPPDAAYIHRAGETARANDPG\DI LLRHDLPLIPAVVKPHILGHVPDYLVPPDAAYIHRAGETARANDPG\DI LLRHDLPLIPAVVKPHILGHVPDYLVPPDAAYIHRAGETARANDPG\DI LLRHDLPLIPAVVKPHILGHVPDYLVPPDAYBPLVPPPQDPPG PLOGREGKKKSSFQITSVITTOVEGGSGGRADEPFROPPTCOPPTG PROGREKKSSFQITSVITTOVEGGGSGGAGGRELDSR BLASLGLGAPTPPGGSGGTPBRGSPGAPSRFRVVKLPHGLGE YRRGRWTCVDVYERDLEPHSFGGLIGGIGGAGGAGGGGGGG BLASLGLGAPTPPGGGGTPBRGSPPPTGPSAGTSRAATPLES RVEARAGGGGATTPPLGREXASPOQREPPETGSSAGTSRAATPLES RVEARAGGGGATPPLGREXASPOQREPPETGSSAGTSRAATPLES RVEARAGGGGATPPLGREXASPOQREPPETGSSAGTSRAATPLES RVEARAGGGGATPPLGREXASPOQREPPETGSSAGTSRAATPLES RVEARAGGGGATPPLGREXASPOQREPPETGSSAGTSRAATPLES RVEARAGGGGATPPLGREXASPOQREPPETGSAGTSRAATPLES RVEARAGGGGATPPLGREXASPOQREPPETGARSAGTSCAATPLES RVEARAGGGGATPPLGREXASPOQREPPETGARSAGTSCAATPLES RVEARAGGGGATPPLGREXADVARLERPETGARATEALATPLAPETERVILLS RELABENAALDGREGLIRALA\SPEGLESAGTSTALTKRORTFTRIPTAVARSPRESPK VQALSNGPWSPGPLPHILLIPSLDGGGGFTTTGTRIANGBAFGRSFCKD VQALSNGPWSPGPLPHILLIPSLDDLDTVVYSTLORTHPRKQ VQPLPLDDSEEK\TYSEKAT\DDITUMHSSCPEVPNOXYKVSYV TAMERKASVSVEQCKPVSVTPQGNDPEYTAKITTLAETERFT\ LETKEKQITRALSKWESSPIREPILLODLDTVVSTLORTHPRKQ RELABERNOTTRINGTYSKRITTSVINNSSCPESTVNASRSPEKCAQORQ RINSAGRSSLPPSNRKSSTPTKREIMITPVTVAVSPKRSEK MISPGFSHILLSKWESSPIREPILLODLDTVVSTLORTHPRKQ VGPLPLDDSEEK\TYSEKAT\DDITUMHSSCPEVPMSVKKVSYV TAMERKSVSVEQCKPVSVTPQGNDPEYTAKIRTLAETERFT\ LETKEKQITASTYRGAAGALLVYDITRRETFRILTSUEDARQHSSSTGG TAMERKSVSVEQCKPVSVTPQGROPPTAALRTLAETERFT\ ELTKEKQITABALGRAPHSSGGRITTGTTRIAPARAGRAGGSGG TAMERAGGGAAGALLVYDITRR	. 6096	2277	575	1
BDSYSQRAVLMEKPDVVVGTPSRILSHLQDGSLKLRDSLKLAN   DEADLLFSFGFRERKSLLCHLPRIYQAFIMSATFNEDVQALI   LILHNPVTLKLQESGLPGPDQLQPQVVCETEBOKFILLYALI   LSLIRGKSLLFVNTLERSYRIRLFILEQFSITFCVIANGELFLRE   CHIISGPNGGFFVGVATATABAVLAPVEKRERGEFPGDXASI   EAGVARGIDPHHVSAVLNFDLPPTPEAYIHRAGRTARANNPGI   LIFVLPTEDFHLGKLEBLLSGERNRGFILLFVQFPMEBLIEGFR   CRDAMBSVTKQALREARLELISGERNRGFILLFVQFPMEBLIEGFR   CRDAMBSVTKQALREARLELISGERNRGFILLFVQFPMEBLIEGFR   CRDAMBSVTKQALREARLELISGERNRGFILLFVQFPMEBLIEGFR   CRDAMBSVTKQALREARLELISGERNRGFILLFVQFPMEBLIEGFR   CRDAMBSVTKQALREARLELISGERNRGFILLFVGFNBEBLIEGFR   CRDAMBSVTKQALREARLELISGERNRGFILLFVGFNBEBLIEGFR   CRDAMBSVTKQALREARLELISGERNRGFILLFVGFNBEBLIEGFR   CRDAMBSVTKQALREARLELISGERNRGFILLFVGFNBEBLIEGFR   CRDAMBSVTKQALREARLELISGERNRGFILLFVGFNBEBLIEGFR   CRDAMBSVTKQALREARLELISGERSPERVEWGLMS    CLAURINGEPEDDGGGGTFRNGSPPGASPFPVKLFHGLE   FRUSPREGERGTCATTVTPLGGGGSFTGTRASTFPLSE   CRDAMBSVTKQALREARLELISGERSPERVEWGLMS    CRDAMBSVTKQALREARLELISGERSPERGGGARSLDBB    ELASLGLGAPTPSGLSGGPTSULPPFTGBGAGSGAGGRSLDBB    ELASLGLGAPTPSGLSGGPTSULPPFTGBAGSGAGGRSLDBB    ELASLGLGAPTPSGLSGGPTSULPPFTGBAGSGAGGRSLDBB    ELASLGLGAPTPSGLSGGPTSULPPFTGBAGSGAGGRSLDBB    ELASLGLGAPTPSGLSGGPTSULPPFTGBAGSGAGGRSLDBB    ELASLGLGAPTPSGLSGGPTSULPPFTGBAGSGAGGRSLDBB    ELASLGLGAPTPSGLSGGPTSULPPFTGBAGSGAGGRSLDBB    ELASLGLGAPTPSGLSGATTPLGRAGGGAGGRSLDBB    ELASLGLGAPTPSGLSGATTPLGRAGGGAGGRSLDBB    ELASLGLGAPTPSGLSGATTPLGRAGGGAGGTSLDBBBBCAGGAGGAGGABLIANALSABARATALISGER   CRDAMBSVATALISGERBSTALIKKGRETSDTPTIMALKELISGERBPTGBALLTVATARSASSPEKCAQGAGABARATALISGERBPTARSASSPEKCAQGAGABARATALISGERBPTARSASSPEKCAGAGAGABARATALISGERBPTARSASSPEKCAGAGAGABARATALISGERBPTARSASSPEKCAGAGAGABARATALISGERBPTARSASSPEKCAGAGAGABARATALISGERBPTARSASSPEKCAGAGAGABARATALISGERBPTARSASSPEKCAGAGAGABARATALISGERBPTARSASSPEKCAGAGAGABARATALISGERBPTARSASSPEKCAGAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1			
DEADLIFSFGFRERKSLICHIPRIYOAFIMSATFMEDUQALI LILHMPVTKKLQESQLPGPDQLQQPQVCETREDRFILLYALI LSLIRGKSLLFWNTLERSYRIRLFILEQESIPTCVLNGBELPLER CHIISQPNQGFYDCVIATDAEVICAPVEGRREGEPEGDKASI RAGVARGIDPHINSAVLARED_PDEAYTHRAGETARANNPOL LIFVLPTEQFHLGKIEELLGERNGGPILLPYQFRMEEIEGFRX CRDAMSSVTYQAIRBARLKEIKELLIJSBKLKTYFEDNIPS\DI LLERDLPLIPBAVYKPHILGHEVPUYPPAKIGLIVPHIKK\GRSC PLVGRPREGSPRTHCAASSTKERNSDPQDSSPFRWVKLPHGLIGE PRIPMEGSPRTHCAASSTKERNSDPQDSSPFRWVKLPHGLIGE YRRGGKKSSFQITSVTTDYRGPGSPGSDFPFYQDFTGE VARRENGESPPTGGGGSTPRNGSSPPGABDPFFYGDPTGE YRRGRTCUDVYERDLEPHSFGGLLGGIRGASGGAGGRELDGR ELASLGIGAPTPPSGLSQGTTSNICSPPPGAPSSFFRWVKLPHGLIGE YRRGRTCUDVYERDLEPHSFGGLLGGIRGASGGAGGRELDGR ELASLGIGAPTPPSGLSQGTSUPNICSPPPGAPSSFFRWVKLPHGLIGE YRRGRTCUDVYERDLERDSPPSGRADFFFYDPQARSFFTGGL EVYPSKAKAEKPPLSASSPQRPPEPETGSSAGTSRATPLES RVZBARAGGSGATTPPLSRRKAVDWRILRHEIGAPREMGQVPPL RPSSPALYFTHDASIVHKSPDPCAAAQKYSLAHSMLAISGR PSSSPALYFTHDASIVHKSPDPCAAAQKYSLAHSMLAISGR PSSSPALYFTHDASIVHKSPDPCAAAQKYSLAHSMLAISGR RELABENAALDQBNGLIRALA\SPEQLGSAGPPRGVPR\LGPP PNSPFYLSLPSTITUPLGLEDGLASAAWPPLPMBALTUPVPFQV VQALSNGPWSPGPLPHLLIIPSLDGGGGGFRTGRQQGAPPGBE QPPPSLDGTPQQ  40ALSNGPWSPGPLPHLLIIPSLDGGGGGFRTGRQQGAPPGBE QPPPSLDGTPQQ VQALSNGPWSPGPLPHLLIIPSLDGGGGFRTGRQQCAPPGBE QPPSLDGTPQQ  6098  168  1074  NYCLRRRSPLEEDSSPGSSSTSLLIKKQRETSUTPIMRALKEL BGKIFRNMGTOTEKRDTSNINPRQTETSVAASRSPEKCAQQRQ RINSASQRSSSLPPSNRKSSTPTKRSIMLTPVTVAYSPKRSPK NLSPGFSHLLSKNRSSPIRRDILLDDLDTYPVSTLQRTMPRRQ QPLPLDDSEEK\TYSEKAT\DDIVNHSSCPBPVPNGVKKVSV TAMEKKSVSYGCKPVSVTPQGNDFSYTAKITLAFTERFP\ ELTKEKQQIRAALSRMPSPGGRITLQTRINQEAFGRSFGKD  NSPGFSHLISKNRSSPIRRDILLDLDLDTYPVSTLQRTMPRRQ RINSASQRSSSLPPSNRKSSTPTKRSIMLTPVTVAYSPKRSPK NLSPGFSHLISKNRSSPIRRDILLDLDLDTYPVSTLQRTMPRQ PLYNDSEEK\TYSEKAT\DDIVNHSSCPBPVPNGVKKVSV TAMEKKSVSYGCKPVSVTPQGNDFSYTAKITLABTERFP\ ELTKEKQQIRAALSRMPSPGGRITLQTRINQEAFGRSFGKD  6000  2  713  FVENSSYRSRADPEFRGRDTMTYAYLFKYIIGDTGVGKSGCLIA QFTDKRPQVHIDLTIGVEFGRRWNIIGKGLIXDLENARQHSSSN  VIMILGNNSDLESGRBVVKREGERAPARE\HIGHTFWILDLENARHSSN	i i			
LILINPYTIKLÓGESCI-GPDOLOGPOVICETREDKFILI/ALI  LSLIRGKSLIPVNTLERSYRIRLPI-GPSIPTCVINGELPIRE  CHI ISOPNOGPYDCVIATDAEVICA-PVEGKREGGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGE	1 1		İ	
LSLIRGESLIFVETLERSYRIRJEPERPSTPTCVLNGELPLER CHIISQPNQGFYDCVLATDAEVICAPVKKRRGRGFKGKKASI BAGVARGIDPHHVSAVLINFDLPFTPEAYIHRAGRTARANNPGI LITVPLPTEQFHLGKIERELLGERINGGFILLFVQFRMERIEGFRY CRDAMRSVTKQAIREARLKEIKRELHBERLATYFENDIPR_NI LLRHDLPLHPPAVVKPHLGHVPDVLVPPALKGLYPPERY CRDAMRSVTKQAIREARLKEIKRSDPQFPFRVVGLPHR LLRHDLPLHPAVVKPHLGHVPDVLVPPALKGLYPPHKK_GRSC CRDAMRSVTKQAIREARLKEIKRSDPQFSPRVVGLPHR LLRHDLPLHPAVVKPHLGHVPDVLVPPALKGLYPPHKK_GRSC PLVGRRRGSGFSFFTKRENSPDGSPFFTVVGLPHRGLGE YRRGRATCVDVYERDLEPHSFGGLLGGIRGASGASGRSLDSE ELASLGIGAPTPPSGGLSGGFBLAFFRANPPHFGGLAGFFQARSFFTNGLG YRRGRATCVDVYERDLEPHSFGGLLGGIRGASGASGRSLDSE ELASLGIGAPTPPSGGLSGGFBLAPPTAFDGPQANSAFFNGLG PROPPPSGLAGGFTARASINAPPTEGFGARSFFTNGLE LVVPSKAKAKKPPLSASSPQRPPPEFTGESAGTSRAATPLPS RVEARLAGGSGATPPLSGRKAVDMRLERMLGAPBENGQVPPLL PROSPPALSTINDSLINKESPEQLASAGPPRGVPR_LGP PNGPFYLSLESLTIVPLGLPGLASAAWPLPMPAALYKEVULKG RELABRNAALEQENGLLRALA_NSPQLASAGPPRGVPR_LGP PNGPFYLSLESLTIVPLGLPGLASAAWPLPMPAALYVPFGV VQALSNOPMSPGFLPHILLIPSLDGGGGGFTTGQQCAPPGEE QPPPSLGFTPQQ  168 1074 NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKEL BGKIFRINGTQTEKBUTSNINPRQTETSVNASRSPBKCAQORQ RIMSASGRSSLPPSMRKSSTPTKREIMITPVTVAYSPKRSPK NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QPLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVBNGVKVSV TAMERKSVSYEQCKPVSVTPQONDPBYTAKIRTLAFTERFF/\QPLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKVSV TAMERKSVSYEQCKPVSVTPQONDPBYTAKIRTLAFTERFF/\QPLPLDGSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKVSV TAMERKSVSYEQCKPVSVTPQONDPBYTAKIRTLAFTERFF/\QPLPLDGSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKVSV TAMERKSVSYEQCKPVSVTPQONDPBYTAKIRTLAFTERFF/\QPLPLDGSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKVSV TAMERKSVSYEQCKPVSVTPQONDPBYTAKIRTLAFTERFF/\ ELTKEKDQIEAALSRMPSPGGRITMTYATJFKYIIGDTGVCKSCCLL QFTDRRPQPVHDLTIGVEFGARMVNIDGRQISKLDIWDTAGQES RSITRSYYRGAAGALLVYDITREFFFNHLTSWLEDARQHSSKN VIMILGNKSDLESRBVKGEGERARAFNHIGLIFMETSAKTACH VIMILGNKSDLESRBVKGEGERARARNIDGRQISLGUAVHTAGQES SCITRSYYRGAAGALLVYDITREFFFNHLTSWLEDARQHSSKN	1			
CHIISOPNQGFYDCUIATDAEVICAPVIGKRRGREPRGUKASI EAGVARGIDPHIVSAVIAFDLPPTEAYTHRAGRTARANNPGI LITPULPTEQPHILGKIELLIGGRRRGPILLIPYOFRMESIEGFR CRDAMBSVTKQAIREARIKSIRRELLISGRRRGPILLIPYOFRMESIEGFR CRDAMSVTKQAIREARIKSIRRELLISGRRRGPILLIPYOFRMESIEGFR LLEHDLPLHPAVVKPHLGHVPDYLVPPALKGLVRPHKK\GRSC PLWGRRREQSPRTHCABSTKERNSDPQDSPPSVUGFLMS 6097 1673 192 APGTMSGGKKKSSFQITSVTTDVEGFOSPGSDSPPTPQPPTGE PRIPMGEPSPDPGGKGTPRNGSPPPGAPSRFRVVKLPHGLGE RASGGKKASSFQITSVTTDVEGFOSPGSSGAGRSLDSR GRAGRTCVDVYSRDLEPBSFGGLLEGIRGASGGAGGRSLDSR ELASLGIGAPTPPSGISGGFTSHIRPPTSPGPQASFFTGGL LVVPSKAKARKPPLSASSPQGRPFBPETGESAGTSRAATPLPS RPSSPALYPTHOASLVHKSGPDFGAVAAGKFSLAHSMLAISGG RELABERAALEQENGILIRALA\SPPQLGSAGPRGVPR\LGFP PNSPFVISIPSITIVPIGLPGIASAAWPLPMPALEVPLYPFGV VQALSNSPWSBGPLPHILIIPSLGGGGFFTTGRQQGAPPGER RELABERNAALEQENGILIRALA\SPPQLGSAGPRGQQAPPGER PNSPFVISIPSITIVPIGLPGIASAAWPLPMPALTVPVPFGV VQALSNSPWSBGPLPHILIIPSLGGGGFFTTGRQQGAPPGER GRIPRNWGTGTKKRDTSNIPPRGTTSTVNASSSPEKCAQQRQ RLNSASQRSSSLPPSNRKSSTPIKEIMITPVTVAYSPKRSFK NLSFGFSHLISKNESSPIKFDILLODLDTVPUSTLQRTNPRKQ VQPLDLDSEGSEV,TYSEKATJUNVHSSCPEPVPNGVKKVSV TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ EITKEKDQIRAALSRMPSSGGRITLQTRINQEAPGRSFGKD NLSPGFSHLISKNESSPIRFDILLIDDLDTVPVSTLQRTNPRKQ QFPPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV TANSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ LETKEKDQIRAALSRMPSSGGRITLQTRINQEAPGRSFGKD NLSPGFSHLISKNESSPIRFDITHTTATRITRFFP\ EITKEKDQIRAALSRMPSPGGRITLQTRINQEAPGRSFGKD TANSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ EITKEKDQIRAALSRMPSPGGRITLQTRINQEAPGRSFGKD CANSCRSSLPPSNRKSSPIRFONITNTSATLFTKFTPF\ EITKEKDQIRAALSRMPSPGGRITLQTRINQEAPGRSFGKD TANSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ EITKEKDQIRAALSRMPSPGGRITLQTRINQEAPGRSFGKD OFTDRRFQPVHOLITGVEGGRAMVNIDGRGLKAGLGUMTTAGQGS RITTSSYYRGAAGALLVDUTTRGFTFTNHLTSWLEDARQHSSEN VUMLIGNKSDLESRRDVKREGGRAPAR\HGLIFWETSAKTAG	1			
EAGVARGIDPHHVSAVLNFDLPPTPEAY HIRAGRTARANNEGI LITVULPTECYHLIKKIERLLIGERNIG PILLFYQFRMERIEGFRY CRDAMRSVTYQAI FREALIKSI KREILLIGERNIG PILLFYQFRMERIEGFRY CRDAMRSVTYQAI FREALIKSI KREILLIGERNIG PILLFYQFRMERIEGFRY LLRHDLPLHPAVVKPHLGHVPDYLVPPALRGLVRPHKK\GRSC FLWGRPREQSPRTHCAASTKERKISDPOESPPEWVGPHSE  APGTMSGGKKSSFQITSYTTDYEGFOSFGASDPPTPQPDTGE PRIPMGEPSPDPGGKGTPRNGSPPPGAPSGFRVVKLPHGLGE YRRGRATCVDVYERDLEPHSFGGLLGEIGASAGGAGGREILDGE ELASLGIGAPTPPSGGLGGTPSKLRPPPTSPGPQARSFTYGLG RVSRAKAGKAPPLSGSPQQRPPEPTGESAGTSRAATPLES RVSRAKAGGSGATPPLSGRKAVVMRILRMEUGAPBERGQVPPLL RPSSPALVFTHDASLHVHKSPPGAVAAQKPSLAHSMLAISGE RELBERNAALEGENGLIRALA\SPEQLGSAGPPRGVPR\LGP PNGPFYLSLESTIVVELGLGASAWPPLPMBALIVPPPGV VQALSNGPWSPGPLPHLLIIPSLDGGGGFFRTGRQQGPFGEE QPPPSLFGTPQQ  MYCLRHRSPLEKDSSPGSSSTSILLIKKQRETSDTPIMRALKKL BGKLFRLMWGTQTEKRITSNINFRQTETSVNASRSPEKCAQQRQ RLNSASQRSSLPPSNRKSSTPTKREIMITPVTVAYSPRRSKK NLSPGFSHLLISINGSSPTRFDILLDLDDLDTVPUSTLQRTNPRKQ \QPLPLDDSEEK\TYSEKAT\DNIVMHSSCPBPUNGVKKVSV TAMERKKSVSYSQCKPVSVTPQGNDPSTTAKLRTLAETERFF\ EGKLFRLWGTGTEKRDTSNINFRQTETSVNASRSPBKCAQQRQ RLNSASQRSSLPPSNRKSSTPTKREIMITPVTVAYSPRRSFK MISPGFSHLLISKNESSPIRFDILLDLDLDTVTVVSTLQRTNPRKQ QFLPLDDSEEK\TYSEKAT\DNIVMHSSCPBPVPNGVKKVSV TAMERKKSVSYSQCKPVSVTPQGNDPSTTAKLRTLAETERFF\ LETKKRQITARASCRSSSTFTKREIMITPVTVAYSPRRSFK NLSPGFSHLISKNESSPIRFDILLDLDLDTVTVVSTLQRTNPRKQ QFLPLDDSEEK\TYSEKAT\DNIVMHSSCPBPVPNGVKKVSV TAMERKKSVSYSQCKPVSVTPQGNDPSTTAKLRTLAETERFF\ LETKERDQIEALSKNPSFGGGRITLGYRINGRAFGRSFGKD  TAMERKKSVSYSQCKPVSVTPQGNDPSTTAKLRTLAETERFF\ LETKERDQIEALSKNPSFGGGRITLGYRINGRAFGRSFGKD  TAMERKSVSYSQCKPVSVTPQGNDPSTTAKLRTLAETERFF\ LETKERDQIEALSKNPSFGGRITLGYRINGRAFGRSFGKD  TAMERKSVSYSQCKPVSVTPQGNDPSTTAKLRTLAETERFF\ LETKERDQIEALSKNPSFGGRITLGYRINGRAFGRSFGKD  TAMERKSVSYSGCRPVSVTPQGNDPSTTAKLRTLAETERFF\ LETKERDQIEALSKNPSFGGRITLGYRINGRAFGRSFGKD  TAMERKSVSYSGCRPVSVTPQGNDPSTTAKLRTLAETERFF\ LETKERDQIEALSKNPSFGGRITLGYRINGLAGRAFGRSFGKD  TAMERKSVSYSGCRPVSVTPQGNDPSTYTAKLRTLAETERFF\ LETKERDQIEALSKNPSFGGRGTTATTATUTSHCRFGKGGR  GETTSKRDQIEALSKNPSFGGRGTTATTATUTSHCRFG	1	İ		
LITVILPTEQPHILGILEGLIGENIGFILLPYQFREBIEGENI CRDAMRSVTKQAIREBARLKEL KRBILLHSEKLKTYFEDNPR\DI LLRHDLPLHPAVVRPHILGHVPDYLVPPALRGUVPPHKK\GRS PLVGRPREQSPRTHCAASSTKERRISDPQDESPPBVGPLMS  6097 1673 192 APGTMSGGKKKSSFQITSVTTDYBGPGSBGSDPPPQPPTGE PRIPNGEPSPDPGGKGTPRNGSPPPGAPSRFRVVKLPHGLGE PRIPNGEPSPDPGGKGTPRNGSPPPGAPSRFRVVKLPHGLGE PRIPNGEPSPDPGGKGTPRNGSPPPGAPSRFRVVKLPHGLGE VRRGRWTCVDVYERDLEPHSFGGLLEGIRGASGAGGRSLDSH ELASLGLGAPTPPSGLSGGFTERAAGGRGAGGRSLDSH ELASLGLGAPTPPSGLSGGFTERAAGGRGAGGRSLDSH CLVVPSKAKAKPPLSABSPQQRPPEPETGSSAGTSRAARTLES RVERRAGGSGARTPPLSRRKAVDMRLRMELGAPBEMGQVPPLL RPSSPALYFTHDASLVHKSPPFCAVAAQKFSLAHSMLAISGH DSDDDGSGSGLVGIDNIKDAMDLVKSHIMFAVRBEVEVLKRQ RELABRNAALBQRNGLLRALA\SPSQLGSAGPPRGVPR\LGPP PNGPFVLSLPSLTIVPLGLPGLASAAWPPLEMPALIVVPVFGV VQALSNOPWSFGPLPHLLIITSLDGGRGFRTGRQQGAPPGEB QPPPSLDGTPQQ  NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTFIMRALKEL BGKIFKNWGTQTEKKDTSNINPRQTETSVNASRSPEKCAQQRQ RLMSASQRSSSLPPSNRKSSTPTKRE IMLTPVTVAYSPKRSPK NLSPGFSHLLSKNESSFTRDILLDDLDTVPVSTLQRTNPRRQ \QPLPLDDSSEK\TYSKAT\DNIVNHSGCPBVPNGVKKVSV TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAFTERFF\ ELTKRKUQIRAALSRMPSPGGRITLQTRLMQEAFGRSFGKD  MISPGFSHLISKNESSFTRDILLDDLDTVPVSTLQRTNPRRQ RLMSASQRSSSLPPSNRKSSTPTKRIMLITVTVAYSPKRSPBK ANGSPGSHLISKNESSFTRDILLDDLDTVPVSTLQRTNPRRQ \QPLPIDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAFTERFF\ \QFLKKBOQIRAALSRMPSPGGRITLQTRLMQEAFGRSFGKD  MISPGFSHLISKNESSFTRDILLDDLDTVPVSTLQRTNPRRQ \QFLPIDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV TANEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAFTERFF\ \QFLKKBOQIRAALSRMPSPGGRITLQTRLMQEAFGRSFGKD  TANEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAFTERFF\ \QFLKKBOQIRAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  TANEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAFTERFF\ \QFTKKBOQIRAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  TANEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAFTERFF\ \QFTKKBOQIRAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  TANEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAFTERFF\ \QFTKKBOQIRAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  TANEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAFTERFF\ \QFTKKBOQIRAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  TANEKNKSVSYEQCKPVSVTPQCNDFBYTAKIRTLAFTERFF\ \QFTKKBOQIRAALSRMP	1			
CRDAMESVTKQAIREARLKEIKREILHSEKIKTYFEDNPR\DI LIRHDLPHHPAVVKPHIGHVEDYLDYPALRGIVRPHKK\GREG PLUGRPREQSPRTICABSTKERNSDPOPSPRVUGPINS  192 APGTMSGGKKKSSFQITSVTTDYEGPGSPGSDPPTPQPPTGE PRIPMGEPSDPDGGKGTPRINGSPPGSPGSSDPPTPQPPTGE PRIPMGEPSDPDGGKGTPRINGSPPGSPGSSBFRVVKLPHGLGE VRRGRWTCVDVYERDLEPHSFGGLLGGIRGAGGGAGGRIDGS ELASLGIGAPTPPSGLSQGPTSWLRPPPTSPGPQARSFTGGLG LVVPSKAKAKPPLSASSPQQRPPBFTGSSAGTSRAATPLES RVEREAGGSGAGGRTPPHSGRKAVDMRLRMELGAPERMGQVPPLL RPSSPALYPTHDASLVHKSPDPFGAVAAQKFSLAHSMLAISGH DSDDDGSGSLVGIDNKIBOAMDLVKSHIMFAVREVEVKLKEG RELAERNAALEGRNGLIARLA\SPEQLGSAGPPRGVPR\LGPP PNGPFVLSLPSLTIVPLGLPGLASAAWPPLEMPALIVPVPPGV VQALSNOPWSGCPLDHILITPSLOGGGGFRTGRQQGAPPGEE QPPPSLPGTPQQ RRINSASQRSSSLPPSNEKSSTPITKEIMHITVYTVAYSPKRSPK RKMSASQRSSSLPPSNEKSSTPTREIMLITVTVAYSPKRSPK NLSFGFSHLISKWESSFTFFDILLDDLDTVPVSTLQRTNPRRQ \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV TAMEKMKSUSYEQCKPVSVTPQGMDFBTTAKITAETERFF/ LITKEKDQI ERALSRMPSPGGRITLQTRLNQEAFGRSFGKD  6099 168 1074 NYCLERISPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKEL EGKIFRNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQGRQ RLNSASQRSSSLPPSNRKSSTPTKRBIMLTPVTVAYSPKRSPK NLSFGFSHLLSKMESSPIRRDILLDDLDTVPVSTLQRTNPRRQ \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV TANSKNKSVSYQCKPVSVTPQGMDFBTTAKITAETERFF/ \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV TANSKNKSVSYQCKPVSVTPQGMDFBTTAKITAETERFF/ \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV TANSKNKSVSYGCKPVSVTPQGMDFBTTAKITAETERFF/ \QFLPKKBQJ ERALSRMPSPGGRTTLQTRLNQRAFGRSFGKD  6000 2 713 FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTCVGKSCLIJ  GFTDKRFQPVHDLTIGVEFGARMVNIOCKQIKLQIWDTAGGBS: UTMLIGNKSDLESRRDVKREEGRAPARE\HGLIFMETSAKTACI  VIMILIGNKSDLESRRDVKREEGRAPARE\HGLIFMETSAKTACI  VIMILIGNKSDLESRRDVKREEGRAPARE\HGLIFMETSAKTACI		j i		
LLRIDLPLHPAVVRPHIGHVPDYLVP PALRGLVRPHKK\GRSC PLVGRPRBQSPRTHCAASSTKERNSDVDGSPFVVGPLMS  6097 1673 192 APGTMSGSKKSSFQITSVTTDVEGPGSPGASDPPTPQFPTGE PRLPNGEPSPDPGGKGTPRNGSPPPGAPSSRFRVVKLPHGLGE YRGGRWTCVDVYERDLEPHSFGGILGGTGRGASGGAGGRSLDSR ELASLGIGAPTPPSGLAGGTSWLRPPPTSPGPQARSFTGGLG RVEREAGGSGARTPLSRKAVVMRLRMELGAPBEMGQVPPLL RPSSPALYFTHDASLVHKSPDPFGAVAAQKKSLAHSMLAISGH PSSPALYFTHDASLVHKSPDPFGAVAAQKKSLAHSMLAISGH PSSPALYFTHDASLVHKSPDPFGAVAAQKKSLAHSMLAISGH PSSPALYFTHDASLVHKSPDPFGAVAAQKKSLAHSMLAISGH PSSPALYFTHDASLVHKSPDPFGAVAAQKKSLAHSMLAISGH PSSPALYFTHDASLVHKSPDPFGAVAAQKKSLAHSMLAISGH PSSPALYFTHDASLVHKSPDPFGAVAAQKKSLAHSMLAISGH PSSPALYFTHDASLVHKSPDPFGAVAAQKKSLAHSMLAISGH PSSPALYFTHDASLVHKSPDPFGAVAAQKKSLAHSMLAISGH PSSPALYFTHDASLVHKSPDPFGAVAAQKKSLAHSMLAISGH PSSPALYFTHDASLVHKSPDPFGAVAQKKGAPPGGEP PNSPFVLSLESLTIVPLGLDGGEGFTTRQQCAPPGGE PNSPFVLSLESLTIVPLGLDGGEGFTTRQQCAPPGGE QPPPSLPGTQQ  PSSPALPTTIVLGLDGGGFFTRQQCAPPGGE  RINSASQRSSSLPPSNRKSSTFTKRSIMLTPVTVAYSPKRSPK NLSPGFSHLLSKNESSPTFKRSIMLTPVTVAYSPKRSPK \QPLDLDDSEK\TYSEKAT\DNIVHSSCPEPVPNGYKKVSV TAMEKNESVSYEQCKPVSVTPQGNDFBYTAKIRTLAFTERFF\ ELTKEKQQIRAALSRMPSFGGRITLQTRLMQRAFGRSFGKD  RINSASQRSSLPPSNRKSSTFTKRSIMLTPVTVAYSPKRSPK RINSASQRSSLPPSNRKSSTFTKRSIMLTPVTVAYSPKRSPK RINSASQRSSLPPSNRKSSTFTKRSIMLTPVTVAYSPKRSPK \QPLDLDDSEK\TYSEKAT\DNIVNHSSCPEPVPNGYKKVSV TAMEKNESVSYEQCKPVSVTPQGNDFBYTAKIRTLAFTERFF\ \QPLDDSEK\TYSEKAT\DNIVNHSSCPEPVPNGYKKVSV TANSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAFTERFF\ \QPLDDSEK\TYSEKAT\DNIVNHSSCPEPVPNGYKKVSV TANSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAFTERFF\ \QPLDDSEK\TYSEKAT\DNIVNHSSCPEPVPNGYKKVSV TANSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAFTERFF\ \QPTDKRFQPVHDLTIGVEFGARMVNIDGRGIKLQIMDTAGGBSI RSITRSYYRGAAGALLVYDITRREFTFNHLTSWLEDARQHSSSNI VIMLIGNKSDLESRRDVKREBGRAPARR\HGLITMSTSATTAGC VITMLIGNKSDLESRRDVKREBGRAPARR\HGLITMSTSATTAGC VITMLIGNKSDLESRRDVKREBGRAPARR\HGLITMSTSATTAGC				
PLVORPREQSPRTHCAASSTKERNSDPQPSPPEVVGPLWS  6097  1673  192  APGTMSGKKKSSFQITSVTTDYBGPGSPGASDPFTPQPPTGE PREPNINGEPSPDPGGGGTPRNGSPPGASDRFTPQPPTTPG PREPNINGEPSPDPGGGGTPRNGSPPGASSRFRVVKLPHGLGE VRRGNTCVDVYERDLEPHSFGGLLEGIRGASGAGGRSLDSF ELASLGLGAPTPPSGLSQGPTSHLRPPFTSGPQARSFTGGLG LVVPSKAKAEKPPLSAGSPQAPPEPETGBSAGTSRAATPLPS RVERRAGGSGARTPLSKKAVDMRLEMBLGAPEEMGQVPPLL RPSSPALYFTHDASLVHKSPDPPGAVAAQKFSLAHSMLAISGF DSDDDSGSGSLVGIDNKIEQAMDLVKSHLMFAVREEVEVLKEQ RELABERNAALDQRIGLIKALA\SPEQLGSAGPPRGVPR\LGPP PNGPFVLSLPSLTIVPLGLDGLGSGAGPPRGVPR\LGPP PNGPFVLSLPSLTIVPLGLDGGGGGFRTGRQQCAPPGEE QPPSLDSTPQQ  6098  168  1074  NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTFIMRALKEL BGKLFFKNWGTQTBKKDTINIPRQTSTSVANSRSPBKCAQQRQ RLNSASQRSSSLPPSINKSSTPTKREIMLTPVTVAYSPKRSPK \QPLPLDDSEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKYSV TANEKNKSVSYGCKPVSVTPQGNDFBYTAKIRTLAETERFF\ ELTKEKDQIRAALSRMPSPGGRITLGTRLINGBAFGRSFGKD  6099  168  1074  NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKEL EGKIFKNWGTQTBKEDTISNINGBAFGRSFGKD  RLNSASQRSSSLPPSINRSSTPTKRBILTPVTVAYSPKRSPK  BETKEKDQIRAALSRMPSPGGRITLGTRLINGBAFGRSFGKD  RLNSASQRSSSLPPSINRSSTPTKRBILTPVTVAYSPKRSPK \QPLDRSSSLPPSINRSSTPTKRBILTPVTVAYSPKRSPK  NISPGFSHLLISKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QPLDRSSSLPPSINRSSTPTKRBILTPVTVAYSPKRSPK  ANSANGSVSSLPPSINRSSTPTKRBILTPVTVAYSPKRSPK  NISPGFSHLLISKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QPLDRSKK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV TANEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\ \QPLDRSKKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\  ELTKBKDQIRAALSRMPSPGGRITLGTRLINGBAFGRSFGKD  TANEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\  ELTKBKDQIRAALSRMPSPGGRITLGTRLINGBAFGRSFGKD  GETDKRQPVHDLTIGVEFGARMWNIDGRGIKLGIMDTAGGBS: RSITRSYYRGAAGALLVYDITRRETFINHLTSWLEDARQHSSSNI  VIMLIGNKSDLEGRRDVKREBGRAPARR\HGLITMETSATTAGC  VIMLIGNKSDLEGRRDVKREBGRAPARR\HGLITMETSATTAGC	1 1			
192 APGTMSGGKKKSSFQITSVTTDYEGPGSPGASDPPTQPPTGE PRIPNGEPSPDPGGKGTPRNESPPGABSSRFRVVKHPIGLGE VRNGRMTCUDVVERDLEPHSFGGLLEGIRGASGGAGGRSLDSH ELASLGLGAPTPPSGLSQGPTSWLRPPPTSPGPQARSFTGGL LVVPSKAKARPPLSARSPQQRPPEPTGESAGTSRAATPLES RVEARAGGSGARTPPLSRKAUDMRLRMELGAPEEMGQVPPLL RPSSPALVFTHDASLVHKSPDPYGAVAAQKPSLAHSMLAISGH DSDDDSGSGSLVGIDNKIEQAMDLVKSHLMFAVREEVEVLKEQ RELAERNAALBQENGLLRALA\SPEQLGSAGPPRGVER\LGPP PNGPPVLSLPSLTIVDGLPGLASAAWPPLPMPALIVVPVPGV VQALSNGPWSFGPLPHLLITPSLDGGGEGFRTGRQQGAPPGEE QPPPSLPGTPQQ  168 1074 NYCLRHREPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKEL EGKIFFKWGTQTEKEDTSNINPRQTETSVMASRSPEKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK NLSFGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRRQ \QPFLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKVSV TAMEKNRSVSYEQCKPVSVTPQGHDFBYTAKIRTLAFTERFF\ ELTKEKDQIRAALSRMPSPGGRITLQTRLNQEAPGRSFGKD  NYCLRHESPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKEL EGKIFFKNWGTQTEKEDTSNINPRQTETSVMASRSPEKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK MLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRQ ELTKEKDQIRAALSRMPSPGGRITLQTRLNQEAPGRSFGKD  NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRQ \QPTDKRFQFYBLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRQ \QPTDKRFQVHDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV TAMEKNSVSYEQCKPVSVTPQGNDFBYTAKIRTLAFTERFF\ BLTKEKDQIRAALSRMPSFGGRITLQTRLNQEAPGRSFGKD  6000 2 713 FVEVSGYRSRADPEPRGRDTMTYAYLFKYTIGDTGVGKSCLIL GFTDKRFQPVHDLTIGVERGARMVNICKGXIKLQIHDTAGGESS VIMLIGNKSDLESRRDVKREBGEAPARR\LGLIFMSTSAKTACI  FVEVSGYRSRADPEPRGRDTMTYAYLFKYTIGDTGVGKSCLIL GFTDKRFQPVHDLTIGVERGARMVNICKGXIKLQIHDTAGGESS VIMLIGNKSDLESRRDVKREBGEAPARR\LGLIFMSTSAKTACI	1			
PRIPINGEPSPDPGGKTPRNGSPPGAPSSFRTVKLPHGLGE  PRIPINGEPSPDPGGKTPRNGSPPGAPSSFRTVVKLPHGLGE  YRRGRWTCVDVYERDLEPHSFGGLLGGIRGASGAGGRSLDSF  ELASLGLGAPTPPSGLSGGFTSWLRPPPTSPGPQARSFTGGLG  RVEREAGGSGRTPPLSRRRAVDMRLRMELGAPERMGQVPPLL  RPSSPALVFTHDASLVHKSPDPPGAVAAQKFSLAHSMLAISGH  RPSSPALVFTHDASLVHKSPDPPGAVAAQKFSLAHSMLAISGH  RELBERNAALEDGEGLIRALA\SPEQLGSAGPPRGVPR\LGPP  PNGPFVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVPPGV  VQALSNGPWSPGPLPHLLIIPSLDGGGEGFRTGRQQGAPPGEE  QPPPSLPGTPQQ  6098  168  1074  NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKEL  BGKIFKNWGTQTEKBDTSNINPRQTETSVNASRSPBKCAQQRQ  RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK  NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ  QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV  TAWEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAFTERFF\  ELTKEKQQIRAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  AVCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKEL  EGKIFKNWGTQTEKBDTSNINPRQTETSVNASRSPBKCAQQRQ  RLNSASQRSSSLPPSNRKSSTPTKRBIMLTPVTVAYSPKRSPK  MLSPGFSHLLSKNBSSPIRFDILLDDLDTVPVSTLQRTNPRKQ  QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV  \[ \begainsagrsslppsnrksstptkrBimltpvtvayspkrspk \begainsagrsslppsnrksstptkrBimltpvtvayspkrspk \begainsagrsslppsnrksstptkrBimltpvtvayspkrspk \begainsagrsslppsnrksstptkrBimltrukerpry\  ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  6100  2 713  FVEVSGYRSRADPEPRGRDTMTYAYLFKYLIIGDTGVGKSCLLI  GFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQINDTAGGBSS  VIMLIGNKSDLESRRDVKREGERAFARR\HGLIFMETSAKTACU  VIMLIGNKSDLESRRDVKREGERAFARR\HGLIFMETSAKTACU	6007	1600		
VRRGRWTCVDVYERDLEPHSFGGLLEGIRGASGAGGRSLDSE  ELASLGLGAPTPPSGLSGOPTSHLRPPPTSOPQARSFTGGL  LVVPSKAKAKPPLSASSPQRPPPETGESAGTSRAATPLPS  RVERARGGSGARTPPLSRKAVUMRLRMELGAPERMGQVPPLL  RPSSPALYFTHDASLVHKSPDPFGAVAAQKFSLAHSMLAISGH  RELABERNAALEQENGLLRALA\SPEQLGSAGPPRGVPLLGPP  PNGPFVLSLPSLTIVPLGLPGLASAAWPPLPMPALLVPVPPGV  VQALSNGPWSPGPLPHILIIPSLDGGGEGFRTGRQQGAPPGEB  QPPPSLPGTPQQ  6098  168  1074  NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKEL  BGKIPKNWGTQTEKEDTSNINPRQTBTSVNASRSPEKCAQQRQ  RLMSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK  NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ  \[ \text{QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV} \]  TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\  ELTKEKDQIERALSRMPSPGGRITLQTRINQEAPGRSFGKD  NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKEL  EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQ  RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK  NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ  \[ \text{QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV} \]  RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK  NLSPGFSHLLSKNBSSPIRFDILLDDLDTVPVSTLQRTNPRKQ  \[ \text{QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV} \]  \[ \text{QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV} \]  \[ \text{QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV} \]  \[ \text{TAMEKNSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\} \]  ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAPGRSFGKD  1000  2  713  FVENSGVRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLIL  GFTDKRPQPVHDLTIGVEFGARMVNIDGQIKLOJWDTAGGGES  RSITRSYYRGAAGALLVYDTYRRETFNHLTSWLEDARQHSSNI  VIMLIGNKSDLESRRDVKREEGRAPARE\HGLIFMETSAKTAC	6097	1673	192	
ELASIGLGAPTPPSGLSQGPTSWLRPPPTSPGPQARSFTGGLG LVVPSKAKAEKPPLSASSPQRPPEPETGESAGTSRAATPLES RVEAEAGGSCARTPPLSRKAVDMRLRMELGAPEEMGQVPPLL RPSSPALVFTHDASIVHKSPDPPGAVAAQKPSLAHSMLAISGH DSDDDSGSGSLVGIDNKIEQAMDLVKSHLMFAVREEVEVLKEQ RELABERNAALBORGLLRALA\SPEQLGSAGPPRGVPR\LGP PNGPFVLSLPSLTIVPJGLPGLASAAWPPLPMPALIVPVPPGV VQALSNGPWSPGPLPHILLIIPSLDGGGEGFRTGRQQGAPPGEE QPPPSLPGTPQQ  6098 168 1074 NYCLRHRSPLEKDSSPGSSTSILLIKKQRETSDTPIMRALKEL BGKIFKNWGTQTEKEDTSNINFRQTETSVNASRSPEKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK NLSPGFSHLLSKNESSPIRFDILLIDDLDTVPVSTLQRTNPRKQ \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV TAMEKNKSVSYEQCKPVSVTPQGNDFSYTAKIRTLAETERFF\ ELTKEKDQIRAALSRMPSPGGRITLQTRLNQEAPGRSFGKD  6099 168 1074 NYCLRHRSPLEKDSSPGSSSTSILLIKKQRETSDTPIMRALKEL EGKIFKNWGTQTEKEDTSNINFRQTETSVNASRSPEKCAQORQ RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK MCSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ PKLTKEKDQIRAALSRMPSPGGRITLQTLDDLDTVPVSTLQRTNPRKQ \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV TANEKNKSVSYEQCKPVSVTPCGNDFFSYTAKIRTLAETERFF\ ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  6100 2 713 FVEVSGYRSRADPEPRGRDTMTYAYLFKYTIIGDTGVGKSCLLI GFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQUWDTAGGSS RSITRSTYNGAAGALUVUTTURRETFNHLLTSWLEDARQHSSSN VIMLIGNKSDLESRRDVKREEGRAPARE\HGLIFMETSAKTACI	i i			
LVVPSKAKAEKPPLSAGSPQQRPPEPTGBSAGTSRAATPLPS RVEARAGGSGARTPELSRRKAVDMRLRMELGAPBEMGQVPPLD RPSSPALYPTHDASLVHKSPDPPGAVAAQKPSLAHSMLAISGH DSDDDGSGSGLVGIDNKIBQAMDLVKSHLMFAVREVEVLKEQ RELABRNAALEQENGLLRALA\SPEQLGSAGPPRGVPR\LGPP PNGPFVLSLPSLTIVPLGLGGLASAAWPPLDMPALIVPVPPGV VQALSNGPWSPGPPLPHLLIIPSLDGGGGFRTGRQQGAPPGEE QPPPSLPGTPQQ  168 1074 NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKEL BGKIPKNWGTOTERKDTSNINPRQTETSVNASRSPEKCAQQRQ RLNSASQRSSSLPPSNRKSSTPIKFEIMLTPVIVAYSPKRSPK NLSFGFSHLLISKMESSPIKFDILLDDLDTVPVSTLQRTNPRKQ QPLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKEL EGKIFKNWGTQTKKEDTSNINPRQTETSVNASRSPEKCAQQRQ RLNSASQRSSSLPPSNRKSSTPIKRBIMLTPVIVAYSPKRSPK NLSFGFSHLLISKNESSPIKPDILLDDLDTVPVSTLQRTNPRKQ QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV \QPLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV \QPLPLDDSEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV \TANEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  6100 2 713 FVEVSGYRSRADDEPRGRITMTYAYLFKYIIIGDTGVGKSCILL GFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQBSI RSITRSYYRGAAGALLVYDTTRRETFNHLTSWLEBARQHSSSNI VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACI VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACI	1 1			
RVEAEAGGSGARTPPLSRRKAVDMRLRMELGAPEEMGQVPPLD RPSSFALYFTHDASLUHKSPDPFCAVAAQKFSLAHSMILAISGH DSDDDSGSGSLVGIDNKIEQAMDLVKSHLMFAVREEVEVLKEQ RELABENAALDQBRGILIRALA\SPEQLGSACPPRGVPR\LGPE PNGPFVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVFPGV VQALSNGPWSPGPLPHLLIIPSLDGGGEGFRTGRQQGAPPGEE QPPPSLPGTPQQ  6098 168 1074 NYCLRHREPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKEL EGKIPKNWGTQTEKBDTSNINPRQTETSVNASRSPBKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK NLSFGFSHLLSKNESSPTRFDILLDDLDTVPVSTLQRTNPRKQ \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\\ ELTKEKDQIEAALSRMPSPGGRITLQTKLNQEAFGRSFGKD  NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKEL EGKIFKNWGTQTEKBDTSNINPRQTETSVNASRSPEKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK GGKIFKNWGTQTEKBDTSNINPRQTETSVNASRSPEKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK NLSPGFSHILSKNESSPIRPDILLDDLDTVPVSTLQRTNPRKQ \QFLPLDDSEEK\TTSEKAT\DNIVNHSSCPBEPVPNGVKKVSV TANSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\\ GETKEKDQIEAALSRMPSPGGRITLQTKLNQEAFGRSFGKD  6100 2 713 FVEVSGYRSRADPEFRGRDTMTYAYLFKYIIIGDTGVGKSCILS GFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESS RSITRSYYKGAAGALLVYDTTRRETFNHILTSWLEDARQHSSN VIMLIGNKSDLESRRDVKREEGRAFARE\HGLIFMETSAKTACI	1 1			
RPSSPALYPTHDASLVHKSPDPPGAVAAQKFSLAHSMLAISGH DSDDDSGSGSLVGIDNKIBQAMDLVKSHLMFAVRERBVULKEQ RELABENAALEQBRGLLRALA\SPEQLGSAGPPRGVPR\LGPP PNGPPVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVPPGV VQALSNGPWSPGPLPHILIIPSLDGGGEGFRTGRQQGAPPGEE QPPPSLPGTPQQ  6098 168 1074 NYCLRHRSPLEKDSSPGSSSTSILIKKQRETSDTPIMRALKEL BGKLPKNWGTQTEKBDTSNINPRQTETSVNASRSPBKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVIVAYSPKRSPK NLSPGPSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV TAWEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ ELTKEKDQI BAALSRMPSPGGRITLQTKLNQEAFGRSFGKD  NYCLRHRSPLEKDSSPGSSSTSILIKKQRETSDTPIMRALKEL EGKIFKNWGTQTEKBDTSNINPRQTETSVNASRSPBKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKRBIMLTPVIVAYSPKRSPK RLNSASQRSSSLPPSNRKSSTPTKRBIMLTPVIVAYSPKRSPK NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV TAMSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ BLTKBKDQIBAALSRMPSPGGRITLQTKINQBAFGRSFGKD  6100 2 713 FVEVSGYRSRADPERFRGDTMTYAYLFKYIIGDTCVGKSCLLL QFTDKRPQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQES: RSITRSYYKGAAGALLLVYDITRRETFRHHLTSWLEDARQUSSNN VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI	!!!			
DSDDDSGSGSLVGIDNKIRQAMDLVKSHLMFAVREEVEVLEQG RELABERNAALBQENGLIRALA\SPEQLGSAGPPRGVPR\LGPE PNGPFVLSLPSLTIVPIGLPGLASAAWPPLPMPALIVPVFPGV VQALSNGPWSPGPLPHLLIIPSLDGGGEGFRTGRQQGAPPGEE QPPPSLPGTPQQ  6098 168 1074 NYCLRHREPLEKDSSPGSSSTSLLIKKQRETSDTFIMRALKEL BGKIPKNWGTQTEKEDTSNINPRQTETSVNASRSPBKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKREIMITPVTVAYSPKRSPK NLSPGPSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QPFPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV TAWEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ ELTKEKDQIERAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKEL EGKIFKNWGTQTEKEDTSNINRRQTETSVNASRSPEKCAQORQ RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QPLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV TANSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ BLTKEKDQIERAALSRMPSPGGRITTLQTLNQEAFGRSFGKD  6100 2 713 FVEVSGYRRADPEPRGRDTMTAYLFKYIIGDTGVGKSCTLL QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQES: RSITRSYYRGAAGALLVYDITRRETFHHLITSWLEDARQUSSNN VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI	!!!		•	
RELABRNALEQBNGLLRALA\SPEQLGSAGPPRGVPR\LGPP PNGPFVLSLPSLTIVPIGLPGLASAAWPPLPMPALIVPVPPGV VQALSNGPWSPGPLPHLLIIPSLDGGGGFFTTGRQQGAPPGEE QPPPSLPGTPQQ  6098 168 1074 NYCLRHRSPLEKDSSPGSSSTSILLIKKQRETSDTFIMRALKEL BGKIPKNWGTQTEKBDTSNINPRQTETSVNASRSPEKCAQQRQ RLNSASQRSSSLPPSNKKSSTPTKREIMLTPVTVAYSPKRSPK NLSPGFSHLLSKNESSPIRFILLIDDLDTVPVSTLQRTNPRKQ \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ ELTKEKDQIRAALSRMPSPGGRITLQTRLNQEAPGRSFGKD  168 1074 NYCLRHRSPLEKDSSPGSSTSILIKKQRETSDTPIMRALKEL EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQ RLNSASQRSSSLPPSNKSSTPTKRBIMLTPVTVAYSPKRSPK NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV TANSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\\ ELTKEKDQIRAALSRMPSPGGRITLQTRLNQBAFGRSFGKD  6100 2 713 PVEVSGYRSRADPEPRGRDTMTYAYLFKYIIGDTGVGKSCTLL GFTDKRFQPVHDLTIGVEFGARMVNIDGRQIKLQIWDTAGQES: RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSNI VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI	1. 1	'		
PNGPPVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVPPGV VQALSNGPWSPGPLPHLLIIPSLDGGGGFRTGRQQGAPPGEB QPPPSLPGTPQQ  MYCLRHRSPLEKDSSPGSSSTSILIKKQRETSDTPIMRALKEL BGKIPKNWGTQTEKBDTSNINPRQTETSVNASRSPEKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK NLSFGFSHLLIKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QPLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV ELTKEKDQIRAALSRMPSPGGRITLQTKLNQRAFGRSFGKD  MYCLRHRSPLEKDSSPGSSTSILIKKQRETSDTPIMRALKEL EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKRBIMLTPVTVAYSPKRSPK NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QPLPLDDSEEK\TYSEKAT\DNIVNHSSCPBEVPNGVKKVSV \QPLPLDDSEEK\TYSEKAT\DNIVNHSSCPBEVPNGVKKVSV TANSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLABTERFF\\ ELTKEKDQIEAALSRMPSPGGRITLQTKLNQRAFGRSFGKD  6100  2  713  PVEVSGYRSRADPEPFGRDTMTYAYLFKYIIGDTGVGKSCILL GFTDKRFQPVHDLTIGVEFGARMVNIDGRQIKLQIWDTAGQESS RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQUBSSN VIMLIGNKSDLESRRDVKREEGRAFARR\GGLIFMETSAKTACI		1		
VQALSNGPWSPGPLPHLLIIPSLDGGGEGFRTGRQQCAPFGEE QPPPSLPGTPQQ  6098 168 1074 NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSUTFIMRALKEL BGKIPKNWGTQTEKBDTSNINPRQTETSVNASRSPBKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK VQFLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV TAWEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ ELTKEKDQIRAALSRMPSPGGRITLQTRLNQEAFGRSFGKD NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKEL EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPBKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV TANEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFP\ ELTKEKDQIRAALSRMPSPGGRITMTYAYLFKYIIGDTGVGKSCLLI QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQES: RSITRSYYRGAAGALLVYDLTRRETFRHHLTSWLEDARQUSSSN VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI	i i			
QPPPSLPGTPQQ  6098 168 1074 NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKEL BGKIPKNWGTQTEKBDTSNINBRQTETSVNASRSPEKCAQQRQ RLNSASQRSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK NLSFGFSHLLIKMESSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QPLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV TAWEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ ELTKEKDQIRAALSRMPSPGGRITLQTKLNQEAFGRSFGKD  NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKEL EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKRBIMLTPVTVAYSPKRSPK RLNSASQRSSSLPPSNRKSSTPTKRBIMLTPVTVAYSPKRSPK NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QPLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV TAMSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ ELTKEKDQIBAALSRMPSPGGRITTLQTKINQEAFGRSFGKD  6100 2 713 PVEVSGYRSRADPSRGRDTMTYALFKYIIGDTGVGKSCLLI QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQES: RSITRSYYRGAAGALLVYDITRRETFHHLTSWLEDARQUSSSN VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI	ļ <u> </u>			
6098 168 1074 NYCLRHRSPLEKDSSPGSSSTSILIKKQRETSDTPIMRALKEL  BGKIPKNWGTQTEKBDTSNINPRQTETSVNASRSPBKCAQQRQ  RLMSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPRRSPK  NLSPGPSHLLSKNESSPIRFDILLODLDTVPVSTLQRTNPRKQ  \[ \text{QFIPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV} \\  TAWEKNKSVSYEQCKPVSVTPQGNDFBTTAKIRTLAETERFF\\  ELTKEKDQIRAALSRMPSPGGRITLQTRLNQEAPGRSFGKD  1074 NYCLRHRSPLEKDSSPGSSTSILIKKQRETSDTPIMRALKEL  EGKIFKNWGTQTEKKDTSNINPRQTETSVNASRSPEKCAQQRQ  RLNSASQRSSSLPPSNRKSSTPTKRBIMLTPVTVAYSPKRSPK  NLSPGFSHLLSKNBSSPIRFDILLDDLDTVPVSTLQRTNPRKQ  \[ \text{QPLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV} \\  TANSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\\  ELTKEKDQIEAALSRMPSPGGRITLQTKLNQEAPGRSFGKD  6100 2 713 FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIGDTGVGKSCTLL  QFTDKRFQPVHDLTIGVEFGARMVNIDGRQIKLQIWDTAGQES:  RSITRSYYRGAAGALLVYDITRRETFHHLTSWLEDARQUSSSN  VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI	1 1	j		
BGKTPKNWGTQTEKBDTSNINPRQTETSVNASRSPBKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKREIMITPVTVAYSPRRSPK NLSPGPSHLILSKNESSPTRFDILLDDLDTVPVSTLQRTNPRKQ \QFIPLDDSEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV TAWEKNKSVSYEQCKPVSVTPQGNDFBTTAKIRTLAETERFF\ ELTKEKDQI RAALSRMPSPGGRITLQTRLNQEAPGRSFGKD  NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKEL EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKRBIMLTPVTVAYSPKRSPK NLSPGFSHILLSKNBSSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QFIPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV TANSKNKSVSYEQCKPVSVTPQGNDFBTTAKIRTLAETERFF\ ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAPGRSFGKD  6100 2 713 PVEVSGYRSRADPEPRGRDTMTYAYLFKYIIGDTGVGKSCLLI QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQES: RSITRSYYRGAAGALLVYDTTRRETFRHHLTSWLEDARQUSSSN VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI	6000	160	1004	
RLNSASQRSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK NLSFGFSHLLISKNESSPTRFDILLDDLDTVPVSTLQRTNPRKQ \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ ELTKEKDQIEAALSRMPSPGGRITLQTKLNQRAFGRSFGKD  NYCLEHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKEL EGRIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV TANSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLABTERFF\\ ELTKEKDQIEAALSRMPSPGGRITLQTKLNQRAFGRSFGKD  6100 2 713 FVEVSGYRSRADPEFFGRDTMTYAYLFKYIIIGDTGVGKSCILS GFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESS RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSNN VIMLIGNKSDLESRRDVKREEGRAFARE\HGLIFMETSAKTACI	0036	708	10/4	
NLSPGFSHLISKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ ELTKEKQQIRAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  6099 168 1074 NYCLRHRSPLEKDSSPGSSTSILIKKQRETSDTPIMRALKEL EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK NLSPGFSHLLSKNBSSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ ELTKEKQQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  6100 2 713 PVEVSGYRSRADPEPRGRDTMTYAYLFKYIIGDTGVGKSCLLI QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQBSI RSITRSYYRGAAGALLVYDITRRETFRHHLTSWLEDARQHSSSN VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI	] ]	j		
QFIPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV   TAMEKINKSVSYEQCKPVSVTPQGNDFBTTAKIRTLAETERFF\   ELTKEKQQIRAALSRMPSPGGRITLQTRLINQEAFGRSFGKO    6099   168	1	ļ		
TAWEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\ ELTKEKDQIRAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  168 1074 NYCLRHRSPLEKDSSPGSSTSTLLIKKQRETSDTPIMRALKEL EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQORQ RLNSASQRSSSLPPSNRKSSTPTKRBIMLTPVTVAYSPKRSPK NLSPGFSHLLSKNBSSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV. TANSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\\ ELTKEKDQIBAALSRMPSPGGRITHQTKINQEAFGRSFGKD QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQES: RSITRSYYRGAAGALLVYDITRRETFHHLTSWLEDARQHSSNN VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI	, ,	1		
ELTKEKDQI RAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  6099 168 1074 NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKEL EGKI FKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQORQ RLNSASQRSSSLPPSNRKSSTPTKRBIMLTPVTVAYSPKRSPK NLSPGFSHLLSKNBSSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QPLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSV. TANSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLABTERFF\\ ELTKEKDQI EAALSRMPSPGGRITLQTKLNQEAFGRSFGKD QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQES: RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSNN VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI	1 !	ļ.		
6099 168 1074 NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKEL EGRIFKNWGTQTEKEDITSNINPRQTETSVNASRSPEKCAQQRQ RLNSASQRSSSLPPSNRKSSTPTKRBIMLTPVTVAYSPKRSPK NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QFLPLDDSEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV. TANSKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLABTERFF\\ ELTKEKDQIEAALSRMPSPGGRITLQTKLNQBAFGRSFGKD QFTDKRFQPVHDLTIGVEFGARMVNIDGRQIKLQIWDTAGQES: RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSNI VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI	ļ i	j		TAMBANASVSYEQUAPVSVTPQGNDFBYTAKIRTLAETERFF\D
EGKFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQ RLMSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPK NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV. TANEKNKSVSYEQCKPVSVTPQGNDFEVTAKIRTLAETERFF\\ ELTKEKQIEAALSRMPSPGGRITLQTKLNQEAFGRSFGKD  713 PVEVSGYRSRADPEPRGRDTMTYAYLFKYIIGDTGVGKSCLLI QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQES: RSITRSYYRGAAGALLVYDLTRRETFRHHLTSWLEDARQHSSNN VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI	6000	7.00	1004	
RLINSASQRSSSLPPSNRKSSTPTKRBIMLTPVTVAYSPKRSPK NLSPGFSHILISKNBSSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QPLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV. TANEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLABTERFF\\ ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD 6100 2 713 FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLI\ QPTDKRFQPVHDLTIGVEFGRRMVNIDGKQIKLQIWDTAGQBS\ RSITRSYYRGAAGALLVYDITRRETFRHLTSWLEDARQHSSSN\ VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI	6033	709	10/4	
NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQ \QFLPIDDSEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV. TANEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\\ ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  6100 2 713 FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIGDTGVGKSCLLI\ QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQES\ RSITRSYYRGAAGALLVYDLTRRETFRHLTSWLEDARQHSSNN\ VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI	1 1			
\QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSV. TAMSKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\\ ELTKEKDQIEAALSRMPSPGGRITLQTKINQEAFGRSFGKD 6100 2 713 FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIGDTGVGKSCLLL\ QFTDKRPQPVHOLTIGVEFGARMVNIDGKQIKLQIWDTAGQES\ RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSNN\ VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI	f 1	į		
TANSKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLÆBTERFF\ ELTKEKDQIEAALSRMPSPGGRITLQTKLNQEAFGRSFGKD 6100 2 713 FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCILL QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQES: RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSNN VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI	i I	İ		
BLTKBKDQIBAALSRMPSPGGRITLQTRLNQBAFGRSFGKD  6100 2 713 FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCILL QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQBSI RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSN VIMLIGNKSDLESRRDVKREEGBAPARE\HGLIFMETSAKTACI	ļ Ī			
6100 2 713 FVEVSGYRSRADPEPRGRDIMTYAYLFKYIIIGDTGVGKSCILL QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQES: RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSN VIMLIGNKSDLESRRDVKREEGRAPARE\HGLIFMETSAKTACI				
QFTDKRFQPVHDLTIGVEFGRRMVNIDGKQIKLQIWDTAGQBS RSITRSYYRGAAGALLVYDITRRETFRHLTSWLEDARQHSSSN VIMLIGNKSDLESRRDVKREEGRAFARR\HGLIFMETSAKTACI			·	
RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSN VIMLIGNKSDLESRRDVKREEGRAPARE\HGLIFMETSAKTACI	6100	2	713	
RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSN VIMLIGNKSDLESRRDVKREEGRAPARE\HGLIFMETSAKTACI		1		QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF
		i		RSITRSYYRGAAGALLVYDITRKETFNHLTSWLEDARQHSSSNM
		!	÷	VIMLIGNKSDLESRRDVKREEGRAFARE\HGLIFMETSAKTACN
VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGFQQSISTSVG				vefafintakeiyrkiqqglfdvhneangikigpqqsistsvgp
SASQRNSRDIGSNSGCC			I	
6101 1 1399 FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPILAFI	6101	1	1399	FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR
1 1 - 1	1	i		GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAQIAEDKPY
				ABLWMGTHPRGDAKILDNRISQKTLSQWIAENQDSLGSKVKDTF

15.7			and the state of t
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
[	amino acid	acquence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			NGNLPFLFKVLSVETPLSIQAHPNKELAEKLHLQAPQHYPDANH
Į			KPEMAIALTPPQGLCGFRPVEEIVTFLKKVPEFQFLIGDEAATH
i	1	1	LKQTMSHDSQAVASSLQSCFSHLMKSBKKVVVEQLNLLVKRISQ
	<u> </u>		QAAAGNNMEDIFGELLLQLHQQYPGDIGCFAIYFLNLLTLKPGE
	İ		AMPLEANVPHAYLKGDCVECMACSDMTVRAGLTPKFIDVPTLCE
			MLSYTPSSSKDRLFLPTRSQEDPYLSTYDPPVPDFTIMKA\EVP
	1	[	G\SVTEYKDLALDSASILLMVQGTVIASTPTTQTPIPLQRGGVL
		Í	FIGANESVSLKLTBPKDLLIFRACCLL
6102	70	2415	QTPQATLAANGAEDSRGGEMLPAGEIGASPAAPCCSESGDERKN
	I	1	LEEKSDINVTVLIGSKQVSEGTDNGDLPSYVSAFIEKEVGNDLK
		1	SLKKLDKLIEGRTVSKMQLEEGVLTISSEIPKRIRSALKNAEES
1	i	ŀ	KQFLNQFLEQETHLFSAINSHLLTAQPWMDDLGTMISQIEEIER
	1		HLAYLKWISQIEKLSDNIQQYLMINNVPKAASTLVSMABLDIKL
	1		QESSCTHLIGFMRATVKFWHKILKDKLTSDFEEILAQLHWPFIA
		1	PPQSQTVGLSRPASAPRIYSYLBTLFCQLLKLQTSHELLTEPK\
		l	HSQKNTLFLPPLLSS/WPIQVMLTPLQKRFRYHPRGNRQTNVLS
		[	KPEWYLAQVLMWIGNHTEFLDEKIQPILDKVGSLVNARLEFERG
	]		LMMLVLEKLATDIPCLLYDDNLFCHLVDEVLLFERELHSVHGYP
	ŀ		GTFASCMHILSEETCFQRWLTVERKFALQKMDSMLSSEAAWVSQ
			YKDITOVDBMKVPDCAETFMTLLLVITORYKNLPTASRKLQFLE
	1	ļ	LQKDLVDDFRIRLTQVMKBETRASLGFRYCAILNAVNYISTVLA
			DWADNVFFLQLQQAALEVFAENNTLSKLQLGQLASMESSVFDDM
			INLLERLKHDMLTRQVDHVFREVKDAAKLYKKERWLSLPSQSEQ
			AVMSLSSSACPLLLTLRDHLLQLEQQLCFSLEKIFWQMLVEKLD
	<b>[</b> .		VYIYQEIILANHFNEGGAAQLQFDMTRNLFPLFSHYCKRPENYF
	<b>.</b>		KHIKEACIVLNLNVGSALTAGKDVLPVQLQGSPPAT
6103	207	2523	ESNSTMTTYLEFIQQNEERDGVRFSNNVWPSSRLEATRMVVPVA
	ĺ		ALFTPLKERPDLPPIQYEPVLCSRTTCRAVLNPLCQVDYRAKLW
			ACNFCYQRNQFPPSYAGISELNQPAELLPQFSSIEYVVLRGPQM
	l		PLIFLYVVDTCMEDEDLQALKESMQMSLSLLPPTALVGLITFGR
	ł		MVQVHELGCEGISKSYVFRGTKDLSAKQLQEMLGLSKVPVTQAT
	}		RGPQVQQPPPSNRFLQPVQKIDMNLTDLLGBLQRDPWPVPQGKR
	Ŀ		PLRSSGVALSIAVGLLECTFPNTGARIMMFIGGPATQGPGMVVG
			DELKTPIRSWHDIDKDNAKYVKKGTKHFEALANRAATTGHVIDI
	[		YACALDQTGLLEMKCCPNLTGGYMVMGDSFNTSLFKQTFQRVFT
			KDMHGQPKMGFGGTLEIKTPR\BIKISGAIGPCVSLNSKGPCVS
	<b> </b>		ENEIGTGGTCQWKICGLSPTTTLAIYFEVVNQHNAPIPQGG\RG
	Ì		A\IQFVTQY\QHSSGQRRIRVTTIARN\WADAQTQIQNIAASFD
	}		QRAAAILMARLAIYRABTEEGPDVLRWLDRQLIRLCQKFGEYHK
j j			DDPSSFRFSETFSLYPQFMFHLRRSSFLQVFNNSPDESSYYRHH
			FMRQDLTQSLIMIQPILYAYSFSGPPEPVLLDSSSILADRILLM
			DTFFQILIYHGETIAQWRKSGYQDMPEYBNFRHLLQAPVDDAQE
1			ILHSRFPMPRYIDTEHGGSQARFLLSKVNPSQTHNNMYAWGQES
· ·			GAPILTDDVSLQVFMDHLKKLAVSSAA
6104	124	732	KVSBYIILSKDKILFHALAMLVLVVSPNSAARGVLRNYWERLLR
			KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL
		,	LDSIFWMAAPKNRRTIBVNRCRRRNPQKLIKVKNNIDVCPECGH
			LKQKHVLCAYCYEKVCKETABIRRQIGKQEGGPFKAPTIETVVL
			YTGETPSEQDQGKRIIERDRKRPSWFTQN
6105	3	989	PLHGACTSLVLQRFCHRRPRPCAPARPEDMRRPAAVPLLLLLCF
			GSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHF
			CGGSLIAEQWVLTAAHCPRNTSBTSLYQVLLGARQLVQPGPHAM
			YARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPD
			PSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDT\PR
			CNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSAGPLV
i l	İ		CLVGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK
	L		COLOSTANDATOROGO CASTAGATIVATABLIBATISTICA

	,		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ar	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ı	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į	to first	amino acid	
i	D .		P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	<u> </u>	\=possible nucleotide insertion)
			LQVQPSEVGRPEVTPPGPGAP
6106	3	1302	GRPPTAPHTGRPPTANRGDPRLDLKRGCARLLTSIESRGRPAAS
0.00	1 -	1 -302	
1	<u>[</u>		AGLRRDRCALRRWPLRRAPLARATRRRAGSPRRCAPRPRACPQG
1	1	ı	WSRARHQPGGLCLLLLLLCQFMEDRSAQAGNCWLRQAKNGRCQV
ł	1		LYKTELSKEECCSTGRLSTSWTEEDVNDNTLFKWMIFNGGAPNC
i	}	1	IPCKETCENVDCGPGKKCRMNKKNKPRCVCAPDCSNITWKGPVC
1		f	GLDGKTYRNECALLKARCKEQPELEVQYQGRCKKTCRDVFCPGS
}			STCV\VDQTNNAYCVTCNRICPBPASSEQYLCGNDGVTYS\SAC
}	Ì	l	HLRKATCLLGRSIGLAYEGKCIKAKSCEDIQCTGGKKCLWDFKV
1		ł	GRGRCSLCDELCPDSKSDEPVCASDNATYASECAMKRAACSSGV
1			
27.00		1,,	LLEVKHSGSCNSISEDTEERREDEDDDDYSFPISSILEW
6107	623	168	SRCSSPRPRPGRGRGK/LSPSKHRKWVEVFKACDEDHKGYLSRE
l			DFKTAVVMLFGYKPSKIEVDSVMSSINPNTSGILLEGFLNIVRK
			KKBAQRYRNEVRHIFTAFDTYYRGFLTLEDFKKAFRQVAPKLPE
L			RTVLEVFREV\DRDS\DGHVSF
6108	3	1348	GGSLRFSPPRVPSCSRVFCPVPPGGCGLPSPMSASRPQSPTTPW
	l :		CLPRRYMKHKRDDGPEKQEDEAVDVTPVMTCVFVVMCCSMLVLL
		İ	YYFYDLLVYVVIGIFCLASATGLYSCLAPCVRRLP\SASAGESA
			LLAPTIPHNSLPYFHKRPQARMLLLALFCVAVSVVWGVFRNEDO
į i			
j	i i		WAWVLQDALGIAPCLYMLKTIRLPTFKACTLLLLVLFLYDIFFV
1			PITPFLTKSGSSIMVEVATGPSDSATREKLPMVLKVPRLNSSPL
•			ALCDRPFSLLGFGDILVPGLLVAYCHRFDIQVQSSRVYFVACTI
	!		AYGVGLLVTFVALALMQRGQPALLYLVPCTLVTSCAVALWRREL
1			GVFWTGSGFAKVLPPSPWAPAPADGPQPPKDSATPLSPQPPSEE
	i ·		PATSPWPARQSPKSRTSERMGAGAPMREPGSPARSEGRDQAQPS
			PVTOPGASA
6109	1	1381	CRSRAGAASGGAILEGTKLRRQRVDTNKPLDPLVPSALRAAMLY
	_		LEDYLEMIEQLPMDLRDRFTEMREMDLQVQNAMDQLEORVSEFF
			MNAKKNKPEWREEQMASIKKDYYKALEDADEKVQLANQIYDLVO
1		-	- · · · · · · · · · · · · · · · · · · ·
1	j		RHLRKLDQBLAKFKMELRADNAGITEILERRSLELDTPSQPVNN
			HHAHSHTPVEKRKYNPTSHHTTTDHIPEKKFKSEALLSTLTSDA
			Skentlgcrnnnstassnnaynvnssqplgsynigslssgtgag
1 3			gi\tmaaaqavqataqmkegrrtsslkasyeafknndfqlgkef
[			SMARETVGYSSSSALMTTLTQNASSSAADSREGRKEKNNNKSSS
<b>,</b>			QQSSSSSSSSSSSSSSSSSSTVVQBISQQTTVVPESDSNSQVDWT
]			YDPNBPRYCICNQVSYGEMVGCDTQDCPIEWFHYGCVGLTEAPK
[ ]			GKWYCPQCT\AAMKRRGSRHK
6110	77	2464	ACPSAATMSDQDHSMDEMTAVVKIEKGVGGNNGGNGGGAFSQ
]	''	7.44	ARSSSTGSSSSTGGGGOESOPSPLALLAATCSRIESPNRNSNNS
1 1			_ = -
!!!			QGPSQSGGTGKLDLTATQLSQGANGWQIISSSSGATPTSKEQSG
[	.		SSTNGSNGSRSSKNRTVSGGQYVVAAAPNLQNQQVLTGLPGVMP
[	i		NIQYQVIPQFQTVDGQQLQFAATGAQVQQDGSGQIQIIPGANQQ
[	i i		IITNRGSGGNIIAAMPNLLQQAVPLQGLANNVLSGQTQYVTNVP
[			VALNGNITLLPVNSVSAATLTPSSQAVTISSSGSQBSGSQPVTS
			GTT1SSASLVSSQASSSSFFTNANSYSTTTTTSNMGIMNFTTSG
[			SSGTNSQGQTPQRVSGLQGSDALNIQQNQTSGGSLQAGQQKBGB
			Q\NQQTQAAPKSI.SRPQLVQGG\QALQ\AFQAAPLSGOTFTTQA
į į			ISQETLQNLQLQAVPNSGPIIIRTPTVGPNGQVSWQTLQLQNLQ
į į			
			VQNPQAQTITLAPMQGVSLGQTSSSNTTLTPLASAASIPAGTVT
		•	VNAAQLSSMPGLQTINLSALGTSGIQVHPIQGLPLAIANAPGDH
			GAQLGLHGAGGDG1HDDTAGGEEGENSPDAQPQAGRRTREACT
	1		CPYCKDSEGRGSGDPGKKKQHICHIQGCGKVYGKTSHLRAHLRW
	1		
			HTGERPFMCTWSYCGKRFTRSDELQRHKRTHTGEKKFACPECPK
			HTGERPFMCTWSYCGKRFTRSDELQRHKRTHTGEKKFACPECPK RFWRSDHLSKHIKTHQNKKGGPGVALSVGTLPLDSGAGSEGSGT
			HTGERPFMCTWSYCGKRFTRSDELQRHKRTHTGEKKFACPECPK

0.70	1 70	Desirable management	Talle and a second control of the second con
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Giutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serire, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	L	\=possible nucleotide insertion)
6111	1637	797	RVDPRVRGAMAPWGKRLAGVRGVLLDISGVLYDSGAGGGTAIAG
l			SVEAVARLKRSRLKVRFCTNESQKSRAKLVGQLQRLGFDISEQE
1	'		VTAPAPAACQILKERGLRPYLLIHDGV\ASEFDQIDTS/STPNC
1		[	VVIADAGESFSYQNMNNAFQVIMELEKPVLISIGKGRYYKETSG
1	ì	1	LMLDVGPYMKALEYACGIKAEVGGKPSPEFFKSALQAIGVEAHQ
1	1		AVMIGDDIVGDVGGAQRCGMRALQVRTGKFRPSDRHHPEVKADG
			YVDNLAEAVDLLLQHADK
6112	77	196	MSSHKSFKSKRFLAKKQKPNRPILQWIWLKTGNKIRHNWK
6113	1779	567	WEGRSWAACGVNLQGAWGERSGVRASEAESPGKRADVSWWSRQL
	1	}	RTMVDHLANTEINSQRIAAVESCFGASGQPLALPGRVLLGEGVL
Í	1		TKECRKKAKPRIFFLFNDILVYGSIVLNKRKYRSQHIIPLEEVT
1	1	}	LELLPETIQAKNRWMIKTAKKSFVVSAASATERQEWISHIEECV
1	1	!	RRQLRATGRPA\STEHAAPWIPDKATDICMRCTQTRFSALTRRH
1	1	1	HCRKCRVVVCAECSRQRFLLPRLSPKPVRVCSLCYRBLAAQQRK
		l .	BEABEQGAGVPRAASHLARPICGRPVEHIMTPTRTRRAAGTATG
[			PAAWSSTPRGWPGLPSTADPRPAEHLSPSQLHCPGPQEGSSRSC
	1	l	PGLRDP1PWNQVQRWGVALSGLPVPFCWTLCPYGFTAGNAFPFR
	<u></u>	<del></del>	KPONTHRSW
6114	818	246	PTSRPRPSPGSPAMSWSACVSAAPSSSWPASSSWPCGPRRCCTR
Ţ.	İ		RRRCSPRCGLAAGSMCSCSPSWRCTPVPACWPSPPP\PAEQVQC
1	1	<b>}</b>	GHLPPHADRRALRLPVAAPARGPGPGHPAGPAGPRPARTPPASP HGPGRPTVPAPPCPLLAATEPTPSRFHORWTREDRMLGRGSOVT
1		!	GRPOWFLRGLVLFSL
6115	324	71	DVCGRVCAHPHLYTHIHMHICAHAC\IHTHAQLC/ITASHALAH
1 2112	344	} ' <sup>+</sup>	SHLYTCMVMLTASHTPSHTHPHTAVHKEHRADVLRGTLTPLR
6116	595	1430	TGVMPPGRWHAA/ISSSGPVFEGARA\LQTVKKEBEDESYTPVQ
97.70	333	1 -330	AARPOTLNRPGOBLFRQLFRQLRYHBSSGPLETLSRLRELCRWN
1	1		LRPDVLSKAQILELLVLEQFLSILPGELRVWVQLHNPESGEE\L
1		1	WPCWRSCRGTLMGHPGGTRALP\EPRCALDGYRS\LRSAQIWSL
1		l	ASPLRSSSALGDHLEPPYEIEARDFLAGQSDTPAAQMPALPPRE
1			GCPGDQVTPTRSLTAQLQETMTFKDVEVTFSQDEWGWLDSAQRN
	· ·	ļ	Lyrdvmlenyrnmaslgk
6117	1433	222	VGVPSPAPPCSWBVGPGGGWTPGILKBGQGGRRTPLLLLATRTR
1		[	GLISLFPPAAMHPAAFFLPVVVAAVLWGAAPTRGLIRATSDHNA
1	1	Ì	SMDFADLPALFGATLSQEGLQGFLVRAHPDNACSPIAP?PPAPV
1	1		NGSVFIALLRRFDCNFDLKVLNAQKAGYGAAVVHNVNSNELLNM
]		l	vwnsebiqqqiwipsvpigersseylralpvybkgarvllvpdn
Ţ	1	<b>[</b>	TFPLGYYLIPFTGIVGLLVLAMGAVMIARCIQHRKRLQRNRLTK
1	[	Į.	\EQLKQI\PTHDYQKGDQYDVCAICLDRYEDGDKLRVLPCAHAY
l	l		HSRCVDPWLTQTRKTCPICKQPVHRGPGDBDQBEBTQGQEEGDB
1	i	1	GEPROHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL
1			SPPSSPVILV
6118	1044	247	STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK
ł		l	KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQEKQERRKGK
1	}	{	EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK
1		ł	NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE
Į	!	l	DSQMBFLBIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP
[			ITWKAKKYLHOLIAANPVLPLVVFANKODLEAAYHITDIHEALA
1	1		II
6119	1217	462	DPREVTENTTKAPAGERTTOPRSSREGTLRSTMEYLSALNPSDL
1	]	i	LRSVSNISSEFGRRVWTSAPPPORPFRVCDHKRTIRKGLTAATR
ł	Ţ	<b>[</b>	OELLAKALETLLINGVLTLVLBEDGTAVDSEDFFQLLEDDTCIM
1	1	f	VLQSGQSWSPTRSGVLSYGLGRBRPKHSKDIARFTFDVYKQNPR
l			DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ
]	1	1	GLGHMLLGISSTLRHAVEGAEQWQQKGRLHSY
L	L	i	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6120	785	179	LERAGGGGLSSRALVGSGACLSLVARANGKGLPRGRKEFVBAVR
	j	ł	VRYVAFRYRTPRAVCLRLWSCRREVIMSGRGKQGGKVRAKAKSR
ł	1	i	SSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAE
i	1	ļ	ILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQG
			G\VLPNIQAVLLPKKTESQKDBGANDP
6121	1612	107	FVRAQARGSRQPVRRPLLGAGSRLRCRSCGRMEPLKVEKFATAN
ĺ	l		RGNGLRAVTPLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKE
			KLMRCSQCRVAKYCSAKCQKKAWPDHKRBCKCLKSCKPRYPPDS
ļ			VRLLGRVVFKLMDGAPSESEKLYSFYDLESNINKLTEDKKEGLR
1	1		QLVMTFQHFMREBIQDASQLPPAFDLFBAFAKVICNSFTICNAB
]		Į	MQEVGVGLYPSISLLNHSCDPNCSIVFNGPHLLLRAVRDIEVGE
1	[	1	ELTICYLDMLMTSEERRKQLRDQYCFECD\CFRCQTQDKDADML
	[		TGDEQVWKEVQESLKKIEELKAHWKWEQVLAMCQAIISSNSERL
	ļ ·	l	PDINIYQLKVLDCAMDACINLGLLEBALFYGTRTMBPYRIFFPG
	ł	l	SHPVRGVQVMKVGKLQLHQGMFPQAMKNLRLAFDIMRVTHGREH
			SLIEDLILLE/AMRRQHQSILRERSQREIRRVSLLNALLRSHT
6122		2324	LCFVSCVNLSYWKFCSVFV
0122	2	2324	RFRKMADGGAASQDESSAAAAAAAADSRMNNPSETSKPSMESGDG
			NTGTQTMGLDFQKQPVPVGGAISTAQAQAFLGHLHQVQLAGTSL
			QAAAQSLNVQSKSNEKSGDSQQPSQPSQQPSVQAAIPQTQLMLA
			GGQITGLTLTPAQQQLLLQQAQAQALLAAAVQQHSASQQHSAA GATISASAATPMTQIPLSQPIQIAQDLQQLQQLQQQNLNLQQPV
·	•		LVHPTINLQPA\OFIISQTPOGQQGLLQA\ONLLTOLPROSOAN
			LLQSQPRI\TLTSQPATPTCTIAATPIQFLPQSQSTPKRIDTPS
			LEEP\SDLEELEQFAKTFKQRRIKLGFT\QGDAGLAMVKLYGND
			FSPTTIFRFBALNLSFKNMCKLKPLLEKWINDAENISSDSSLSS
			PSALNSPGIEGLSRRRKKRTSIEA\NIRVALEKSFLEN\QKPTS
			EEITMIADQLNMEKGVIRVWFCNRRQKEKRINPPSSGG\TSSSP
			IKAIPPSPTSLVATTPSLVTSSAATTLTVSPVLPLTSAAVTNLS
			VTGTSDTTSNNTATVISTAPPASSAVTSPSLSPSPSASASTSEA
			SSASETSTTOTTSTPLSSPLGTSQVMVTASGLQTA/AQLLPPKG
			AAQLPANASLAAMAAAAGLNPSLMAPSQFAAGGALLSLNPGTLS
			GALSPALMSNSTLATIOALASGGSLPITSLDATGNLVFANAGGA
			PNIVTAPLFLNPQNLSLLTSNPVSLVSAAAASAGNSAPVASLHA
			TSTSAESIONSLFTVASASGAASTTTTASKAQ
6123	3	2944	HLLHRWFGTDMQMINFTTGBFQLTBACPYLGTHSEESRFGILHL
			HLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFG
			ARELLKVGGRLPGAGGSLRFKVPBSTLMDCRRQLKDSKQILSIT
			Knpkvenigplpitvsslkingyncogygprvldchopsldpnt
	I		SRDISIVFTPDFTSSWVIRDLSLVTAADLEPRFTLMVTLPHHLL
	1		PLCADVVPGPSWBESFWRLTVFFVSLSLLGVILIAFQQAQYIIM
			BFMKTRQRQNASSSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS
	1	_	DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK
ļ		•	HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI
i			SLRYASGINVNLQKNLTLPKNLLNKERNTLKNTIVFSNPSSBCS
			MKEGIQTCMFPKBTDIKTSENTAEFKERELCPLKTSKKLPENHL
			PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK
- 1	ĺ		PSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEKREGNL
į	1		QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS
1	1		SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK
	1		KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM
Į	İ		VDAQHFLPAGDSVSQNDFPSKAPISLNLSHNICNPMTGNSLPQY
i	ł		AEPSCPSLPAGPTGVERDKGLYSPGDLWPTPPVCVTSSLNCTLE
ļ	1		NGVPCVIQESAPVHNSFIDWSATCEGQPSSAYCPLBLNDYNAPP
j			RENMNYANGFPCPADVQTDFIDHNSQSTWNTPP\NMPAS\WGNA
I	İ		QFPSSSRPYLKSTPKACLPMSGLFGPI\WAP\QSDVYENCCPIN

		1 3/-6-3 3	[ Nation and a second manufacture of small manufacture]
SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
ì	location	corresponding to first	L=Leucine, M=Methionine, N=Asparagine,
1	corresponding	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	to first	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l .	amino acid	sequence	Codon, /=possible nucleotide deletion,
l .	sequence	sequence	\=possible nucleotide insertion)
<u> </u>	sequence	<del> </del>	PTTEHSD/THMENQA\VVCKEYYPGF\NPFRAYMNLDIWTTT\A
l			NRNANFPLSRDSSYCGNV
6124	1573	236	SDEALRLAGERCMGRVQLFEISLSHGRVVYSPGEPLAGTVRVRL
6124	1	2.30	GAPLPFRAIRVTCIGSCGVSNKANDTAWVVRBGYFNSSLSLADK
ŀ	}	ł	GSLPAGEHSFPFQFLLPATAPTSFEGPFGKTVHQVRAAIHTPRF
ŀ	l	ſ	SKDHKCSLVFYILSPLNLNSIPDIEQPNVASATKKFSYKLVKTG
ĺ		ļ	SVVLTASTDLRGYVVGQALQLHADVENQSGKDTSPVVASLLQKV
1		{	SYKAKRWIHDVRTIAEVEGAGVKAWRRAQWHEQILVPALPQSAL
i	l .	l	PGCSLIHIDYYLQVSLKAPRATVTLPVFIGNIAV/NPCPSBPPA
l		į.	RPGAASWGPTPGG\PSAPPQEEAEARAAAGGPHFLDPVFLSTKS
	}	ł .	HSQRQPLLATLSSVPGAPEPCPQDGSPASHPLHPPLCISTGATV
i	ł		PYFARGSGGPVPTTSTLILPPEYSSWGYPYEAPPSYEQSCGGVB
1		l	PSLTPES
6125	1	904	KTCPKLTCAFTVSVPDSCCRVCRGDGELSWEHSDGDIFRQPANR
	1	1	EARHSYHRSHYDPPPSRQAGGLSRYPGARSHRGALMDSQQASGT
l			IVQIVINNXHKHGQVCVSNGKTYSHGESWHPNLRAFGIVECVLC
1	{		TCNVTKQECKKIHCPNRYPCKYPQKIDGKCCKVCPG/KKAKEBI
			PGQSFDNKGYFCGBETMPVYESVFMBDGBTTRKIALETERPPQV
ļ		1	EVHVWTIRKGILQHFHIEKISKRMFEELPHFKLVTRTTLSQWKI   PTEGEAQISQMCSSRVCRTELEDLVKVLYLERSEKGHC
- C136	1224	389	RLLSBAPCPRSRRRFOMNPBWGOAFVHVAVAGGLCAVAVFTGIF
6126	1224	307	DSVSVOVGYEHYARAPVAGLPAFLAMPKNSLVNMAYTLLGLSWL
	1		HRGGAMGLGPRYLKDVPAAMALLYGPVQWLRLWTQWRRAAVLDQ
1	1		WLTLPIFAWPVAWCLYLDRGWRP\WLFLSLECVSLASYGLALLH
			POGFEVALGAHVVPAVGQALRT\HRHYG/SATPSATYLALGVLS
	}		CLGFVVLKLCDHQLARWRLFQCLTGHFWSKVCDVLQFHFAFLFL
ì	}		THENTHPREHPSGGKTR
6127	1335	463	VLPRRCLVFVVNTMDSSREPTLGRLDAAGFWQVWQRFDADEKGY
i i	}	·	IERKELDAFFLHMLMKLGTDDTVMKAMLHKVKQQFMTTQDASKD
ł			GRIRMKELAGMFLSEDRNFLLLFRRENPLDSSVEFMQIWRKYDA
1	<b>,</b>	ţ	DSSGFISAAELRNFLRDLFLHHKKAISEAKLEEYTGTMMKIFDR
	ļ	j	NKDGRLDLNDLARILALQENFLLQFKMDACSTBKRKGDFEKIFA
Į.		ļ	YYDVSKTGALEGP\EVDGFVKDMMELVQPSISGVDLDKFREILL
L	<del> </del>	843	RHCDVNKDGKIQKSBLALCLGLKINP TCRMSRROLKRWVWSSQOVQARGRNVRAPRLGKIAMGLKMSSKD
6128	2511	( 043	SPGSLDGRAWEDAQKPQSAWCGGRKTRVYATSSKRAPPSEGTRR
1			GGAARPEKTAEBGPPAAPGSLRHSGPLGPHACPTALPEPQVTSA
J	1	1	MSSQVVGIEPLYIKAEPASPDSPKGSSETETEPPVALAPG\PAP
1	1	1	TRCLPGHKEERDGEGAGPGEQGGKLVLSSLPKRLCLVCGDVAS
1	[		GYHYGVASCEACKAFFKRTIQGSIBYSCPASNBCBITKRRRKAC
1		1	QACRFTKCLRVGMLKEGVRLDRVRGGRQKYKRRPEVDPLPFPGP
1	1		FPAGPLAVAGGPRKTAAPVNALVSHLLVVEPBKLYAMPDPAGPD
1	{	}	GHLPAVATLCDLFDREIVVTISWAKSIPGFSSLSLSDQMSVLQS
1			VWMEVLVLGVAQRSLTLQDELAFABYLVLDEEGARPAGLGELG\
1	Į.	1	AALLQLVRRLQALRLEREBYVLLKALALANSDSVHIEDEPRLWS
ł	1		SCEKLIHEALLEYBAGRAGPGGGAERRRAGRLLLTLPLLRQTAG
	L		KVLAHFYGVKLEGKVPMHKLFLEMLRAMMD
6129	1764	771	ARFARSAHEGKMPKKKTGARKKAENRREREKQLRASRSTIDLAK
1		]	HPCNASMBCDKCQRRQKNRAFCYFCNSVQKLPICAQCGKTKCMM
1	1	1	KSSDCVIKHAGVYSTGLAMVGAICDFCKAWVCHGRKCLSTHACA
]			CPLTDAEC\VECERGVWDHGGRIFSCSFCHNFLCEDDQFEHQAS
j	l .	1	CQVLEAETPKCVSCNRLGQHSCLRCKACFCDDHTRSKVFKQEKG
			KOPPCPKCGHETOETKDLSMSTRSLKFGROTGGEEGDGASGYDA
}	1	}	YWKNLSSDKYGDTSYHDEEEDEYEARDDREEEDBGRKDSDTESS DLFTNLNLGRTYASGYAHYEEQEN
6130	<del> </del>	577	GRGGTMREYKVVVLGSG\GVGKSALTV\QFVTCTFIEKYDPTIE
6130	3		QUODITAMINA A DOOG (DADIOMITA (AL LICITIBATIDE LIP

	T		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding to first	to first	L-Leucine, M-Methionine, N-Asparagine,
1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
	ocquence	<del> </del>	\=possible nucleotide insertion)
1	1	}	DFYRKBIEV\DSSPSVAGISWTQQGTEQF\ASMRDLYIKKGQGC ILVYSLVNQQSPQ\DIKPMRDQIIRVKVSBKVPVI\LVGN\SVD
1	}		LESEREVSSSEGRALAEBWGCPFMBTSAKSKTMVDELFAEIVRO
1		ŀ	MNYAAQPDKDDPCCSACNIO
6131	3	1811	SSPREKTSDSSHRPSRHCPLFLRLVGLSPFSYLCVPPSRPVPGS
	1	1012	PRSLSAMRLLPLAPGRLRRGSPRHLPSCSPALLLLLVLGGCLGVF
ļ			GVAAGTRRPNVVLLLTDDQDEVLGGMTPLKKTKALIGEMGMTFS
İ	j .	ļ	SAYVPSALCCPSRASILTGKYPHNHHVVNNTLEGNCSSKSWOKI
l			QEPNTFPAILRSMCGYQTFF\AGKYLNEYGAPDAGGLEHVPLGW
1			SYWYALEKNSKYYNYTISINGKARKHGENYSVDYLTDVLANVSL
i			DFLDYKSNFEPFFMMTATP\APHSPWTAAPOYOKAFONVFAFRN
I			KNFNIHGTNKHWLIRQAKTPMTNSSIQFLDNAFRKRWQTLLSVD
1	· ·	·	DLVEKLVKRLEFTGELNNTYIFYTSDNGYHTGQFSLPIDKROLY
			BFDIKVPLLVRGPGIKPNQTSKMLVANIDLGPTILDIAGYDLNK
1			TOMOGMELLPILRGASNLTWRSDVLVEYQGEGRNVTDPTCPSLS
	*		PGVSQCFPDCVCKDAYNNTYACVRTMSALWNLQYCBFDDQEVFV
! :			EVYNLTADPDQITNIAKTIDPELLGKMNYRLMMLQSCSGPTCRT
			PGVFDPGYRFDPRLMFSNRGSVRTRRFSKHLL
6132	96	1241	AAGLLPPGLVPEDPRRTRNLLPPGIQGPPFALSRPLFSCVESGW
			AWEAMEPEFLYDLLQLPKGVEPPAEEELSKGGKKKYLPPTSRKD
			PKFEELQKPA\VLMEWINATLLPEHIVVRSLEEDMFDGLILHHL
	*		FORLAALKLEAEDIALTATSQKHKLTVVLEAVNRS\CSWRSGRP
			SGA/WESIFNKDLLSTLHLLVALAKRFQPDLSLPTNVQVEVITI
			ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVFDKLPKLAPEKVNA
			VKEAIVNFVNQKLDRLGLSVQNLDTQFADGVILLLLIGQLEGFF LHLKEFYLTPNSPAEMLHNVTLALELL/IGRGPAQLPC/LALK/
			TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTPHGAPN
6133	2	4256	FVHGSMADTDLFMECERERLEPWQKISDVIEDSVVEDYNSVDKT
	ū		TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
			KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
			IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
			STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
			TATOPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSTASFVT
			vkrpgvtgensnevaklvntlntipslgqspgpvvvsnnssah\
			GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTHAL
	İ		RCHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
			/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
			GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
			LDQQNGKVDGHTICQHCYRQFSTPFQLQCHLRNVHSPYESTTKC
			KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
			VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVOPLFAKDKIEHKLOHHKTPRKPKOLEGLKPGTKVTIRA
	1		SRGQPRTVPVSSNDTPPSALQEAPLTSSMDPLPVFLYPPVORS
	1		IQKRAVRKMSVMGRQTCLBCSFEIPDPPNHFPTYVHCSLCRYST
i	ľ		CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
	1		SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
	j		NVKNMYPPPSFPTNKAATVKSAGATPABPRELLTPLAPALPSPA
[			STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTOEPE
	Ī		LASGGGGGGGGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPO
	į		RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP
j	]		VNEETLEQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
Ì	İ		VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
ļ	1		DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
ļ	ļ	•	RGQMDQPANMPDSILLEAKRSGYSDDEIMELWSTRVWOKHTACO
ł	İ		RSKGMLVMDCHRTHLSBEVLAMLSASSTLPAVVPAGCSSKIOPL
			Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z

	·		the fact that the design the
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	1	1	
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
		į	DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
1 .	İ	ŀ	LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
J	l	i	PYGFEEADLDLMEI
6134	2	4256	PVHGSMADTDLFMECEERELBPWQKISDVIEDSVVEDYNSVDKT
0.33	_		TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
1	ļ	į.	KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
			,
	i	į.	PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
1 .		j .	IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
1			STMPVRPTTNTFTTVIPATLTTRSTVPQSQSQQTKSTPSTSTTP
İ .			TATOPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
1		ł	VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
			GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
1	}	1	RGHMCYCCPRMVEYQKKGKSLDSBPSVPSAAKPPSPBKTAPVAS
i I			/THPSSTPIPALSPPY/TKVPRPNENVGDAVQTKLIMLVDDFYY
		ļ	GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVB
1			LDOONGEVDGHTICOHCYRQFSTPFQLQCHLRNVHSPYESTTKC
•	•	į	KICEWAPESEPLFLOHMKDTHKPGEMPYVCOVCQYRSSLYSEVD
		1	
1			VHPRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
1			CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
- 1		Į.	SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
į.		İ	IQKRAVRKMSVMGRQTCLECSFBIPDFPNHFPTYVHCSLCRYST
l .		<b>,</b>	CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
Ĭ.			SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
1		<u> </u>	NVKNMYPPPSFPTNKAATVKSAGATPABPEELLTPLAPALPSPA
1	Ì		STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQRPE
	•		LASCGCGCGCCCKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
ľ		ļ.	RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP
1		l '	VNEETLFQKATKIGRSLEGGPKISYEWAVRFMLRHELTPHARRA
ĺ			VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
		1	DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
i	ł	Į.	RGQMDQPANMPDSILLBAKESGYSDDEIMRLWSTRVWQKHTACQ
1	İ	ł	RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
1	}	ł	DVCIRTVKNFLHKKWKEQAREMADTACDSDVILQLVLVWLGEV
l			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
i	}	1	LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
1	Į	]	FYGFREADLDLMBI
6135	2	4256	FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
1	ł	ł	TTV5VSQQPVSAPVPIAAHASVAGHLSTSTTV5SSGAQN5DSTK
	1		KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
l.	İ	1	PVOVMONANHVTSSPVASOPIFITTQGPPVRNVRPVQNAMNQVG
1			IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
	l	İ	STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
1			TATOPTSLGOLAVOSPGOSNOTTNPKLAPSPPSPPAVSIASPVT
	I	I	1
1	]	1	VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
1		[	GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
1	]	1	RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
	1	I	/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
I	1	1	GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
1	1	· ·	LDQQNGBVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
}	[	1	KICEWAPESEPLFLOHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
ł	1.	1	VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
ì	]	1	
i		1	CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
1	1		SRGQPRTVPVSSNDTPPSALQBAAPLTSSNDPLPVFLYPPVQRS
i	j.	l	IQKRAVRKMSVMGRQTCLECSFRIPDFPNHFPTYVHCSLCRYST
i	I	Ī	CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT

	1. 1. 1. 1. N. 3.		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible rucleotide insertion)
			SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
I			nvknmypppsfptnkaatvksagatpaepeklltplapalpspa
ì			STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQRPE
	Ì		LASGGGGGGGGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
			RRIRRWLRRFQASQGENLEGKYLSFEAREKLAEWVLTQRBQQLP
l			VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
			VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
ļ			DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
ĺ	ĺ	1	RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
{	,		RSKGMLVMDCHRTHLSEEVLANLSASSTLPAVVPAGCSSKIQPL
I	1		DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
1		}	LGVIGDCPELVQRSPLVASVLPGPDGNINSPTRNADMQEELIAS
1	l	1	LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
i			FYGFREADLDLMEI
6136	1704	539	FGVRMALEGMSKRKRKRSVQEGENPDDGVRGSPPEDYRLGQVAS
l .		į	SLPRGEHHSRGGTGRLASLFSSLEPQIQPVYVPVPK\ESALASA
		Ì	DLEEEIHQKQGQKRKNSQPGVKVADRKILDDTEDTVVSQRKKIQ
1		·	INQEBERLKNERIVFVGNLPVTCNKKKLKSFFKEYGQIESVRFR
}		1	SLIPAEGTLSKKLAAIKRKIHPDQKNINAYVVFKERSAATQALK
l		İ	RNGAQIADGFRIRVDLASETSSRDKRSVFVGNLPYKVEESAJEK
İ		Ì	HPLDCGSIMAVRIVRDKMTGIGKGFGYVLFENTD8VHLALKLNN
			SELMGRKLRVMRSVNKEKFKQQNSNPRLKNVSKPKQGLNFTSKT
1			
			AEGHPKSLFIGEKAVLLKTKKKGQKKSGRPKKQRKQK
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPRQGQELMAKALES
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPRQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYEDIARNINSSCRPGPGAWLRVV
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNLIVAMCLA\LLGLPGKAQBLQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPRQGQBLMAKALES LSCPRDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYBDIARNINSSCRPGPGAWLRVV LEKPFGHDHPSAQQLATELGTFFQBBEMYRVDHYLGKQAVAQIL
6137	141	2656	RALRKRRCGPGERGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNI.IVAMCLA\LLGLPGKAQELQGHVS\IILAGEQI.GDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPEQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPPAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHPSAQQLATELGTFFQEBEMYRVHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPRQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHYSAQQLATELGTFFQBERHYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTBVLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPRQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALMKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKRPFGHDHPSAQQLATELGTFPQBEEMYRVDHYLGKQAVAQIL PFRDQMRKALDGLWMRHHVERVEIIMKETVDABGRTSFYEEYGV IRDVLQNHLTEVLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPRQGQELMAKALES LSCPKDMAPSHCAEHKOQFLQLSQYRQLKTAKDYQALMKDIEAQ LQHAGLREAGGIPYFSVPPPAYEDIARNINSSCRPGGAWLRVV LEKPFGHDHPSAQQLATELGTFFQEBEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVBRVEIIMKBTVDABGRTSFYEEYGV IRDVLQNHLTBVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDKRVGYARILFKNQACCVQSEKHWAAAQS
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNLIVAMCLA\LLGLPGKAQBLQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPRQGQELMAKALES LSCPRDMAPSHCAEHKDQFLQLSQYRQLKTARDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYEDIARNINSSCRPGPGAMLRVV LEKPFGHDHPSAQQLATELGTFFQBBEMYRVDHYLGKQAVAQIL PFRDQMRKALDGLMNRHHVBRVBIIMKBTVDABGRTSFYBEYGV IRDVLQMHLTBVLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSBQVRRELQKPDSFHSLTPTPAGVLVHIDNL RWEGYPFILMSGKALDKRVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPRQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYBDIARNINSSCRPGPGANLRVV LEKPFGHDHPSAQQLATELGTFFQBBEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDABGRTSFYBEYGV IRDVLQNHLTBVLTLVAMBLPHNVSSAEAVLRHKLQVPQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTPAGVLVHIDNL RWEGVPFILMSGKALDKRVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRRLFRPSLPSSWKEMBGPPG LRLPGSPLSDYYAYSPVRERDAHSVILSHIPHGRKNPPITTENL
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNI.IVAMCLA\LLGLPGKAQELQGHVS\IILAGEQI.GDLAKK YLWQG\LFQLYLDEAGRGRSFSFHGAALTAPRQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFCHDHYSAQQLATELGTFFQBEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTTFFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKRMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIFMGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEYSSGRLFFS
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPRQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTARDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHYSAQQLATELGTFFQBERMYRVHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDABGRTSFYEEYGV IRDVLQNHLTEVLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL ORGSAVVGQYQSYSEQVRRELQKPDSFHSLTTFFAGVLYHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYVAYSPVRERDAHSVLLSHIFHSRKNPFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGGPGPMPGDFQVLRAKYRESSLVSAWSBELISKL
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNLIVAMCLA\LLGLPGKAQBLQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPRQGQELMAKALES LSCPRDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHPSAQQLATELGTFPQBBEMYRVDHYLGKQAVAQIL PFRDQMRKALDGLWNRHHVERVEIIMKETVDABGRTSFYEEYGV IRDVLQNHLTEVLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL ORGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTPAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVPHIGHGDLGSPAVLVSRNLFRPSLPSSWKRMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIPHGRKNFPITTENL LASWNFWTPLLBSLAHKAPRLYPGGAENGRLLDFEPSSGRLPFS QQQPBQLVPGPGPGPMPBDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQPHLALSGGSSPVALFQQLATAHYGFPW
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKRQBLQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPRQGQELMAKALES LSCPRDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYEDIARNINSSCRPGPGAMLRVV LEKPFGHDHPSAQQLATELGTFFQBBEMYRVDHYLGKQAVAQIL PFRDQMRKALDGLMNRHHVBRVBIIMKBTVDABGRTSFYBEYGV IRDVLQHILTBYLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSBQVRRELQKPDSFHSLTPTPAGVLVHIDNL RWEGYPFILMSGKALDKRVGYARILFKNQACCVQSEKHMAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYVAYSPVRERDAHSVLLSHIFHSRKNPFITTENL LASWNPWTPLLBSLAHKAPRLYPGGAENGRLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSBELISKL ANDIERTAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPN AHTHLWLVDERCVPLSDPRSNFQGLQAHLLQHVRIPYYNIH\AM
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPRQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYBDIARNINSSCRPGPGAWLRVV LEKPFGHDHPSAQQLATELGTFFQBBEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDABGRTSFYEBYGV IRDVLQNHLTBVLITLVAMELPHNVSSAEAVLRHKLQVPQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTPAGVLVHIDNL RWEGYPFILMSGKALDKRVGYARILFKNQACCVQSEKHMAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIPHGRKNPPITTENL LASWNFWTPLLBSLAHKAPRLYPGGARMGRLLDFFPSSGRLFFS QQQPBQLVPGPGPGPMPSDFQVLYRAKYRESSLVSAWSEBLISKL ANDIBATAVRAVRFGQPHLALSGGSSPVALFQQLATAHYGFPW AHTHLWIVDERCVPLSDPRSNFQGIQAHLLQHVRIPYYNH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPRQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTARDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYBDIARNINSSCRPGPGAWLRVV LEKPFGHDHPSAQQLATELGTFFQBBEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDABGRTSFYEEYGV IRDVLQNHLTBVLITLVAMBLPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDKRVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKKMBGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIPHGRKNPPITTENL LASWNFWTPLLBSLAHKAPRLYPGGAENGRLLDFEPSSGRLPFS QQQPBQLVPGPGPPMPGDFQVLRAKYRESSLVSAWSEBLISKL ANDIEATAVRAVRRFGQPHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPRSNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRNSLSLPILINRAKKV
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNI.IVAMCLA\LLGLPGKAQELQGHVS\IILAGEQI.GDLAKK YLWQG\LFQLYLDEAGRGRSFSFHGAALTAPRQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFCHDHYSAQQLATELGTFFQBEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFPITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEPSSGRLFFS QQQPEQLVPGPGPGPMPGDFQVLRAKYRESSLVSAWSBELISKL ANDIEATAVRAVRFFGGFHLALSGGSSPVALFQQLATAHYGFPN AHTHLWLVDERCVPLSDPRSNFQGIQAHLLQHVRIPYYNIH\AM PVHLQQRLCABEDQGAHTYAREISALGANSSFDLVLLGMGAGH TASLFPQSPTGLDGEQLVVITTSPSQPHRRNSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKAQBLQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALMKDIEAQ LQHAGLREAGGIPYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHPSAQQLATELGTFFQBBEMYRVDHYLGKQAVAQIL PFRDQMRKALDGLWNRHHVERVEIINKETVDABGRTSFYEEYGV IRDVLQNHLTBVLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL OGGSAVVGQYQSYSEQVRRELQKPDSFHSLTTTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKRMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIPHGRKNFPITTENL LASWNPWTPLLBSLAHKAPRLYPGGAENGRLLDFEPSSGRLFPFS QQOPBQLVPGPGPGPMPGDFQVLRAKYRESSLVSAWSEBLISKL ANDIBATAVRAVRRFGQPHLALSGGSSPVALFQQLATAHYGFPW AHTHLWIVDERCVPLSDPSSNFQGLQAHLLGWVRIPYYNTH\AM PVHLQQRLCABEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLWMGRMKREITTLVSRVGHEPKKWPISGVLPHSQQLVWYMDY DAFLG
6137	141 4587	934	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKAQBLQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPRQGQELMAKALES LSCPRDMAPSHCAEHKDQPLQLSQYRQLKTARDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYBDIARNINSSCRPGPGAMLRVV LEKPFGHDHPSAQQLATELGTFFQBBEMYRVDHYLGKQAVAQIL PFRDQMRKALDGLMNRHHVBRVBIIMKBTVDABGRTSFYBEYGV IRDVLQNHLTBVLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSBQVRRELQKPDSFHSLTPTPAGVLVHIDDL RWEGYPFILMSGKALDBRWGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYVAYSPVRERDAHSVLLSHIPHSRKNPFITTENL LASWNPWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPBQLVPGPGPGPMPSDFQVLRAKYRBSSLVSAWSBELISKL ANDIBATAVRAVRRFGQPHLALSGGSSPVALFQQLATAHYGFPN AHTHLWLVDERCVPLSDPSNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCABEDQGAHIVAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRNSLSLPI.INRAKV AVLVMGRMKREITTLVSRVGHRPKKWPISGVLPHSQLVWYMDY DAFIG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHPSAQQLATELGTFFQBEEMYRVDHYLGKQAVAQIL PFRDQNKKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLITLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGYPFILMSGKALDBRVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIPHGRKNPPITTENL LASNNFWTPLLESLAHKAPRLYPGGRENGRLLDFEPSGRLFFS QQQPEQLVPGPGPGPMPBGPQVLRAKYRESSLVSAWSBELISKL ANDIERTAVRAVRRFGQPHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPRSNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPGSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSQLVWYMDY DAFIG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPRQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYBDIARNINSSCRPGPGAWLRVV LEKPFGHDHPSAQQLATELGTFFQBEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTBVLITLVAMELPHNVSSAEAVLRHKLQVPQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTPAGVLVHIDNL RWEGYPFILMSGKALDKRVGYARILFKNQACCVQSEKHMAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHLFHGRKNPPITTENL LASWNFWTPLLESLAHKAPRLYPGGARMGRLLDFFFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLARKYRESSLVSAWSEELISKL ANDIEATAVRAVRFFQPHLALSGGSSPVALFQQLATAHYGFPW AHTHLWIVDERCYPLSDPRSNFQGIQAHLLQHVRIPYYNTH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLWGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGISFSPHGAALTAPRQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYBDIARNINSSCRPGPGAWLRVV LEKPFGHDHPSAQQLATELGTFFQBEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTBULTLVAMBLPHNVSSAEAVLRHKLQVPQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVPHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMBGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIPHGRKNPPITTENL LASWNFWTPLLBSLAHKAPRLYPGGAENGRLLDFEPSSGRLPFS QQDEQLVPGPGPGPMPGDFQVLAKYRESSLVSAWSEBLISKL ANDIEATAVRAVRRPGQPHLALSGGSSPVALFQQLATAHYGFPW AHTHLWIVDERCYPLSDPRSNFQGLQAHLLQHVRIPYYNH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSPDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRNSLSLPI.INRAKKV AVLWGRMKREITTLVSRVGHEPKWPISGVLPHSQQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLHELKNKEIHFQRRRTCAL TLRAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKAQBLQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALMKDIEAQ LQHAGLREAGGIPYFSVPPFAYEDIARNINSSCRPGPGAMLRVV LEKPFGHDHPSAQQLATELGTFPQBBEMYRVDHYLGKQAVAQIL PFRDQMRKALDGLWNRHHVERVEIIMKETVDABGRTSFYEEYGV IRDVLQNHLTEVLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL ORGSAVVGQYQSYSEQVRRELQKPDSFHSLTTTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVPHIGHGDLGSPAVLVSRNLFRPSLPSSWKRMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIPHGRKNFPITTENL LASWNPWTPLLESLAHKAPRLYPGGAENGRLLDFEPSSGRLPFS QQQPBQLVPGPEGPGPMPBDFQVLRAKYRESSLVSAWSEBLISKL ANDIBATAVRAVRRFGQPHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPRSNFQGLQAHLLGHVRIPYYNTH\AM PVHLQORLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLWGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLHHELKNKEIHFQRRRTTCAL TLRAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPBLHEDLHNEK ELIKELEQSLASWTONLKELQTMKADLTRHVLVEDVWVLKEQIE
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKAQBLQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPRQGQELMAKALES LSCPRDMAPSHCAEHKDQPLQLSQYRQLKTARDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYBDIARNINSSCRPGPGAMLRVV LEKPFGHDHPSAQQLATELGTFFQBEEMYRVDHYLGKQAVAQIL PFRDQMRKALDGLMNRHHVBRVBIIMKBTVDABGRTSFYBEYGV IRDVLQNHLTBVLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSBQVRRELQKPDSFHSLTPTPAGVLVHIDDL RWEGYPFILMSGKALDBRWGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYVAYSPVRERDAHSVLLSHIPHSRKNFPTTTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFBYSSGRLFFS QQQPBQLVPGPGPGPMPSDFQVLRAKYRBSSLVSAWSBELISKL ANDIBATAVRAVRFFGQFHLALSGGSSPVALFQQLATAHYGFPN AHTHLWLVDERCVPLSDPSSNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCABEDQGAHIVAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRKSLSLPI.INRAKKV AVLVMGRMKREITTLVSRVGHBPKKWPISGVLPHSGQLVWYMDY DAFIG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTKSLHELKNKEIHFQRRRTTCAL TLRAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVIKAQSEDPLPELHBDLHNEK ELIKBLBQSLASWTONLKELQTMKADLTRRULVEDVWVIKEQIE ELHRQWEDLCLRVAIRKQBIEDRLNTWVVFNEKNKELCAWLVQM
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKAQBLQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYILDEAGRGHSFSPHGAALTAPRQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYBDIARNINSSCRPGPGAWLRVV LEKPFGHDHPSAQQLATELGTFFQBBEMYRVDHYLGKQAVAQIL PFRDQMRKALDGLMNRHHVBRVEIIMKBTVDABGRTSFYBEYGV IRDVLQNHLTBYLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSBQVRRELQKPDSFHSLTPTPAGVLVHIDNL RWEGYPFILMSGKALDBRWGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYVAYSPVRERDAHSVLLSHIFHGRKNFPTTTENL LASNNFWTPLLESLAHKAPRLYPGGAENGRLLDFEYSGRLPFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRBSSLVSAWSBELISKL ANDIBATAVRAVRRFGQPHLALSGGSSPVALPQQLATAHYGFPN AHTHLWLVDERCVPLSDPBSNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCABEDQGAHTYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRNSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHBPKKWPISGVLPHSQLVWYMDY DAFIG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLRAGEKILLTTDLKTKESVGRRISGLQDSWDMBPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPBLHEDLHNEK ELIKELBQSLASWTONLKELQTMKADLTRHVLVEDVWMULKEQIE HLHRQWEDLCLRVAIRKQERBERLQXMCMBEBINLFSENKLQLKQMGDQL
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPRQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYBDIARNINSSCRPGPGAWLRVV LEKPFGHDHPSAQQLATELGTFFQBEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTBVLTIJVAMELPHNVSSAEAVLRHKLQVPQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTPAGVLVHIDNL RWEGYPFILMSGKALDBRVGYARILFKNQACCVQSEKHMAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIPHGRKNPPITTENL LASMNFWTPLLESLAHKAPRLYPGGRENGRLLDFFPSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQPHLALSGGSSPVALFQQLATAHYGFPW AHTHLWILVDERCVPLSDPESNFQGIQAHLLQHVRIPYYNH\AM PVHLQQRLCABEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRMSLSLPLINRAKKV AVLWGRMKREITTLVSRVGHEPKKWPISGVLPHSQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCKKKI KELKSRLQVLKAQSEDPLPBLHEDLHNEK ELIKELEQSLASWTONLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIBDRLNTWVYFNEKNKELCAWLVQM RNKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQRGMGDQL IKASNKSRAABIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPRQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYBDIARNINSSCRPGPGAWLRVV LEKPFGHDHPSAQQLATELGTFFQBEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTBVLITLVAMELPHNVSSAEAVLRHKLQVPQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTPAGVLVHIDNL RWEGYPFILMSGKALDKRVGYARILFKNQACCVQSEKHMAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIPHGRKNPPITTENL LASWNFWTPLLESLAHKAPRLYPGGRENGRLLDFFPSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRFFQPHLALSGGSSPVALFQQLATAHYGFPW AHTHLWIVDERCYPLSDPRSNFQGIQAHLLQHVRIPYYNHINAM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRNSLSLPLINRAKKV AVLWGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ PQSTVETWDQCEKKIKELSRLQVLKAQSEDPLPBLHEDLHNEK ELIKELBQSLASWTONLKELQTMKADLTRHVLVEDVWVLKEQIE HLHRQWEDLCLRVAIRKQRIEDRLNTWVVFNEKNKELCAWLVQM KNKVLQTADISIEEMIEKLQKDCMBEINLFSRNKLQLKQMGDQL IKASNKSRAAEIDDKLNKLNDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQRRLAEQQD
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKAQBLQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPRQGQELMAKALES LSCPRDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYEDIARNINSSCRPGPGAMLRVV LEKPFGHDHPSAQQLATELGTFPQBEEMYRVDHYLGKQAVAQIL PFRDQMRKALDGLWNRHHVERVEIINKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL ORGSAVVGQYQSYSEQVRRELQKPDSFHSLTTTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVPHIGHGDLGSPAVLVSRNLFRPSLPSSWKRMESPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIPHGRKNFPITTENL LASWNPWTPLLESLAHKAPRLYPGGAENGRLLDFEPSSGRLPFS QQQPBQLVPGPGPGPMPBDFQVLRAKYRESSLVSAWSEBLISKL ANDIEATAVRAVRRFGQPHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPRSNFQGLQAHLLGHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLWGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTTRSLHHELKNKEIHFQRRRTTCAL TLRAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCCKKIKELKSRLQVLKAQSEDPLPBLHEDLHNEK ELIKELEGSLASWTONLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQRIEDELNTWVVFMKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRABIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARISESELSKPVVYDVCODQEIQRRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKAQBLQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHPSAQQLATELGTFFQBEEMYRVDHYLGKQAVAQIL PFRDQMRKALDGLWNRHHVERVEIIMKETVDABGRTSFYEEYGV IRDVLQNHLTEVLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLWHIDNL RWGGYPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIPKSRKNFFTTTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPBQLVPGPGFGPMPGDFQVLRAKYRESSLVSAWSEBLISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALPQQLATAHYGFPN AHTHLWLVDERCVPLSDPRSNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEBDQGAHIYAREISALGANSSFDLVLLGMCADGH TASLFPQSFTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLWGRMKREITTLVSRVGHEPKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTKSLHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPBLHBDLHINEK ELIKELBQSLASWTONLKELQTMKADLTRHVLVEDVWYLKRQIE HLHRQWEDLCLRVAIRKQBIEDRLNTWVVFNEKNKELCAWLVQM RNKVLQTADISIEEMIEKLQKDCMBEINLFSENKLQLKQMGDQL IKASNKSPAABIDDKLNKINDRWQHLFDVIGSRVKKLETFAFI QQLDKNMSNLRTWLAR IESELSKPVVYDVCDDQEIQRRLAEQQD LQRDIEQHSAGVESVFNICDVILHHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWOKFLDDYSRFBDWLKSAB
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNNILIVAMCLA\LLGLPGKAQBLQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSPHGAALTAPRQGQELMAKALES LSCPRDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIPYFSVPPFAYEDIARNINSSCRPGPGAMLRVV LEKPFGHDHPSAQQLATELGTFPQBEEMYRVDHYLGKQAVAQIL PFRDQMRKALDGLWNRHHVERVEIINKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL ORGSAVVGQYQSYSEQVRRELQKPDSFHSLTTTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVPHIGHGDLGSPAVLVSRNLFRPSLPSSWKRMESPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIPHGRKNFPITTENL LASWNPWTPLLESLAHKAPRLYPGGAENGRLLDFEPSSGRLPFS QQQPBQLVPGPGPGPMPBDFQVLRAKYRESSLVSAWSEBLISKL ANDIEATAVRAVRRFGQPHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPRSNFQGLQAHLLGHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLWGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTTRSLHHELKNKEIHFQRRRTTCAL TLRAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCCKKIKELKSRLQVLKAQSEDPLPBLHEDLHNEK ELIKELEGSLASWTONLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQRIEDELNTWVVFMKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRABIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARISESELSKPVVYDVCODQEIQRRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			NOREBFEGTRESILVWLTBMDLQLTNVEHFSESDADDKMRQLNG
		•	FQQEITLNTNKIDQLIVFGEQLIQKSEP\LDAVLIEDELEELHR
			YCOEVFGRVSRFHRRLTSCTPGLEDEKEASENETDMEDPREIQT
			DSWRKRGESEEPSSPQSLCHLVAPGHERSGCETPVSVDS\IPLB
	ł		WDHTGRRGGPSSSH\EEDBEAQYY\SALSGKSISDGHSWHVPDS
	ł		PSCPEHHYKOMEGDRNVPPVPPASSTPYKPPYGKLLLPPGTDGG
	1		KEGPRVLNGNPQQEDGGLAGITEQQSGAFDRWEMIQAQEL\HNK
		]	LKIKQNLQQLNSDISAITTWLKKTRABLEMLKMAKPPSDIQBIB
			LRVKRLQEILKAFDTYKALVVSVNVSSKEFLQTESPESTELQSR
	ì	1	LRQLSLLWEAAQGAVDSWRGGLRQSLMQCQDFHQLSQNLLLWLA
	1		SAKNRRQKAHVTDPKADPRALLECRRELMQLEKELVERQPQVDM
1	Ì		LQEISNSLLIKGHGEDCIEABEKVHVI\EKKLKQLREQVSQDLM
ļ ·		•	ALQGTQNPASPLPSFDEVDSGDQPPATSVPAPRAKQFRAVRTTE
1			GEEETESRYPGSTRPQRSFLSRVVRAALPLQLLLLLLLLLACLL
i		<u> </u>	PSSKEDYSCTQANNF\ARSFYPMLRYTNGPPPT
6139	52	1131	LGDWVWSRTCGVLETPTSVLRRARARGPCPTDSKWALPRLREGE
1	Ì	1	TERRPWHASSWKTL/LAGWIGGAASVIVGHPLDIVKTRLQAGVG YGNTLSCIRVVYRRESMFGFFKCMSFPLASIAVYNSVVFGVFSN
1		į	TORFLSQHRCGRPEASPPRTLSDLLLASMVAGVVSVGLGGPVDL
1			IKIRLQMQTPPVSGRQPRFEVQGSGSCG\BPAYQGPVHCITTIV
		1	RNEGLAGLYRGASAMLLRDVPGYCLYPIPYVFLSEWITPEACTG
	İ		PSPCAVWLAGGMAGAISWGTATPMDVVKSRLQADGVYLNKYKGV
			LDCISQSYQKEGLKVFFRGITVNAVRGFPMSAAMFLGYELSLQA
	}	į.	IRGDHAVTSP
		136	RPELELWRLRSRSWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP
6140	694	136	RCQRP/QPPAPEPSSPNAAVPEAIPTPRAAASAALBLPLGPAPV
İ			SVAPQAEAEARSTPGPAGSRLGPETFRQRFRQFRYQDAAGPREA
			FRQLREL/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR
]			ARRIBRATOVRITG
6141	2	984	AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS
9141		}	ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFEIS
l			PSEILYCTINTPKIDMERLIGGQLGLEDFIFAHVKGIEKEVNVY
		1	KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI
ļ	1		NGENIVGWRHYDVAKKLKELKKEBLFTMKLIBPKKAFEIELRSK
1			AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD
1		1	VLELYMGIRDIDLATIMFEAGKDKVNPDEFAVALDETLGDFAFP
Ì		j	DEFVFDVWGVIGDAKRRGL
6142	116	602	BARGROVCGAKCCGDAPHVENREEBTARIGPGVMESKEERALNN
]		1	LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR
			FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMBKL
1		1	REKQLSHSLRAVSTDPPHHDHHDEFC\LMP
6143	2802	270	FRMRIPLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q
	1		\QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED
		1	LLINEWEASKCNIVCTOPRRISAVSLANKVCDBLGCENGPGGRN
1	1		SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM
1			FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLIIMSATVDSE
1			KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC
1	1	1	QKFLEERERYTINVTSKAGGIKKYQRYIPVQTGAHADLNPFYQK
1		}	YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIBGAVLI
1	1	ĺ	FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF
I	1		TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS
1	i	ł	QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD
	1	ſ	YSVPRILRVPLEBLCLHIMKCNLGSPEDFLSKALDPPQLQVISN
	1	1	AMNILRKIGACBLNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF
		1	GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL
		1	TIYNAYLGWKKARQEGGYRSBITYCRRNYLNRTSLLTLEDVKQB
L			

		• • •	· -
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
'	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		amino acid	P=Proline, Q=Glutamine, R=Arginine,
	to first		S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	W=Tryptopnan, ralyrosine, Asonthown,Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\-possible nucleotide insertion)
			LIKLVKAAGPSSSTTSTSWEGNRASQTLSFQEIALLKAVLVAGL
	Į.	1	YDNVGKIIYTKSVDVTBKLACIVETAQGKAQVHPSSVNRDLQTH
	ì	1	GNLLYQEKIRYARVYLRETTLITPFPVLLFGGDIEVQHRERLLS
		1	IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENDKI
	· ·		
			LOIITELIKTENN
6144	1289	568	SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPYQN
	i.	1	VSASGGARHGGRGSGGPVICTYGPDLFPLVA\TIGAAFVAKVMS
	1	1	VGDRTVTLGINDTAGSERYEAMSRIYYRGAKAAIVCYDLTDSSS
		1	FERAKFWVKELRSLEBGCQIYLCGTKSDLLBEDRRRRRVDFHDV
	•		QDYADNIKAQLFETSSKTGQSVDELFQKVARDYVSVAAFQVMTB
	1	1	DKGVDLGOKPNPYFYSCCHH
			GGMDLSBLERDNTGRCRLSSPVPAVCRKRPCVLGVDRAGRGPVL
6145	1109	196	GGMDP2RPRMMLGKCKT225AAbAACKWZhCATGADFWGRGBAT
			GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKMEDT
	1		DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYALD
			QGVNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALYPV
			\VSAASICAKVARDOAVKKWOFVEKLQDLDTDYG\SGYPNDPQD
	l	1	/TKAWLKEHVEPVF\GFP\QFVRF\SWRTAQTI\LEKEAEDVIR
	1	1	EDSASENQEGLRKITSYFLNEGSQARPRSSHRYFLERGLESTTS
	į –	ĺ	L
	<u> </u>		LKKKGKEKARAQQVEALPGPSLDQWHRSAGEEEDGPVLTDEQKS
6146	428	781	LKKKGKKAKAQQVEALPGPSILQWIKGAGEEEDGFVII DISUKS
	l .	1	R/YPGHEAHDQGG\WDARQSIIRKVVDPETGRTRLIKGDGEVLE
•	1	1	BIVTKERHRBINKQATRGDCLAFQMRAGLLP
6147	1	2304	GTROLPPPSPGSGPGDSPEGPRGEAPERREKAHGMLKLYYGLSE
	_	1	GEAAGRPAGPDPLDPTDLNGAHFDPEVYLDKLRRECPLAQLMDS
	1	1	RTDMVRQIRALDSDMQTLVYENYNKFISATDTIRKMKNDFRKMB
	İ		DEMORLATNMAVITOFSARISATIOORHERITKLAGVHALLRKL
	1	1	QFLFELPSRLTKCVELGAYGQAVRYQGRAQAVLQQYQHLPSFRA
	) .	1	IQDDCQVITARLAQQLRQRFREGGSGAPEQABCVELLLALGEPA
	i .	i	EKLCKEPLAHARGRLEKELRNLEAELGPSPPAPDVLEFTDHG\S
		1	KKPCKKATAHAKOKURURURURURURURURURURURURURURURURURURU
	1	1	SGFVGGLCQVAAAYQELFAAQGPAGAEKLAAFARQLGSRYFALV
	•	1	ERRLAGEGGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT
	1	1	EIVERVARERIGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGP
	1		GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF
	1		CSOGVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLLLS
	1	[	RLCLDYETATISYILTLTDBQFLVQDQFPVTFVSTLCARARETA
	I		RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLBPRNVRAVMKRV
	1	I	VEDITAIDVQVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG
	1	1	GGDMCIWASHGASSVARASVREPQGNKSPRMNTKRAGECLCPRS
	1	}	COLUMN TO THE PURE OF THE PURE OF THE STREET
	Ī	1	CSFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS
			CILPLPHSTGSINSDHVPTK
6148	3056	353	VPAVGGTFADGAMGEABKFHYIYSCDLDINVQLKIGSLEGKREQ
	1		KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT
			SYKAPSTRWNWNEWLKLPVKYPDLPRNAQVALTIMDVYGPGKAV
			PVGGTTVSLFGKYGMFRQGMHDLKVWPMCRSQMDQKPTKTPGRT
			SSTLSEDOMSRLAKLTKAHROGHMVKVDWLDRLTFREIEMINES
			THE CONTRACT THE PROPERTY OF T
1		1	VKRSSNFMYLMGGFRCVKCDDKEYGIVYYBKDGDBSSPILTSFB
1	I		LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ
1	1	1	LKNIVSYPPSKPPTYREQDLVWEFRYYLTNQDKALTKILTSVIW
			DLPOGAKOALALLGKWKPMDVEDSLBLLSSHYTNPTVRRYAVAR
1			LRQADDEDLIMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS
	1		ENVSNSGINSARIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG
	Ī	ļ	PUANUSCHISCHEL ZONG CHANGE STATE AND
i		1	ENLEODLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK
ŀ			THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM
	1	1	KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLBPQVK
l	1	•	KMACKED GINKKKKINITERITE STATES TO THE STATES OF THE STATE
			IRGIIPRTATI,FKSALMPAOLFFKTEDGGKYPVIFKHGDDLRQD
			IRGIIPBETATIFKSALMPAQLFFKTEDGGKYPVIFKHGDDLRQD QLILQIISLMDKLLRKENIDLKLTPYKVLATSTKHGFMQFIQSV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			PVAEVLDTEGSIONFFRKYAPSENGPNGISAEVMDTYVKSCAGY
ţ			CVITYILGVGDRHLDNLLLTKTGKLFHIDFGYILGRDPKPLPPP
ı		į	MKLNKEMVEGMGGTQSEQYQEFRKQCYTAFLHLRRYSNLILNLF
1			SLMVDANIPDIALEPDKTVKKVQDKFRLDLSDEBAVHYMQSLID
			ESVHALFAAVVEQIHKFAQYWRK
6149	1	1413	RVDPRVRENGTANPI KNGKTSPASKDQRTGKKTSVQGQVQKGND
i		1	BSESDFBSDPPSPKSSBBBEQDDEEVLQGEQGDFNDDDTEPENL
Į	, ·		GHRPLLMDSEDEEEEEKHSSDSDYEQAKAKYSDMSSVYRDRSGS
1	}	İ	GPTQDINTILLTSAQLSSDVAVETPKQEFDVFGAVPFFAVRAQQ
1	1		POQEKNEKNLPOHRFPAAGLEQEEFDVFTKAPFSKKVNVQECHA
1		1	VGPEAHTIPGYPKSVDVFGSTPFQPFLTSTSKSESNEDLFGLVP
	1		FDEITGSQQQKVKQRSLQKLSSRQRRTKQDMSKSNGKRHHGTPT STKKTLKPTYRTPERARRHKKVGRRDSOSSNEFLTISDSKENIS
1	1	}	VALTDCKDRCNVLOPEESLLDPFGAKPFHSPD\LSWHPP\HOGL
1	:		s\diradhnt\vlpgr\pronslhgsphsadvlkmodfgavp/f
1			LTELVVQSITPHQSQQSQPV\BLDPFGAAPFPSKQ
6150	372	37	MSNIKKYIIDYDWKASIEIEIDHDVMTEEKLHQINNFWSDSEYR
0250	}	]	LNKHGSVLNAVLIMLAQHALLIAISSDLNAYGVVCEFDWNDGNG
	ł		QEGWPPMDGSEGIRITDIDTSGIF
6151	1555	521	DSNQQSVSGTAASTLLHSFKATIYYQGTGHVQQFYGVTSPYSQT
1			TPPIVQSYAQPSLQYIQGQQIFTAHPQGVVVQPAAAVTTIVAPG
	1		QPQPLQPSEMVVTNNLLDLPPPSPPKPKTIVLPPNWKTARDPEG
1	l ·	,	KIYYYHVITRQTQWDPPTWESPGDDASLRHEAEMDLGTPTYDEN
1	[	. *	PMK\ASKKPKTAEADTSSELAKKSKEVFRKEMSQFIVQCLNPYR
1 .			KPDCKVG\RITTTEDFKHLARKLTHGVMNKELKYCKNPE\DLBC
	<b>{</b>	*	NENVKHKTKEY I KKYMQKFGAVYKPKEDTEFRVTVGPGWEDGWS
L			GKTDSRERKSCGPFCSTPVSTVLLMIHHPGEFNPADVN
6152	1366	648	NRTWSTPSTWMGVALPPLCSTGPWPVTRQITARTTCGAVPAKCP
			PWC/DVHEPRCQPPDCHGHGTCVDGHCQCTGHFWRGPGCDELDC
i			GPSNCSQHGLCTRTGCRCDAGWTGSNCSRECPLGWHGPGCQRPC
ł	{		KCKHHCPCDPKTGNCSVSRVKQCLQPPEATLRAGELSFFTRTAW LALTLALAFLLLISTAANLSLLLSRAERNRRLHGDYAYHPLQEM
·	Ī		NGEPLAARKEQPGGAHNPFKD
6153	2	3368	GRVGARSPGRAYALLLLLI CFNVGSGLHLQVLSTRNENKLLPKH
"		2300	PHLVRQKRAWITAPVALLEGEDLSKKNPIAKIHSDLAEERGLKI
1	ł		TYKYTGKGITEPPFGIFVFNKDIGELNVTSILDREETPFFLLTG
1			YALDARGNNVKKPLELRIKVLDINDNEPVFTQDVFVGSVERLSA
1			AHTLVMKINATDADEPNTLNSKISYRIVSLEPAYPPVFYLNKDT
}			GEIYTTSVTLDREEHSSYTLTVEARDGNGBVTDKPVKQAQVQIR
Ì			ILDVNDNIPVVENKVLEGMVBENQVNVEVTRIKVFDADBIGSDN
1			wlanftpasgneggyfhietdaqtnegivtlikevdyremknld
[	ľ		FSVIVANKAAPHKSIRSKYKPTPIPIKVKVKNVKEGIHFKSSVI
			SIYVSESMDRSSKGQIIGNFQAFDEDTGLPAHARYVKLEDRDNW
1			ISVDSVTSBIKLAKLPDFESRYVQNGTYTVKIVAISKDYPRKTI
}			TGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLDGHPN
[			SGPFSFSVIDKPPGMAEKNKIARQESTSVLLQQSEKKLGRSBIQ
}			FLISDNQGFSCPRKQVLTLTVCEVLHGS\GCREAQHDSYVGLGP
1			AAIALMILAPLLLLLVPLLLLMCHCGKGAKGFTPIPGTIEMLHP
			WNNEGAPPEDKVVPSPLPVDQGGSLVGRNGVGGMAKEATMKGSS
			SASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAI\MTTE
1	]		TTITARATGASRDVAGAQAAAVALNBEFLKNYFTDKAASYTERD
			ENHTAKDCLLVYSQERTESLNASIGCCSFIEGELDDRFLDDLGL
			KFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTM VNSENTYSSGSSFPVPKSLOEANAEKVTOEIVTERSVSSRQAQK
1			VNSENTISSGSSPPVPKSLQEANAEKVTQEIVTEKSVSSKQAQK VATPLPDPMASRNVIATETSYVTGSTMPPTTVILGPSQPQSLIV
	i		TERVYAPASTLVDQPYANEGTVVVTERVIQPHGGGSNPLEGTQH
L			TEMATURES THANKS TAMBERT ANA TEMATKE UCACOUSTS TREATING

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, P=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\-possible nucleotide insertion)
		1	LQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
			APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGH
			SNSTITTSSTRVTKHSTVQHSYS
6154	3660	2146	KKKTKMKNTLQKTVNPGANPKPTISDKSHLLQMVSKLDLTDAKN
	ļ		SDTAHIKSIBITSILNGLQASBSSAEDSBQBDERGAQDMDNNGK
		1	EESKIDHLTNNRNDLISKEEQNSSSLLEENKVHADLVISKPVSK
			SPERLEKDIEVISEDTDYEEDEVTKKEKDVKKDTTDKSSKPQIK
			RGKRRYCNTRECLKTGSPGKKEBKAKNKESLCMENSSNSSSDED
			EBBTKAKMTPTKKYNGLEEKRKSLRTTGFYSGFSEVABKRIKLL
			NNSDERLONSRAKDRKDVWSSIQGQWPKKTLKELFSDSDTEAAA
			SPPHPAPERGVARESLQTVAREESCSPSVELEKPPPVNVDSKPI
			ERKTVEVNDRKABFPSSGSNFSA+IPLPYLHLNRLHQSL+QKGS
	j		RQQSSVTVSEPLAPNQBEVRSIKSETDSTIEVDSVAGELQDLQS
	1		ERE*LASRP*CQCELEQ**SARTRTS*KSLYRSEKSERCSGRRK
			FIKKABKKP*SNSGKQQKEGK
6155	869	121	HLLPELRGKSWITMKYVFYLGVLAGTFFFADSSVQKBDPAPYLV
			YLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRVRDG
			TEQTINPIQIVRYWNYSHSAPQDDIMLIKLAKPAMLNPKVQALN
	ļ		P\PTTNVRPGTVCLLSGLDWSQENSGRHPDLRQNLEAPVMSDRE
	f		CQKTBQGKSHRNSLCVKFVKVFSRIFGBVAVATVICKDKLQGIE VGHFMGGDVGIYTNVYKYVSWIENTAKDK
			GTSTVTMATKKHFSIILNLLGMLLKKDNQDTRKLLMTWALEVAV
6156	5725	3984	VMKKSETYAPLFCLPSFHKFCKGLLADTLVEDVNICLQACSSLH
	Ì		ALSSSLPDDLLORCVDVCRVQLVHRGTCIRQAFGKLLKSIPLGV
	,		FLSNNNHTEIQEISLALRSHMSKAPSNTFHPQDFSD/VISFILY
٠.,	ł		GNSHRTGKDKWLERLFYSCQRLDKRDQSTIPRNLLKTDAVLWQW
	l	1	AIWEAAQFTVLSKLRTPLGRAQDTFQTIEGIIRSLAGHTLNPDQ
	1	1	DVSQWTTADXDEGHGNNQLRLVLLLQYLENLEKLMYNAYEGCAN
	j	İ	ALTSPPKVIRTFLYTNROTCODWLTRIRLSIMRVGLLAGOPAVT
	} .	ļ	VRHGFDLLTEMKTTSLSQGNELEVSIMMVVEALCELHCPEAIQG
			IAVWSSSIVGKHLLWINSVAQQAEGRFEKASVEYQEHLCAMTGV
	1	l	DCCISSPDKSVLTLASAGCKSASLKHCLNGESRKSVLSKPTDSS
	İ		PEVINYLGNKACECYISTADWAAVQEWQNAIHDLKKSTSSTSLN
			LKADPNYIKSLSSFESGKFVECTEQLELLPGENINLLAGGSKEK
	1		IDMKKILIRNM
6157	946	329	MANRGPSYGLSREVQEKIEQKYDADLENKLVDWIILQCAEDIBH
6157	346	349	PPPGRAHFOKWIMDGTVICKLINSLYPPGQEPIPKISESKMAFK
	ľ		OMEQISQFLKAAETYGVRTTDIFQTVDLWEGKDMAAVQRTLMAL
		<b>\</b>	GSVAVTKDDGCYRGBPSWFHRKAQQNRRGFSEBQLRQGQNVIGL
	[		OMGSNKGASQAGMTGYGMPRQIM*DAASCP
6158	441	1482	LGSLIVLSLHCKVIFSSQSLERAMKEKAVDLVPILAQNPGLAQN
0700		1402	PILEGKOHNONTGVDPIIDHVQDRKTD/SRSKSPHKKRSKSRER
			RKSRSRSHSRDKRKDTRBKIKEKERVKEKDREKEREKEREKE
	l		KERGKNKDRDKEREKDREKDKEKDREREREKEHEKDRDKEKEKE
	1	l	QDKEKEREKDRSKEIDEKRKKDKKSRTPPRSYNASRRSRSSSRE
			RRRRRSRSSRSPRTSKTIKRKSSRSPSPRSRNKKDKKREKERD
	İ	1	HISERRERESTSMEKSSNDRDGKEKLEKNSTSLKEKEHNKEPD
	1		SSVSKEVDDKDAPRTEKNKIQHNGNCQLNEENLSTKTEAV
6150	l	ļ	
6159	53	84	AVIAPLHISLGDRARPYLKNTEKSSTTCSRRRNQSFPPVMSLTH
	1		RLHLCKYNGCAVSNVCRFWEGRPLPLMIVVPYTLPVSLPVGSCV
	1		IITGTPILTFVKDPQLEVNFYTGMDEDSDIAFQFRLHFGHPAIM
			NSCVFGINRYBEKCYYLPFEDGKPFELCIYVRHKEYKVMVNGQR
	1		IYNPAHRFPPASVKMLQVFRDISLTRVLISD*GRCVRITAVQEF
	l		DVSVSCDCTTAYQPG
6160	1626	1790	AGAKPFP*F*KVADAQPTESEKEIYNQVNVVLKDAEGILEDLQS
	1	1	YRGAGHEIREAIQHPADEKLQEKAWGAVVPLVGKLKKFYEFSQR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide location	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1		corresponding to first	H-Histidine, I-Isoleucine, K-Lysine, L-Leucine, M-Methionine, N-Asparagine,
}	corresponding to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	bequence	\=possible nucleotide insertion)
ļ	Bequence	<del> </del>	LRAALRGLIGALTSTPYSPTQHLEREQALAKQFABILHFTLRFD
ł			ELKMTNPAIONDFSYYRRTLSRMRINNVPAEGENEVNNELANRM
}			SLFYARATPMLKTLSDATTKFVSENKNLPTENTTDCLSTMASVC
	İ		RVMLETPEYRSRFTNEETVSFCLRVMVGVIILYDEVHPVGAFAK
			TSKIDMKGCIKVLKDQPPNSVEGLLNALRYTTKHLNDETTSKQI
ľ	Ĭ	1	ksmlq+qlltlvnkg
6161	455	1569	PVSGSESSLRRAWASILRLMLGPRVAVSILCEDGISH*LLEKH*
	1		KSHVLEPLSSLALERQCLALSLDWSTGKTGRAGDQPLKIISSDS
1			TGQLHLLMVNETRPRLQKVASWQAHQFEAWIAAFNYWHPRIVYS
	1	ļ	GGDDGLLRGWDTRVPGKFLFTSKRHTMGVCSIQSSPHREHILAT
1	1	1	GSYDEHILLWDTRNMKQPLADTPVQGGVWRIKWHPFHHHLLLAA
l			CNHSGFKILNCQKAMEERQEATVLTSHTLPDSLVYGADWSWLLF
			RSLQRAPSWSFPSNLGTKTADLKGASELPTPCHECREDNDGEGH
ļ.		Ì	ARPOSCMKPLTECHRKNGTWLQATAATTRDCGVNPBBADSAFSL
<u> </u>			LATCSFYDHALHLWEWEGN
6162	1	586	RTIHATGRAGASPMHRLIVWRLAEANKOHVRCOKCLEFGHWIYE
1	Į.		CTGKRKYLHRPSRTAKLKKALKEKENKLLLQQSIGETNVERKAK
			KKRSKSVTSSSSSSSSSSSSSSSSSSSESETSTSSSSEDSDTDESS
			SSSSSASSTTSSSSSDSDSDSSSSSKQ*HQHR*QL*R*TTKEE
	3,003	785	RKEIRLLHSYWTDGLKTIM RIRSTTEGCAVRLHPTONTGKARIMILLSVSLGRHWAPTYKPFL
6163	1081	/85	TPVVFVFFFPFFHRKE*VMOKNFMKSREDEWMEKINNLHVQRAD
ŀ			MNRLIMNYLVTEGFKEAAEKFRMESGIEPSVDLETLDERIKIRE
Ì			MILKGOIOEAIALINSLHPELLDTNRYLYFHLOQOHLIELIROR
			ETRAALEFAQTQLAEQGEESRECLTEMERTLALLAFDSPRESPF
ł	ł		GDLLHTMOROKVWSEVNOAVLDYENRESTPKLAKLLKLLLWAON
			ELDOKKVKYPKMTDLSKGVIEEPK
6164	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
			SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
i		ĺ	VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
	ļ	į	NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
			WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
			YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
			GYEPPLTNVFTMQWPLTLFATCLPNQTVLKIWDSVPFEGSEIIL
			RVSLAIWAKLGEQIECCETADEFYSTMGRLTQENLENDLLQSHE
1	}		LMQTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSVSGRHS
			KARDSDBENDPDDEDAVVNAVGCLGPFSGFLAPBLQKYQKQIKE PNEBQSLRSNNIAELSPGAINSCRSBYHAAFNSMMMBRMTTDIN
			ALKROYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN
			HILLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
· '		1	PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNKASKTNGLGAA
1			RAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
1			VOAKLGALELNORDAAABTELRVHPPCQRHCPEPPSAPBENKAT
		F	SKAPQGSNSKTPIPSPPPSVKPLRKSATARNLGLYGPTERTPTV
			HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQKYQRN
1			GGERFG
6165	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
			SCISRTAPRILCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
1	1		VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
Ì			NPDDDSMGIQIVKDLHRTGCSSYCGQBAEQDRVVLKRVLLAYAR
J	ļ		WNKTVGYCQGPNILAALILEVMEGNEGDALKIMIYLIDKVLPBS
1			YPVNNLRALSVDMAVPRDLLRMKLPELSQHLDTLQRTANKESGG
i			GYEPPLINVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
}			RVSLAIWAKLGEQIECCETADBFYSTMGRLTQEMLENDLLQSHB
1	Į	1	LMQTVYSMAPFPFFQLAELREKYTYNITPFPATVKPTSVSGRHS
l			KARDSDERNDPDDRDAVVNAVGCLGPFSGFLAPELQKYQKQIKB
	· · · · · · · · · · · · · · · · · · ·		<u> </u>

		• •	·
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
j	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bequence	\=possible nucleotide insertion)
ļ	sequence		
1	l	ĺ	PNEEQSLRSNNTAELSPGAINSCRSEYHAAFNSMMMERMTTDIN
I		1	ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN
}			HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYKDLKTKLNS
	i	ļ	PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKINGLGAA
ł		Ì	EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
	•	ľ	VQAKLGALBLNQRDAAAETELRVHPPCQRHCPEPPSAPEENKAT
	ŀ	•	SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
}	}	1	HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN
1	j		GGERFG
6166	2	1206	HKLWRTVAMAGAEWKSLEECLEKHLPLPDLQEVKRVLYGKELRK
1		1	LDLPREAFEAASREDFELQGYAFEAAEEQLRRPRIVHVGLVONR
1	i		IPLPANAPVAEQVSALHRRIKAIVEVAAMCGVNIICFORAWTMP
I	]	į	FAFCTREKLPWTEFABSAEDGPTTRFCOKLAKNHDMVVVSPILE
	1		RDSEHGDVLWNTAVVISNSGAVLGKTRKNHIPRVGDFNESTYYM
1	į	1	EGNIGHPVFQTQFGRIAVNICYGRHHPINWIMYSINGABIIFNP
1	Ĭ	l	SATIGALSESLWPIKARNAAIANHCFTCAINRVGTEHFPNEFTS
			GDGKKAHQDFGYFYGSSYVAAPDSSRTPGLSRSRDGLLVAKLDL
1			I
1			NLCQQVNDVWNFKWTGRYEMYARELAEAVKSNYSPTIVKE*PAS
	1000		VPALG
6167	1220	1844	YGIVTGPSLCAGDKQPKKQEKNPVLVSPEFVDEALCACEEYLSN
1			LAHMDIDKDLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTQ
1 .	'		VQRCEDILQQLQAVVPQIDMEGDRNIWIVKPGAKSRGRGIMCMD
1 .	<b>,</b>	}	HLEEMLKLVNGNPVVMKDGKWVVQKYIERPLLIFGTKFDLRQWF
		·	LVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDK*APLYLTPEGWS
ł	}		LFLQRYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDMEG
1			DRNIWIVKPGAKSRGRGIMCMDHLBEMLKLVNGNPVVMKDGKWV
			VQKYIERPLLIFGTKFDLRQWFLVTDWNPLTVWFYRDSYIRFST
1		ĺ	Obestknitok
6168	84	1392	VWPVPSVSAMPPKKQAQAGGSKKAEQKKKEKIIBDKTFGLKNKK
i			GAKQQKFIKAVTHQVKFGQQNPRQVAQSEABKKLKKDDKKKELQ
ł			ELNELPKPVVAAQKISKGADPKSVVCAFFKQGQCTKGDKCKFSH
			DLTLERKCEKRSVYIDARDEELEKDIMDNWDEKKLEEVVNKKHG
Ĭ			RABKKKPKTOIVCKHFLBAIENNKYGWFWVCPGGGDICMYRHAL
l			PPGFVLKKKKKKKKKRDBISL*DLIERERSALGPNVTKITLESF
1	ļ		LAWKKRKROBKIDKLEODMERRKADFKAGKALVISGREVFEFRP
1			ELVNDDDERADDTRYTOGTGGDEVDDSVSVNDIDLSLYIPRDVD
	j		ETGITVASLERFSTYTSDKDENKLSEASGGRAENGERSDLEEDN
			EREGTENGAIDAVPVDENLFTGEDLDBLREELNTLDLEE
6169	112	662	APAAAMAERPEDLNLPNAVITRIIKEALPDGVNISKEARSAISR
1 7107	***	002	AASVFVLYATSCANNFAMKGKRKTLNASDVLSAMEEMEFORFVT
I .			
			PLKEALEAYRREQKGKKEASEQKKKDKDKTDSEEQDKSRDEDN DEDEKRLEEERONEEEEVDN+KGRETVAPWKVPLEMRRATCFCK
			APPCWAB
6170	62	667	STKVMLPNTGRLAGCTVFITGASRGIGKAIALKAAKDGANIVIA
	•		AKTAQPHPKLIGTIYTAABBIEAVGGKALPCIVDVRDEQQISAA
1			VEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG
1	] .		TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWFKQHCGRW*VV
L			G*GDGLCLICFELNLCMSDVITICT
6171	382	941	HFMQSDVELDCDIBPCGHTKFPPTLPLSTTVIVCSCHPVATAST
			MAEAFSKTTSBEDQSIQEPKBANSMTAQKQKK*GLRGSRRRHAN
			SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD
1			RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESOGT
			NATLRYTKSK
6172	651	54	GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREBAQR
'-	224	J3	SAQERKERLERALEENRLIPTELEREALALQGSLEFDDAGGEGV
1			
L			TSHVDDEYRWAGVEDPKVMITTSRDPSSRLKMFAKELKLVFPGA

SEQ	Predicted	Predicted end	Amino agid compat ambalala desal ambala
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C-Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	sequence	\=possible nucleotide insertion)
<b> </b>	Jequence		QRMNRGRHEVGALVRACKANGVTDLLVVHEHRGTPVGLIVSHLP
ł	ŀ		
ļ			FGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRV
1	}		SDILRYLFPVPKDDSHRVITFANQDDYISFRHHVYKKTDHRNVB LTEVGPRFELKLYMIRLGTLEQEATADVEWRWHPYTNTARKRVF
1			•
6173	3	288	LSTE*AAPRPLGQLL
1 02/3	,	400 .	SVDHREVQVLSQSMPLTPHQAVLRGBRPYMCVECGKCPGRSSHL
I			LQHQRIHTGEKPYVCSVCGKAFSQSSVLSKHRTIHTGEKPYECN ECGKAFRVSSDLAQHHKIHTGEKPHECLECRKAFTQLSHLIQHQ
	İ		RIHTGERPYVCPLCGKAFNHSTVLRSHQRVHTGEKPHRCNECGK
	·		TFSVKRTLLQHQRIHTGEKPYTCSECGKAPSDRSVLIQHHNVHT GEKPYECSECGKTFSHRSTLMNHERIHTEBKPYACYECGKAFVQ
j .	ļ		HSHLIQHQKVHRKL*PTCVLSVGSALAGVPTSFSISVSTLERSP
1			MCAVYVGRPSARAQSLVNTGQPTQVRSPMSVMSVKKPLE
6174	1060	959	PRPPGKRWMVAGLGNPGLPGTRHSVGMAVLGQLARRLGVAESWT
1 02/7	1000	,,,,	RDRHCAADLALAPIGDAQLVLLRPRRLMNANGRSVARAAELFGL
•			TAREVYLVHDBLDKPLGRLALKLGGSARGHNGVRSCISCLNSNA
J ,			MPRLRVGIGRPAHPEAVQAHVIGCFSPARQELLPLLLDRATDLI
i .			LDHIRERSQGPSLGP*H*WFSKKA
6175	2204	334	RYPRADPRSRSGOPRAEGIGAFAEGPLRAMAAPVKGNRKOSTEG
		221	DALDPPASPKPAGKONGIONPISLEDSPEAGGEREEEOEREREO
Į i			AFLVSLYKFMKERHTPIERVPHLGFKQINLWKIYKAVEKLGAYE
1			LVTGRRLWKNVYNELGGSPGSTSGATCTRRHY*RLVLPYVRHLK
			GEDDKPLPTSKPRKQYKMAKENRGDDGATERPKKAKEERRMDQM
<b>f</b> 1			MPGKTKADAADPAPLPSQEPPRNSTEQQGLASGSSVSFVGASGC
			PEAYKRLLSSFYCKGTHGIMSPLAKKKLLAQVSKVEALQCQBEG
1			CRHGAEPQASPAVHLPESPQSPKGLTENSRHRLTPQEGLQAPGG
ļ			SLREEAQAGPCPAAPIFKGCFYTHPTEVLKPVSQHPRDFFSRLK
ĺ			DGVLLGPPGKEGLSVKEPQLVWGGDANRPSAFHKGGSRKGILYP
			KPKACNVSPMAKVPAESPTLPPTFPSSPGLGSKRSLERRGAAHS
			GKRLRAVSPFLKEADAKKCGAKPAGSGLVSULLGPALGPVPPEA
			YRGTMLHCPLNFTGTPGPLKGQAALPFSPLVIPAFPAHFLATAG
			PSPMAAGLMHFPPTSFDSALRHRLCPASSAWHAPPVTTYAAPHF
			FHLNTKL
6176	1040	402	PLSALRAMAEVHVIGQIIGASGFSESSLFCKWGIHTGAAWKLLS
			GVREGQTQVDTPQIGDMAYWSHPIDLHFATKGLQGWPRLHFQVW
			SQDSFGRCQLAGYGFCHVPSSPGTHQLACPTWRPLGSWREQLAR
			AFVGGGPQLLHGDTIYSGADRYRLHTAAGGTVHLBIGLLLRNFD
			RYGVEC*GTLPPTSPPSTPRTPSDGGGWHSGQKHRL
6177	1400	992	VPIESLVGKVHNFPLIAFYCCEKGKRQPHKSLHDRCFGEALDPN
		i	CSHCYLDQIKRSDFLGFSGYSPHFVAISTNSEHKMQPSSMQQAL
			PSQ*PYWTDPRPALVPCCSHRPDVHRSRPGPGLPGTSGCSDRPP
[ ]			VCPI
6178	1027	254	STORGGIKGVARAASLVGRRRAGTGMALLLCLVCLTAALAHGCL
			HCHSNFSKKFSFYRHHVNFKSWWVGDIPVSGALLTDWSDDTMKE
]	}		LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELR
			NIFREQVHLIQNAIIESRIDCQHRCGIFQYETISCNNCTDSHVA
1	•		CFGYNCESSAQWKSAVQGLLNYINNWHKQDTSMRPRSSAFSWPG
	ļ		THRAAPAPLVLPALRCLEPPHLANLSLEDAA+CLKQH
6179	806	276	RGETREMAGNLLSGAGRRLWDWVPLACRSFSLGVPRLIGIRLTL
	1		PPPKVVDRWNEKRAMFGVYDNIGILGNFEKHPKELIRGPIWLRG
	i		WKGNELQRCIRKRKNVGSRMFADDLHNLNKRIRYLYKHFNRHGK
			FR+KRKLRTSEKAHLSPWRRETVLPPVRKRLCIFSVIKWGPFGI
6180	156	1833	DHHILKAASTTHVCARGNIPAIPNTRCLEC*ATATPSSLECON*
	135	1033	SHLSLCPLPATTSGLTPNSMIPEKERQNIAERLLRVMCADLGAL
			SVVSGKEPLKLAQTLVDSGARYGAFSVTBILGNFNTLALKHLPR
	!	i	MYNQVKVKVTCALGSNACLGIGVTCHSQSVGPDSCYILTAYQAE
	<u></u>		MINA WAY A CONTORNATION TO A LOUD OF A CANADOLI TO LA ICUS OF A CANADOL

PCT/US00/34263

	1	<u>'</u>	<u> </u>
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ĺ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sedreuce	Codon, /=possible nucleotide deletion,
	sequence	L	\=possible nucleotide insertion)
1			GNHIKSYVLGVKGADIRDSGDLVHHWVQNVLSEFVMSEIRTVYV
}	1		TDCRVSTSAFSKAGMCLRCSACALNSVVQSVLSKRTLQARSMHE
)	i		VIELLNVCEDLAGSTGLAKETFGSLEETSPPPCWNSVTDSLLLV
ł		ł	HERYEQICEFYSRAKKMNLIQSLNKHLLSNLAAILTPVKQAVIE
1	ļ		LSNESQPTLQLVLPTYVRLEKLFTAKANDAGTVSKLCHLFLRAL
I	ł	1	KENFKVHPAHKVAMILDPQQKLRPVPPYQHEEIIGKVCELINEV
i	ļ	1	KESWAEBADFBPAAKKPRSAAVENPAAQEDDRIGKNEVYDYLQE
1			PLFQATPDLFQYWSCVTQKHTKLAKLAFWLLAVPAVGARSGCVN
L			MCEQALLIKRRELLSPEDMNKLMFLKSNML
6181	169	1032	TRTLLSPVLLPGPRWKPWRRRPMGPLALPAWLQPRYRKNAYLFI
1	[		YYLIQFCGHSWIFTNMTVRFFSFGKDSMVDTFYAIGLVMRLCQS
1	!		VSLLELLHIYVGIBSNHLLPRFLQLTERIIILPVVITSQEEVQB
į.	Ì		KYVVCVLFVFWNLLDMVRYTY9MLSVIGISYAVLTWLSQTLWMP
ľ	ĺ		IYPLCVLAEAFAIYQSLPYFESFGTYSTKLPFDLSIYFPYVLKI
	•		YLMMLPIGMYFTYSHLYSERRDILGIFPIKKKKM*STAFQCDTR
63.00			KDRLWIQCSK*NTGSILVEKFLVF
6182	1769	1224	AS*IDYQLNTLLKEFQLTEENTKLRYLTCSLIEDMAAAYFPDCI
j .	1		VRPFGSSVNTFGKLGCDLDMFLDLDETRNLSAHKISGNFLMEPQ
			VKNVPSERIATQKILSVLCECLDHFGPGCVGVQKILNARCPLVR
]			FSHQASGFQCDLTTNNRIALTSSELLYIYGALDSRVRALVFSVR
		•	CWARAHSLTSSIPGAWITNFSLTMMVIFFLQRRSPPILPTLDSL KTLADAEDKCVIEGNNCTFVRDLSRIKPSQNTETLRLLLKEFFE
			YFGNFAFDKNSINIRQGREQNKPDSSPLYIONPFETSLNISKNV
			SQSQLQKFVDLARESAWILQQEDTDRPSISSNRPWGLVSLLLPS
1			APNRKSPTKKKSNKFAIETVKNLLESLKGNRTENFTKTSGKRTI
			STOT
6183	1118	452	HLDRYIKSPGSGSSTPAPPSHLLLYLLHPOSTRTMGCCGCSRGC
		,	GSGCGGCGSGCGGCGSGCGCGSGCGCGSGCGCGGCGGCGG
}			RCYVPVCCCKPVCSWVPACSCTSCGSCGGSKGGCGSCGGSKGGC
			GSCGCSQSSCCKPCCCSSGCGSSCCQSSCCKPCCCQSSCCVPVC
l			CQSSCCKPCCCQSNCCVPVCCQCKI*GSGPRPSGFSCLVKAFLM
			VP
6184	ī	2191	IVTVREEDGAPAVAPPGVVVSRANKRSGAGPGGSGGGGARGARE
1			EPPPPLQAVLVADSFDRRFFPISKDQPRVLLPLANVALIDYTLE
			PLTATGVQETFVFCCWKAAQIKEHLLKSKWCRPTSLNVVRIITS
			ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALREHR
]			LRRKL+KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL
			HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA
]			QLFTDNFDYQTRDDFVRGLLVNKRILGNQIHMHVTAKKYGARVS
[			NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG
<b>i</b> !			PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD
<u> </u>			NVVLDQTYLWQGVRVAAGAQIHQSLLCDNABVKERVTLKPRSVL
			TSQVVVGPNITLPEGSVISLHPPDABBDBDDGBFSDDSGADQEK
			DKVKMKGYNPABVGAAGKGYLWKAAGMNMEBEBELQQNLWGLKI
			NMEBBSESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR
			GKEENISCDNLVLBINSLKYAYNISLKEVMQVLSHVVLEFPLQQ
			MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED
			FFLEHBALGISMAKVLMAFYQLBILAEBTILSWFSQRDTTDKGQ
			QLRKNQQLQRFIQWLKEABEESSBDD
6185	791	44	PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG
			IPFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFPFQR
			HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF
	1		GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK
			REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR
			GCQEAEMQTPRRIGWGWYHTLTLYLWBEK
6186	569	238	VYGIDSSNTNTHGABERNRKLKKHWKI/CHAQSRLDVNGLALKMA

SEQ	Predicted	Predicted end	I Amire and a company of the company
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1 .	corresponding	to first	Laterday M. Matting at the control of the control o
]	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *⇒Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Deque	\=possible nucleotide insertion)
<del></del>	1	<del></del>	KERKVKNKVKNKADTEEVFNNSPTNQEKMPTSAILPDFSGSVIS
	1		NIRNOMETLHSQPHQEENLCFENSFSLINLLPINAVEPTSSQQI
1	l .	ļ	PRETSEANKERRKMTSKSSESNIYSPLTSFITADSELHDIIKD
4	1		LEDCLMVGLHTCGDLAPNTLRIFTSNSEIKGVCSVGCCYHLLSR
	İ		EFENQHKERTQEKWGPPMCHYLKEERWCCGRNARMSACLALERV
	1 .		AAGQGLPTESLFYRAVLQDIIKDCYGITKCDRHVGKIYSKCSSF
1			LDYVRRSLKKLGLDESKLPBKIIMNYYEKYKPRMNBLRAFNMLK
1			VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLFDPVKSPRCYA
ŀ			VIALKKQQ+FPLKQIIRCISL+DSAGCAEEVSVGDGGPALRDAP
		-	PSGSRVGSRYD
6187	1701	771	DAWGPETRLARILNPDSFIEPRPGRLPELEATRPHMEPKASCPA
1	j l		AAPLMERKPHVLVGVTGSVAALKLPLLVSKLLDIPGLEVAVVTT
1			ERAKHFYSPQDIPVTLYSDADEWEMWKSRSDPVLHIDLRRWADL
1	]		LLVAPLDANTLGKVASGICDNLLTCVMRANDRSKPLLFCPAMNT
	1		AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGDEGLGAMAEVG
1	1	ı	TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEWVQAKSVKMDV
i	i		GKIGGYPHLINGGPALSLPRGQACSRLNWTEGPGLSFFQPGEAA
	L		A
6188	238	1534	KGFVNAGPLMAKLQVSPQWKAPEMSQICLSCGHPSA*GPRWASW
			NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCMQEMG
ı	1		NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYEKKKYMDRSLD
			INAFRKEKDDKWKRGSEPVPEKKLEPVVPEKVKMPQKKEDPQLP
	! !		RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTLEKDLDLLASV
1	i .		PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEPGSKSEEIGKK
	}		QLSKDSILSLYGSQTPQMPTQAMFMAPAQMAYPTAYPSFPGVTP
1.	1		PNSINGSMMPPPVGMVAQPGASGMVAPMAMPAGYMGGMQASMMG
1			VPNGMMTTQQAGYMAGMAAMPQTVYGVQPAQQLQWNLTQMTQQM
6189	1297		AGMNFYGANGMMNYGQSMSGGNBQAANQTLSPQMWK
8105	1297	793	LGBPLGDLCELIPGDVQQLQMGEVHPGTGAQGSAAQSVAGEVQL
1			TQLSHARQRPSCQGSQLIALDLQHMDISRQPRWQHVQPVARQVQ
			RAQQAQLARGVAVHLWAGDAVVAEVELLQEVGGGKVFAANACDL
			VVQDHEGAHAARQATGHALQRVIVQVRRVQPLBAL*RVPSGLPR
		•	RVRAFMILHNQITGIGREDFATTYFLEKLNLSYNRITSPQVHRD AFRKLRLLRSLDLSGNRLHMLPPGLPRNVHVLKVKRNKLAALAR
1 1			GALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQ
'	]		LTBIPEGLPESLEYLYLQNNKISAVPANAFDSTPNLKGIFLRFN
]		<b>-</b>	KLAVGSVVDSAFRRLKHLQVLDIRGNLRFGDISKDRGRLGKEKE
	}		BEEEDEVEREETR
6190	66	1309	ILVGNVSFLLSPAEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQ
	1	<del></del>	GLHCETCKEGFY_NYTSGLCQPCDCSPHGALSIPCNSSGKCQCK
) l	[		VGVIGSICDRCQDGYYGFSKNGCLPCQCNNRSASCDALTGACLN
			CQENSKGNHCEECKEGFYQSPDATKECLRCPCSAVTSTGSCSIK
( l			SSELEPECDQCKDGYIGPNCNKCENGYYNFDSICRKCQCHGHVY
	l		PVKTPKICKPRSGECINCLHNTTGFWCENCL*GYVHDLBGNCIK
] ]	1		KVILPTPEGSTILVSNASLTTSVPTPVINSTFTPTTLQTIFSVS
	ľ		TSENSTSALADVSWTQFNIIILTVIIIVVVLLMGFVGAVYMYRE
	]		YONRKLNAPFWTIELKEDNISFSSYHDSIPNADVSGLLEDDGNE
	]		VAPNGQLTLTTPIHNYKA
6191	1212	1511	VNLCHGGLLHLSTHHLGIKPSMH*LFFLMLSFPHLTPOOPKCPS
	ļ		MIDWIKKIWYIYTMEYYATIKRNBIMFFAGTWMEMEAIILSKLM
	j		QDYMFSLISGS
6192	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSBPESDGRAGIEAVGSAAEE
1	İ		KGGLVSDAYGEDDFSRLGGDKDGYEERKDKNSRQSEDDDSETEK
		i	PEADDPKDNTEAEKRDPORLVASFSERVRNMSPDEIKIPPEPPG
			RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI
			QFCAIDELGTNYPKDMFDPHGWSEDSYYBALAKAQKIEMDKLEK

Degiming				
NO: location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence sequenc	SEQ	Predicted	predicted end	Amino acid segment containing signal peptide
Cocresponding   cofirms   corresponding   cofirms   corresponding   cofirms   common acid   creidue of   amino acid   sequence   cocon,			•	
L=Leucine, M=Methionine, N=Asparagine, points animo acid residue of amino acid residue of amino acid sequence   P=PTO-Oline, Q=Olinamine, R=Asparinine, points animo acid sequence   P=PTO-Oline, Q=Olinamine, N=Valine, amino acid sequence   P=PTO-Oline, Q=Olinamine, V=Valine, amino acid sequence   P=PTO-Oline, Q=Olinamine, V=Valine, amino acid sequence   P=PTO-Oline, Q=Olinamine, V=Valine, amino acid sequence   P=PTO-Oline, Q=Olinamine, V=Valine, v=Val	NO:			
amino acid residue of amino acid residue of amino acid sequence  #### PPPCOLINE, Q-GIUTANINE, R-ARTSININE, ####################################		1		1
amino acid residue of amino acid sequence discovery tryptophan, Y-Tyrosine, X-Eubknown, Y-Stop Codon, Y-possible nucleotide deletion, Y-possible nucleotide de	ļ		1 -	
residue of amino acid sequence Codon, /=possible mucleotide deletion   Acceptable mypossible mucleotide insertion   Acceptable mypossible mucleotide insertion   Acceptable mypossible mucleotide insertion   Acceptable mypossible		l .		
amino acid sequence   Sequence	i .			
Sequence   Sequence				
BSAIFUTTIAQPTILITTATLPAVVITTISASGERTIVISAVGT   TVKKAKQ				
6193 3 950 TREGGRINGKRINTSSLAVVARDSSPESDGRAGTKAVGSJARE  KOGLVSDAYGEDDFSRLGGDEDGYRSBEDDENSRQSEDDDSSTEK  PEADDPKDNTEARKRDPQBLVASFSBEVRINSFDERKTPEPEPG  RCSNHLQDKLGKYRRKIKKERADMNYI IGRKREFRINSTYRHALA  AKKERTKIEFYTGTKGGTTINTSTTTTTASTAVADQKRKSKW  DSAIFYTTIAQPTILITTATIPAVTVTYTSAGSKTTVISAUGT  IVKKAKO  6194 3 950 TREGGRINGKRAVLSSLAVVARDSSPESUSEAGIEAVGSAARE  KOGLVSDAYGEDDFSRLGGDEDGYBERBDENSRQSBEDDISFTEK  PEADDPKDNTEARKRDPQELVASFSREVERASTERVGSAARE  KOGLVSDAYGEDDFSRLGGDEDGYSBERBDENSRQSBEDDISFTEK  PEADDPKDNTEARKRDPQELVASFSREVERASTERVGSAARE  KOGLVSDAYGEDDFSRLGGDEDGYSBERBDENSRQSBEDDISFTEK  PEADDPKDNTEARKRDPQELVASFSREVERASTERVGSAARE  KOGLVSDAYGEDDFSRLGGBEDGYSGREADIERVGSAARE  KOGLVSDAYGEDDFSRLGGBEDGYSGREADIERVGSAARE  KOGLVSDAYGEDDFSRLGGBEDGYSGREADIERVGSAARE  KOGLVSTAYGENDFSRLGGBEDGYSGREADIERVGSAARE  KOGLVSTAYGENDFSRLGGBEDGYSGREADIERVGSAARE  KOGLVSTAYGENDFSRLGGBEDGYSGREADIERVGSAARE  KOGLVSTAYGENDFSRLGGBEDGYSGREADIERVGSAARE  KOGLVSTAYGENDFSRLGGBEDGSBERGEBDDSSTERL  AKKERKERVTEFYTGTKKGTTTNATSTTTTTASTAVADAGKRKEK  AKKERKERVEFYTGTKKGTTTNATSTTTTTASTAVADAGKRKEKE  AKKERKERVEFYTGTKKGTTTNATSTTTTTASTAVADAGKRKEKE  AKKERKERVEFYTGKKGTTTNATSTTTTTASTAVADAGKRKEKE  AKKERKERVEFYTGKKGTTTNATSTTTTTASTAVADAGKRKEKEN  AKKERKERVEFYTGKKGTTNATSTTTTTASTAVADAGKRKEKEN  AKKERKERVEFYTGKKGTTTNATSTTTTTASTAVADAGKRKEKEN  AKKERKERVEFYTGKKGTTTNATSTTTTTASTAVADAGKRKEKEN  PEADDPFUTLAVVETNATSTTTTASTAVADAGKRKEKEN  FEADDPFUTLAVVETNATSTTTTATSTAVADAGKRKEKEN  FEADDPFUTLAVVETNATSTTTTATSTAVADAGKRKEKEN  FEADDPFUTLAVVETNATSTTTTATSTAVADAGKRKEKEN  FEADDPFUTLAVVETNATSTTTTATSTAVADAGKRKEKEN  FEADDPFUTLAVVETNATSTTTATSTAVADAGKRKEKEN  FEADDPFUTLAVVETNATSTTTTATSTAVADAGKRKEKEN  FEADDPFUTLAVVETNATSTTTATSTAVADAGKRKEKEN  FEADDPFUTLAVVETNATSTTTATSTAVADAGKRKEKEN  KOLLMANINGSOLLAVETNATSTAVATATSTAVADAGKRKEKEN  KOLLMANINGSOLLAVETNATSTAVATATSTAVADAGKRKEKEN  KOLLMANINGSOLLAVETNATSTAVATATS		-		AKKERTKIEPVIGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
6193  3 950  TREGGREMAGKRAVIZSIANVARDSSPESOGRAGITEAVGSAREE  KOGLVSDAYGEDDESRLGODEDUSTEK  PEADDPKONTEARKROPQBLIVASFSERVINNSFDEIKTIPPRPPG  RCSNHLQDKIQKIYRKIKGRADMSVIIQRKREFRINSTYRLII  QPCAIDELGTYPKROMPOPHERBEDSYYRALBAQKIRHDKURK  AKKERTKIEFVTGTKKGTTTNATSTTTTTTTTATAVADAQKRKSKM  DSAITVTTIAQPTTLITTATIPAVVTVTTSASGSKTVISAVGT  IVKKAKO  6194  3 950  TREGGREMAGKKNVLSSLAVVAEDSEPBSDGRAGIEAVGSAREE  RGGLVSDAYGEDDESRLGGDEOGYBEBEDDSSRGSRGBDDDSBTEK  PEADDPKONTEARKROPQELVASFSBRVRINSPDEIKIPPPPG  RCSNHLQDKIQKIYRKKIK REGMONNYIIQKREFRINSTYTELSI  QPCAIDELGTYPTYPKOMPOPHISSBSYYRALAKAQKIEMDKURK  AKKERKIEFVTGTKGTTTNATSTTTTTSADADAQKRKSKM  DSAIPVTTIAQPTILITTATIPAVVTVTTSASGSKTVISAVGT  IVKKAKO  6195  736  235  VANGLQSIMPKFYCDYCDTYLTHDSPSVRTHCGGRRHKENVKD  YYQKNMBEQAQSILIKITAAPQOGKIEPTPFSAPPAGAMITEP  PENGEHPPMHQDPPMRPBAPHMOPTPRGMTPTPFSAPPAGAMITEP  PENGEHPPMHQDPPMRPBAPHMOPTPRGMTPTPFAGAREP  PENGEHPPMHQDPPMRPBAPHMOPTPRGMTPTPLQEEDSH  QRLIMGIAWSELKOHFLHILQGVEKKKIEQMILDTICKLEUSH  HIVSTANKRIMISSWLAHPSISASAAPRAVITELLGTIESS  RHIVTRLDGVYKKQPRNSHINKSSPSVEPLDIAVTIELITIESS  MQALYPFBGHINVDARFVERSALAKHTAMLLGI  6197  3 819  ADDPGTTERMWSKYTPPENTISTITENDELGERGRYG  PIUDVYI PILDTYTRRGRPAYUQPEDVRDAEDALYINLIKRVOG  RGIRIGFAGGRETTPOGMKSKRRHEDGSSDIRRERGSSPGRTPS  RSSSWGENBRRSDSLKESSHRPSVEGGKSRGKSLEPRSTSARQ  SRTYPRHFGSRGRSRSSLGKSRSSICKGRGSGKYGNSGTKS  RSSSWGENBRSDSLRSSHRPSVEGGKSRGKSLEPRSTSARQ  SRTYPRHFGSRGRSRSSLGKSRSSICKGRGSGKYGNSGTKS  RSSSWGENBRRSDSLRSSHRPSVEGGKSRGKSLEPRSTSARQ  SRTYPRHFGSRGRSRSSLGKSRSSICKGRGSGKYGNSGTKS  RSSSWGENBRSSSSRRRSSSLGKSRSSICKFASSSRSS  RSSSWGENBRSSSGRRRSSSLGKARGSTERGRSSSRSSRSS  RSSSWGENBRSSSSRRSSSRSSRSSRSSRSSRSSRSSRSSRSSRSSRS				DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
### REGILVEDAYGEDDEST-LEGDENGY-BERUSHS-DEST-LEY PEPPOR RCSNHLQOKTQKI, YRRKI KROHMNY I I GRKREFRNES I YEKLI OPCALDELG-TNYEKNHOPEH-SHEDS-YYRALABAQKI KROKLEN AKKERKIKEPYTETKAGTTUNYEKNHOPH-SHEDS-YYRALABAQKI KROKLEN AKKERKIKEPYTETKAGTTUNYEKNTYTTTATS-TAVADAQKEKSKW DSAI-PYTTIAQPTILITTATLPAVOTVUTTSAGS-KTTVI ISANGT IVKKAKO DSAI-PYTTIAQPTILITTATLPAVOTVUTTSAGS-KTTVI ISANGT IVKKAKO SUGU-SDAYGEDOFEN-LGGENGY-BERDENSENG-BEDDIS-BTEK PERADDE-KOMTRAKKENU-SI-SLAVYAREDSEPES-GGE-BI-EX-VGSAAKE KOGLVSDAYGEDOFEN-LGGE-GGGT-SHEDEN-BRAGNER-BRADE-PRADDE-KOMTRAKKEN-SHENGH-PREDIKT-PEPPOR RCSNHLQDKI QKLYERKI KROMDANY I I QKKKEPNNPS I YEKLI QFCANDL-GKTAYEKNU-STATUT-STAVADAQKE KSK BAJ-PYTTIAQPTILITTATL-AVVOTVTTSAGS-KTTVI ISANGT IVKKAKO BAJ-PYTTIAQPTILITTATL-AVVOTVTSAGS-KTTVI ISANGT IVKKAKO SAKKERKKER-PYTGTKKGTTINATS-TITTA-STAVADAQKE KSK BAJ-PYTTIAQPTILITTATL-AVVOTVTSAGS-KTTVI ISANGT IVKKAKO BAJ-PYTTIAQPTILITATUR-AVVOTVTSAGS-KTTVI ISANGT IVKKAKO SAKKER-KKER-PYTGTKKGTTINATS-TITTA-STAVADAQKE KSK BAJ-PYTTIAQPTILITATUR-BYT-VTTV-TSAVADAQKE KSK BAJ-PYTTIAQPTILITATUR-BYT-VTTV-TSAVADAQKE KSK BAJ-PYTTIAQPTILITATUR-BYT-VTTV-TSAVADAQKE KSK BAJ-PYTTIAQPTILITATUR-BYT-VTTV-TSAVADAQKE KSK BAJ-PYTTIAQPTILITATUR-BYT-VTTV-TSAVADAQKE KSK BAJ-PYTTAQPTILITATUR-BYT-VTTV-TSAVADAQKE KSK BAJ-PYTT-BYT-BYT-BYT-BYT-BYT-BYT-BYT-BYT-BYT-	ì		1	IVKKAKQ
PRADDPKOMTERARROPOGLUASPSERVENNSSPORTET PPEPPER RCSNHLQKTQKLYBRIKEGDMYNYI IQRKREPRNPSTYBKLI QPCAIDELGTNYPKOMPDHYNI IQRKREPRNPSTYBKLI QPCAIDELGTNYPKOMPDHYNI IQRKREPRNPSTYBKLI AKKERTKIEFYTGTKKGTTTMATSTTTTTASTAVADACKREKRW DSAITYTTLACPTTLITTATLPAVTUTTTSASGKKTVISAUGT IVKKAKQ  6194 3 950 TRGGGNAGKKNVLSSIAVYABDSEPBSDGRAGIENVGSAARE RGGLVSDAYGBDDPSRLGGDBOGYBBEDRSTRGSBDDSTTEK RGGLVSDAYGBDDPSRLGGDBOGYBBEDRSTRGSBDDSTTEK RGGLVSDAYGBDDPSRLGGDBOGYBBEDRSTRGSBDDSTTEK RCSNHLQDKIQKLYBRKIKEGMMNYI IQRKKEPRNPSI YSKLI QPCAIDELGTNYPROMPDHOWSBDSYYRALAKAGKIBDDLERDK AKKERTKIEFYTGTKGTTTANSTTTTTASTAVADAQKRISK AKKERTKIEFYTGTKGTTTANSTTTTTASTAVADAQKRISK DSAIPYTTAQFTITLTTTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKQ  6195 736 235 VANGLGSNMPKPYCDVCDTYLTHDSPSVRRTHCSGRRHKENKO YYQKWMBQAQSLIDKTTAAPQOKLTPPTSAAPPDAGAMIPPP PSILGEPRRGHMPAPHNOGPPMMPMGPPPRGMMPVGPAPCMRP PMGBBMPMMPGPPMMPPRARPMNOYPTRPGMTEPDR PSILGEPRRGHMPAPHNOGPPMMPMPAPPRAGNIEPBLTPFLQEEDSH QRLIMGHMVSELKDHFLRRLGGVEKKKIEQWLLDYISKLDLICE HIVSTNMRKBUNJSWLUKHNSRGSAARFAUHTSTLLETAVITL MKDLDNYERBRINLSSWLUKHNSRGSAARFAUHTSTLLETAVITL MKDLDNYERBRINLSSWLUKHNSRGSAARFAUHTSTLLETAVITL MKDLDNYERBRINLSSWLUKHNSRGSAARFAUHTSTLLETAVITL MKDLDNYERBRINLSSWLUKHNSRGSAARFAUHTSTLLETAVITL MKDLDNYERBRINLSSWLUKHNSRGSAARFAUHTSTLLETAVITL MKDLDNYERBRINLSSWLUKHNSRGSAARFAUHTSTLLETAVITL MKDLDNYERBRINLSSWLUKHNSRGSAARFAUHTSTLLETAVITL MKDLDNYERBRINLSSWLUKHNSRGSAARFAUHTSTLLETAVITL MKDLDNYERBRINLSSWERREPESPEDIRBRSFSGRREFTS SQRUKNERSDSLKSSENRFSPSGRERSPSGRREFTS SGRUGNBRRRSDSLKSSENRFSPSGRERSPSGRREFTS RSSWGRNRRSDSLKSSENRFSPSGRERSPSGRREFTS SSWGRNRRSDSLKSSENRFSPSGRERSPSGRREFTS SSRUGNBRRSSDSLKSSENRFSPSGRERSPSGRREFT SSSWGRNRRSDSLKSSENRFSPSGRERSPSGRREFT SSSWGRNRRSDSLKSSENRFSPSGRERSPSGRREFT SSSRGRREFTSGRREFTSGRERGREFTHANSPSGRAFT GVPSLLLVATURHBLETAFPETLOPHDVBRERGRAFT GRAPPPTPSGRAFTHANSPSTAT GVPSLLLVATURHBLETAFFELDPTLOPHDTLGNNYBGARSE RSHPPPPPPSPSPSPSPDSPROGREFTSLTVASSLCLFARAGOFT LACGULWFSGVGHTWSGNATHLVSSLLTTLLKQLEPTAWDSGTT GVPSLLLVATURGGPTTATAUHTBURHBRREFTLEFTRNAVDRREF SARGFULGSRAVITATEGREFTURHDBETTRANTLTG GVPSLLLVATURGGPTTATAUHTBURHBRUCHSRADGGFT GGGEKTYLT	6193	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIRAVGSAAEB
RCSHHLQDRIQGLURRITERSHOWNYIJQRKRRPRNESIYERLI  QPCAIDELGTNYPKOMPDPHGSEDSYYRALARQKIENDKLEK AKKERKIEFYTGTKKGTTTMATSTTTTATAVADAQKRSKM DSA17VTTIAQPTILTTTATLPAVVTVITSASGSKTVUISAVGT IVKKAKQ  6194 3 950 TRGGSNEMAGKKNVLSILAVYARDSEBERSIRGASGEDDSBTEK PGADDPKDNTRAEKRDPQELVASFSBRVRNMSPDEIKIPPEPPG RCSHHLQDKIQKLYBRKIKGSMNAVITJURKKRPRNESIYSKGLI QPCAIDELGTNYPPDMEPPHGWERGYYKRAGKIKAQKIENDKLEK AKKERTKIEFYTGTKKGTTTNATSTTTTTASTAVADAQKRSKM DSA17VTTIAQPTILTTATTLPAVVVITSASGSKTVUISAVGT IVKKAKQ  6195 736 235 VANGLQSNMPKPYCDYCDTYLTHDSPSYRRGTICSGRRHKENVKD YYQKWHEBDAQSLIDKTTAAPQQGKIPPTPFSAPPPAGAMIPPP DSILGEPRRGMHPAPHINGBPYMSPPPSAPPPAGAMIPPP PSILGEPRRGMHPAPHINGBPYMSPPPSAPPPAGAMIPPP PSILGEPRRGMHPAPHINGBPYMSPPPSAPPPAGAMIPPP PSILGEPRRGMHPAPHINGSPPMSHRFSPPROMPYVPAPCGMRP PMGGHPMRMGPPPMSPRPPARMWYTTFLQEDSH 6196 1512 623 KTGKRRSANYUNILDNASQYISHLEKRRIGSPRHTPLQEDSH RGGHLMGLMVSELKHHLRIGOVEKKI GAULDYISKILDLIC HIVSTIMKKHILISHDALHUNISGCAABFAVFHIMTRILGAUNSL FLPLPPGPHTLHTILGVCLPLHNILLHCIDSCYLLLTETAVIRL MKOLDNITEKNEKLKFSITVRIPPLIGGVEKKI GAULDYISKILDLIC HIVSTIMKKHILISHDULHUNISGCAABFAVFHIMTRILGATNSL FLPLPPGPHTLHTILGVCLPLHNILLHCIDSCYLLLTETAVIRL MKOLDNITEKNEKLKFSITVRIPPLIGGLICELMDHPMSNIISS NHUTRILIQNYKKQPRSSMINKSSSVEFLPINYFIELITDIESS NQAIFPFEGENADARTVRIPMTSILTIKADALTRYBILLITDIESS NQAIFPFEGENADALTHYDEFILITOILESS RGAPSTERANGSKEKKLGERINGSISKSGKEKSSPRKGTSSSFGKR SSRGENRRRSDSLEESSHRRFSYSGKKRSKSEPRRSSSSRRK SSRGENRRRSDSLEESSHRRFSYSGKKRSKSEPRGTSSSTKS RSHGRIEDDSTARSPCKSPKRGTNESTATAVADARTPERDLERGERG SRTPRRNFSSGKRSKEKSCRERKSGLERRSTAARG SRTPRRNFSSGKRSKEKSCRERKSGLERRSTAARG SRTPRRNFSSGKRSKEKSCRERKSGLERRSTAARG SRTPRRNFSSGKRSKEKSCRERKSGLERRSTAARG SRTPRRNFSSGKRSKEKSCRERKSGLERRSTAARG SRTPRRNFSSGKRRKSGKERRSTAARG SRTPRRNFSSGKRKRKSCRERKSGLERRSTAARGOFTL LACCULMFSGVGHTWSQAATHIVSSLLATLLQLELPTARAGOFT UKCHANGENGTATATAGGFIVETVLAWHLLKTPRSPPTTLPPERRRGSY SRQPSTYSEMBEKLEDDFILDSHTYRSSLCLARAGOFTL LACCULMFSGVGHTWSQAATHIVSSLLATLLQLELPTARAGOFT UKCHANGENGTATATAGGFIVETVLAWHLLKTPRSPPTTLPPERRRGSF SRGPSTYSEMBEKLEDDFILDSHTYRINGERGRINDANTARG SRGPSTYSEMBORGRERGRINGTLINGTHETTVUCHTINIERM RKCTEWPPERPORATORPLL				KGGLVSDAYGEDDFSRLGGDEDGYKBEDENSRQSEDDDSETEK
OPCAIDELGTNYPROMPPHGMERDSTYRALARAQKIRMDKLEK ARKERTRIEPTTGTKKGTTTNATSTTTTATSTAVADAQKRYSKW DSA17VTTLAQPTILITTATLPAVTVUTTSASGSKTTVISAVCT IVKKAKQ  6194 3 950 TRGGGNARAGKKNVLSSLAVYARDSEPBSDGEAGIEAVGSAARE KGLVSDAYGRDDPSRLGGDEOGYEBEEDRSNGSEDDDSTTEK RGGLVSDAYGRDDPSRLGGDEOGYEBEEDRSNGSEDDDSTTEK PEADDPKDNTRAEKRDPQELVASFSBRVENNSPDBIKLPPEPPG RCSNHLQDKIQKLYBRKIKEGMMNYII LQRKKEPRNPSIYEKLI OPCAIDELGTNYPROMPPHGMERDSTYRALARAQKIRMDKISK AKKERTKIEFTTRATTTAVADAQKRYKSKW DSAIPVTTLAQPTILITTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKO DSAIPVTTLAQPTILITTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKO 1VKKAKO 6195 736 235 VANGLQSNMPKPYCDVCDTYLTHDSPSVRKTHCSGGRRHKENVKD YYQKMMERQAGSLIDKTTAAPQGGKIPPTPSARP PEAGMIPPP PSGEBMPMMERQPPMSPPARPMYDTRPGMTRPDR PSGEBMPMMERQPPMSPPARPMYDTRPGMTRPDR 6196 1512 623 KTGGRESSAVYENILDSAGGYISMLEKRHIJGERUTPLAQEEDSR CRLLMGLMSVELKDHPLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVBTHNRKEHLBISWLHHDSRSSAARFAVFHIMTILGATUSL FLEIPPOPHTHI-HILLQCUCLEHNLLHGCTDGSVLLLTETAVIRL MKOLDNTEKNRKLKFSIIVRLPPLIGGKICLEHNDHMSSNIISR NALYPPEGENNVDASFVERALKHTAMILGG. HIVBTHRICHNYKLGPSTVERPRTSLFIRNVADATRPEDLREEFGRYG PIVDVYTLPLDFYTRRREGFATVQFEDVRDARDALYBLIBLRSNIVCG RQIBLIQFAQGDRRTFCQMKSKERREGSPSDBIRRSRSFSGRTTSS RSSSWGRMERRSSSLSKERREFSTSGERSKSLEPRRSTSGRG SRTYRRNFGSGRGSRGKSLQKSRSGIGSGSSGNGKYDSGTKS RSSSWGRMERRSSSLSKERRFSTSGERSKSLEPRRSTSGRG SRTYRRNFGSGRGSRGKSLQKSRSGIGSGSSSGNGKYDSGTKS RSHGRHSDBIARSPCKSPKGTTNFETVQTAKHSHRSRSTARQ SRTYRRNFGSGRGSRGKSLQKSRSGIGSGSSSGNGKTSGTKS RSHGRHSDBIARSPCKSPKGTTNFETVQTAKHSHRSRSTARQ SRTYRRNFGSGRGSRGKSLQKSRSGIGSGSSGNGKTSGTKS RSHGRHSDBIARSPCKSPKGTTNFETVQTAKHSHRSRSS KRINERSDBEGGGALDMCCGRRINGHLOPPTVURALDRAELDDSGTW GVPSLLLIVPLSGGLVLVTTLWHILLATPPSPPTPLEPBERRGPF RSHRADDSEGGALDMCCGRRINGHLOPPTVGREGGTIMSPRRSS ARBYLLGASRVIARAGKHINGHCPPTVMKALDLSGTM GVPSLLLIVPLGGGLVLVTTLWHILLATPPSPPTPLEPBERRGPF RGGEBKYVIATQGPIVSTVADPRHMWGRHTPILVRITIBBM BKCTEWPRPDQKTPDRAVLLTURDPLHLINGKBERADAGGFHANTI VHCSAGIGRTCCPLARGLGRANVULTURERDAYBRASGGRHAPII VHCSAGIGRTCCPLARGLGCHASGHGVILAREKKA MIGHEBORYDFVHHVMSLYEKQLSHOGSPE MIGHEBORYDFVHHVMSLYEKQLSHOGSPE MIGHEBORYDFVHHVMSLYEKGLSHOGPE			i	
AKKERTRIEFVTGIKKSTTINATSTTTTTASTAVADAQKRISKW DSAIPVTTIAQPTILTTATLPAVVTVITSASGSKTTVISAVGT IVKKAKQ 6194 3 950 TEGGGKMAGKKNVLSSIAVYAEDSEPRSUGAGIEAVGSAARE RGGLVSDAVGBOPSRIGGDBOYGEREBYSRQSBODDSTEK PRADDPKOMTRAERRDPQELVASFSRRVENNSPDEIKIFPEPPG RCSSHLOGAVIQLVERKI KERMANNYI 1QAKKERPUPSIYKELI OPCAIDELGTNYPKOMFDPHGHSBDSYYRALAKAQKIEMDKLEK AKKERIKIEFVTGTKAGTTINATSTTITTASTAVADAQKRISKM DSAIPVTTLAQPTILTTIALPAVIVTYTSASGSKTTVISANGT IVKKAKQ 6195 736 235 VANOLGSNMPKPYCDVGUTYLTHDSPSVEKTHCGGRRHKENVKD YYQKWHSBQAGSLIDKITAAPOQOKIPPTPSSAPPAGAMIPPP PSLPGPPRPGHMPAPHINGGPPMPMMPVGPPAPGMPVGPAPGMRT PMGGHPMMPQPPMPMPPHPAPHINGPPPMPMMPVGPAPGMPVGPAPGMRT EMGGHPMNPQPPMPMPPPPRPSAPPAGAMIPPP RMGGHPMNPQPPMPMPVGPAPAMVPTREOMITEDR 6196 1512 623 KTGKRRSAAYVENLIDNAGQVISHLEARRIGSPRITJCQEEDSI CRILMGIMVSELKOPHLRIGOVEKKI EXQULLYTISKLIDLIC HIVSTNNRKSHLISHVLHNDSRGSAARFAVFHINTRILGAUENSI PLPLPPOPTHILITLIGVGLELQLEHRILLIGLEQUELLITETAVIRL MKOLDNTEKNEKLKPSIIVRIPPLIGQKICCHMHDHPMSSNIISR NHVTRILQNYKKQPRASMINKSSSVEFLPINYPITILTILISAVSI. FLPLPPOPTHITHITLIGVGLEPHANLLIGGE RMGLIPPHGGPRASMAVKRILGSBARFAVFHINTRILGATVSI. HIVSTNILIQNYKKQPRASMINKSSSVEFLPINYPITILITILISCU RMGLIPPHGGPRASMAVKRILGDEINNABERGRYG RNGALYPPEGENOVABERVERARAKHTANLIGI RMGLIPPHGGBPRTYCQMSKERRIGGSBARFAVFHINTRILITILISCU RGGERVILIDTYTRREGRAVVOFBUVINDERALKYRAVGE RCHERTON RESERVATION REPROMENTATION	Į			
DSA12VITIAQFTILITITATLPAVVIVITSASGSKITVISAVGT IVKKNKQ  TREGGNEMAGKENVLSSLAVVAEDSEPESDEGGIEAVGSAAEB KGGLVSDAYGEDDFSRLGGBEOGYEREDENSRQGSDUDSETER PEADDPENDTRABKERDGELVASFSRENNSPDEIKLFPEPEP RCSHHLODKIQKLYERKIKEGHMYMYITORKEFRAPSIYSKLI OPCAIDELGTNYPKOMFDPHGWSBGSYYRALAKAQKIEMDKLEK AKKERIKEPYTGYKKGTITMISTITITATAVADAQKERSKN DSA1PVITIAQPTILITTATLPAVVIVVTSASGSKTTVISAVGT IVKKAKQ  6195 736 235 VANGLQSNMPKPYCTYCDTYLINDSPSVRTHCSGRKHKENVKD YYQKMMEQAQSLIDKTTAAFQQKIPPTPSAPPPAGAMIPPP PSLEGEPREGNMPAPHNGGPPMWPMFPPPGMPYGRPCHGMP PMGGBMPMMFQPPMMPPARPMWVPTRPGMTPDR 6196 L512 623 KTGKRRSAVYUNILIBABEQYISINLEANLISPELTPLIQEEDSH QRLIMGIMYSEKKDHPLRHLQGVEKKKLEQWILDYISKLDLIC HIVBTNWKGINLESWLHPNSGSSAFPAVHTHTELEATNSL PLELPPGPPTTLHTILGQCLCHLMHHMSSNILHFEANLISPLITYLIQEEDSH MKOLDNTEKNBELKESIIVELPPLIGGKICCHLMHMSMINITISK NHAVTELLQHYKUQPRASMIKNSSPSTELPINYTIETITDIESS NQALYPPEGGBUNDARFVERALKHTANLIGL 6197 3 619 ADPEGTESAVMSKYTTRPGTSLFILWADATRPEDLABEFGGYG PIVDVYIPLDFYTRREGGRAYQFBVRABEDALYNLNRKWVCG RQIHIQPAQGDRATTCGMKSKRRHCSSPSDHRRSBFSGRATTAS SKIGKRHSDSIASSHRRFSTSGSKERSEPRRSSFSGKRTSFRSRS SKIGKRNSBGSIASSHRRFSTSG KERGSSEPROFTSSTARG SRTYRRFSSRGRBKSSLOKESSSISLITVASSLCLFAASQFI LACGULMFSGYCHIMSQNATNIVSSLILAQUEPTAMHDSGTW SKRALESPSTISPACFLLKKLPALEGGTLPHPDTICRNYEGARSE RENHAADDEGGALIMCCSSRIPEGPQFIVMGARSELGDSQ REMPPPPPPSPSDPAQKYPDFTVPFTVPDCHNDLGGNYGSRBS SRCPSTYSEMMERISLORENSLITVASSLCLFAASQFI LACGULMFSGYCHIMSQNATNIVSSLILAQUEPTAMHDGETW GVPSLILVFLSGGIVUTTLVWHLLRQUEPTPVPDCWDLKPPRBS AREVILSASRVIJARGHLRKALDPFLAQAEFFEIPMNYDDRKFY DIPGLVRKNYKTILPRPHERVCLTSQDEPDFLSSYINANIVIG GGEEKYYIATGGFVSTVADPWRNWQBRTFIIVMITNIBEMN EKCTEWPREQVANDGETTVQKVHTTEDVRILALBLEKSGTERR GLKTYWFTSWPDKTFYSMPDKTFURVERBAAQQGEFTCAPII VHCSAGIGRTGCFIATSICCQOLRGGWVDILKTTCQLREGGFGAPII VHCSAGIGRTGCFIATSICCQOLRGGGWVDILKTTCQLREGGFGAPI UHCSAGIGRTGCFIATSICCQOLRGGGWVDILKTTCQLREGGFCAPII VHCSAGIGRTGCFIATSICCQOLRGGGVVDILKEKKA		!		1 = ·
Tykkako				<u> </u>
6194 3 950 TREGGNEMACKUNUSSLAVYARDSEPENSIGEAGIEAVGSAARE KGGLVSDAYGRDDPSRLGGDEDGYEREEDESSIGEAGIEAVGSAARE PEADDPKORTRAEKGDPGELVASFSARVRIMSPDETKLTPPEPPG RCSHILQDKIQKIYEKRI KEGHDMYI IJQRKREFRIPSTYSKLI OPCAIDELGTHYPKONDPHGMSBDSYYRALAKAGKIBMUKIEK AKKERTKIEFYTGTKGTTTNATSTTTTASTAVADAGKEKSKM DSAAIPYTITAQPTHITTATLPAVVTVTTSASGKTTVISAVGT IVKKARQ  6195 736 235 VANGLGSNMPKYCDYGDTYLTHDSPSYRKHTKSGRRKKENVKD YYRKWMBEAQASLIDKTAAFQOGEIPPTPSAPPPAGMTPPP PSLDGPPRPGMMPAPHNGGPPMMPMMGPPPCMMPYGPAPGMRP PMGGHMPMRGPPPMMPMPMPPDRMMPMGPPPCMMPYGPAPGMRP EMGGHMPMRGPPPMMPMPMPPRPMMPMPTPPMMPMPDRPDGMRP EMGGHMPMRGPPPMMPMPMPMPMPMPMPMPMPMPMPMPMPMPMPM	1			• • • • • • • • • • • • • • • • • • • •
RGGLVSDAYGEDDESRLGSDEDGVERBEDENSRQSEDDDSSTER PRADDPKONTRAEKRDPQELVASTSERVRMSPDEIKIPPEPPG RCSHHLQDKIQKLVPKSKIKKSMOMNYIIQKKREPRNPSIYSKLI QPCAIDELGTNYPKDMFDPHGMSBGSYYRALAKAGKIBMDKLEK AKKRETKIERVTGIYKGTTMATITTTATSTAVADAGKRSKM DSAIPVTILQPTILITTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKQ  6195 736 235 VANGIGJSMMFKPYCDYCDTYLTHDSPSVRRTHCSGRRHKENVKD YYQKWMSEQAQSIJDKTTAAPQQGKIPPTPFSAPPPAGAMTPPP PSLPGPPRPGMMPAPHMGGPPMPMPMPPPPGMPPVGPAPGMRP PMSGEMPMMPGPPMMRPPPPGMMPVGPAPGMRP PMSGEMPMMPGPPMMRPPPARSMVPTIROMTPPDR 6196 1512 623 KTGKRSAAYVRNILDNASQVISMLERRNIGSPLTPLLQBEDSH QRILMGIMVSEK,DHFLENLGGVKIKE,DMILDTISKLLDLIC HIVETNMKKEINLHSWVLHFNSRGSAARFAVFHIMTRIEATNSI, FLEPLPPGFMTLHTILGVQCLPLHNILHCIDGSVLLLTETTAVIRL MKDLADNTERNBELK,RESIIVRLPPLLGGKICRLMDHPMSNNISS NHVTRLLQNNYKKQPRNSMINKSSPSVEFLPIMYFIEILTDIESS NQALYPPEGGIDMYDABPVERAALMTALLGGL  6197 3 619 ADPEGTEZAVMSRYTRPENTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLLDFYTRREGGFAZVQFEDVRDAEDALNILMRKWVCG RQIKIGPAQGDRTFCQOKSKERNDSSDNHRRSSPSQRTTRS RSSWGRNRRSDSLKESRHRFFSYEGSKSGRSSLPRSTSARQ SRTYRRN*GSRGRSRSKSLQRSKSICPRSTSARQ SRTYRRN*GSRGRSRSKSLQRSKSICPRSTSARQ SRTYRRN*GSRGRSRSKSLQRSKSICPRSTSARQ SRTYRRN*GSRGRSRSKSLQRSKSICPRSTSARQ SRTYRRN*GSRGRSRSKSLQRSKSICPRSTSARQ SRTYRRN*GSRGRSRSCSLPRSTVTNSSLCLPAASQTL LACULWFSCYGHIRUGNATHLUSSLLTLLKQLEFTAMLOSGTW GVPSLLLVFLSGGLVLVTTLWHILLRTPRPFPTPLPPDRORGSV SRQPSPTYSEMMEKIEDDPLLDDPYPTPPPDROMIX KPEADP SRQPSPTYSEMMEKIEDDPLLSVSTLANDINGR SRQPSPTYSEMMEKIEDDPPLLSSYLMANTIRG VGGEKVYIATQGPIVSTVADPWRMUWQRHTPIIVATINISRMM KKCTEVMPBEQVAYDGWSITVQKVIHTHDSYRRLISLKSGTEER GLKHYWFTSSPDQKTLPRDAPPLLLHUREWERAAQGGGPHCAPII VHCSAGIGRTGCTIATSICCQOLROBGVVDLIKTTCQLRQDRGG GLKHYWFTSSPDGNYLVFRADAPSEVVLAREKA				
PRADDRONTBARKUDOPELVASFSIRVRIMSPDRIKITPPPPG RCSNHLODKIQKLYBRIKKEMDMYNIJORKKEPRNPSIYEKLI OPCAIDELGTNYPKOMPPPHOWERDSYYRALAKAQKIEMDKLEK AKKERTEIBFYTGTKKGTTTMATSTTTTTASTAVADAQKRSKM DSAIPYTIIAQPTILITTATLPAVUTYTTASGSKTTVISAVGT IVKKAKQ  6195 736 235 VANGLQSIMPKPYCDYGUTYLITHDSPSVRKTHCSGRRHKENVKD YYOKWMBEDAQSI,DKTTAAPOQOKIPPTPFSAPPPAGAMTPPP PSLPGPPRPOMMPAPHMGPPMMMGPPPMMMPPPAGAMTPPP PSLPGPPRPOMMPAPHMGPPMMMGPPPMMMPVGPAPGMRP PMGGHMMMPQPMMPPRARMMVPTREOMITPLUQEEDSH CRILMGLMVSELKDHPLRHLGVVEKKKIEGMULDYISKLIDLIC HIVETINMKEINLESWULHFNSRGSAAFEAVFHIMTRILLGATINSL FLPLPPOPHTLHITILGVCLPLINLLHCIDSGVLLLTETAVIRL MKOLDNTEKNSKLKESIJVRLPPLIGGKICRIMDHPMSNIISK NHUTRILLONYKKOPRINSMINGSSYVEFLDIMYPTEILTDIESS NQALYPPEGHDNVDAEFVERAALKHTAMLIGL 6197 3 619 ADPEGTERAVMGRYTRPRITSLETIRNVADATREPDIRREFGRYG PIVDVIJLDHYTRGPRGFAVVEPDVDAEDALINLANKKWCG RQIEJGAQQDIKTPQOMSERRRPSYSQSKGRSKSLPRRSTSARQ SRTPRRNFSGRGRSKSLORESKSIGKSGSSSPQKOTSSGTKS RSSWGENRRRDSLKESRHRPSYSQSKGRSKSLPRRSTSARQ SRTPRRNFSGRGRSKSLORESKSIGKSGSSSPQKOTSSGTKS RSHGRHSDSILRSPCKSPRGYTNFETKVQTAKHSHFRSHSRSS YRHKN9W SRAPENFSGRGRSKSLORESKSIGKSGSSSPQKOTSSGTKS RSHGRHSDSILRSPCKSPRGYTNFETKVQTAKHSHFRSHSRSS YRHKN9W 6198 111 1912 SEAALSFSFTSPACYLLRKLPALEDGTLPHPUTLGMNYEGARSE RENNHADDESGGALDMCCSSRLPGLOPGIVMRALDEAGGLOGG RMPPPPPPSPPSPAPPAQRAYDRGSHITVRSSLCLFAASOPT, LACGVLMFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHILLRTPREPPTPLPPEDRRGSV SRQPSFTYSEMMBERLEDDFILLDPYPTPTPPPDRRGSV SRQPSFTYSEMMBERLEDDFILLDPYPTPTPPPPDRRGSV SRQPSFTYSEMMBERLEDDFILLDPYPTPTPPPPPRPRSS AREYLLSASRVLQABEHHEKALDPFILQAEFFILMNING GGEKVYIATIGPPVSTVADFWRMWQRSTFILVKININIEMM EKCTEYMPEGVANDENSTYQKVIHTEDYRLKLISLKSGTEER GLKHYWFTSMPDQKTPDRAPPLLHUREWERAAQOEGHCAPII VHCSAGIGPTGCFIATSICCQOLROBGVVDILKTTCQLRQDRGG GLKHYWFTSMPDQKTPDRAPPLHURBEWRAUGEFFILAWTINGLKSGTEER GLKHYWFTSMPDGKTPDRAPPLHURBEWRAUGEFFILAMYIRG GLKHYWFTSMPDGKTPDRAPPLHURBEWRAUGEFFILAMYIRG GLKHYWFTSMPDGKTPDRAPPLHURBEWRAUGEFFILMNINGR	6194	3	950	
RCSHHLQDKIQKLYBRIKERMMNYI IORKREPRN9SIYEKLI  QPCAIDELGTNYPKIMPDHSSEDSYYBALARAQKIEMDKLEK AKKERTEIEVTGTKKGTTTMATSTTTTTHSTAVADAQKRESKM DSAIPVTITAQPTILITTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKQ  6195 736 235 VANGLQSMMPKPYCDYCDTYLTHDSPSVRRTHCGGRKHKENVKD YYQKWHSEQAQGSLIDKTTARPQOKIPPTPSAPPPAGAMTPPP PSLEGPREGMMPAHMGGPPWMPWMSPPPAGAMTPPP PSLEGPREGMMPAHMGGPPWMPWMSPPPAGAMTPPDR 6196 1512 623 KTGKRESAAYVENILDNAEQVISNLEARMIGPRITPLIQEEDSH QRILMGIMVSEKUDHFLRHLQGVEKKIERMIJDTISKLDLIC HIVSTNURKHNILSSWLHFINSGSARFAVFHIMTRILEATNSL FLPLPDPPPHTHETILGVQCLPLHALGTDSVGLILTTATNSL HIVSTNURKHNILSSWLHFINSGSARFAVFHIMTRILEATNSL HIVSTNURKERILGVQCLPLHALGTDSVGLILTTATNISL MKDLDNTEKNEKLKPSIIVRLPPLIQQKICRLMDHPMSSNIISR NHVTRLLQNYKQPRNSMINKSSFSVEFDJHYFIEILTTDIESS WQALYPPEGHDWYDABFPHAHATMLIGL 6197 3 819 ADPESTERAVMSRYTRPENTSLETERNADATTPENTLREFGRYG PIVDVYIPLDPYTRRPRGFAYVQFBUVADADALYNLNKWYCC RGILGPAQGDRRTPCQMKSKERPCSPSDHRRESSPSGRTER ESSMCENRRRSDSILKESHRRFSYSGUKERSKSLDRRSFSRS SRTPRRMSGRGRGSKSLORRSKSILGRSSSFSKPRRFSTSARG SRTPRRMSGRGRGSKSILGRSKSILGRSSSIGKSLGPRSSTSARG SRTPRRMSGRGRGSKSILGRSKSILGRSSSIGKSLGPRSSSSS KRHENTSSGRGLBKSSILGRSKSILGRSSIGKSLGPRSSSS KRHENSM 6198 111 1912 SEAALSFSFTSPACFILKKLPALEDGTLPHDTILGMYBGARSE RENHAADDSEGGALDMCCSBRLFGLPQP IVMRALDEARGLQDSQ RRMPPPPPPPSPSDPAQKPPPRGASSILTVRSSLCLFAASQPL LACGVLMFSGYGRINGGSWATMLVSSLLTLLKQLEFTAMLDSGTW GVPSLLLVFLSGGLVLVTTLVWHILKFPPEPPPPLPPPDRFRGSV SRQPSFTYSEMMBERIEDDPPLLSSTLTVRSLCLFAASQPL LACGVLMFSGYGRINGGSWATMLVSSLLTLLKQLEFTAMLDSGTW GVPSLLLVFLSGGLVLVTTLWHILKFPPEPPPPLPPPDRFRGSV SRQPSFTYSEMMBERIEDDPPLLSSTLTVRSPCDVLKFRBSS AREVLSSGSWYLGARELHEKALDPFILQAEFFRIMMFVDFKEY DIPGLUVKNYKKTILPPHERVCLTALAPEPPPPLPPPPDRFRGSV SRQPSFTYSEMMBERIEDDPPLLSSTLANDTRG GGERKYIANTGGPTVSTVAAPFWRWWQRHTPILVALTINIEMM EKCTEVWPERQVAYDGEITVQKVIHTEDYFLRLISLKSGTEER GLKHYWFTSWPDGKYTDPAPPLLHLURBWERAAQGGFHCAPII VHCSAGIGFTGCFIATSICCQOLROGGVVDILKTTCQURGG MQHCBQYQFVHWMSLYKRQLSHQSFB MQHCBGYGFFWFWFRSSSSSWWLGAEDIKKIFFFKETLGFGAFSEVVLAREKA				
OPCAIDBLIGTNYPROMEDHIGHSENSYMALAKAQKIEMMUKLEK AKKERTKIEFYTGTKRGTTINATSTTTTTASTAVADAQKREKM DSAIPYTTIAQPTILITTATLPAVVTVTTSASGEKTTVISAVGT TVKKAKQ  6195 736 235 VANGLQSNMPKYCDYCDTYLTHDSPSVRKTHCGGRKHKENVKO YYQKMMBQAQSI.DKTTAAPQOGKIPPTPSAPPPAGAMIPPP PSLDGPPREGMMPAPHINGGPPMMPMUPPPROMMPVGPAPCMRP PMGGMMMMRQDPPMMPPAPHINGPPPROMMPVGPAPCMRP PMGGMMMMRQDPPMMPPAPHINGPPPROMMPVGPAPCMRP PMGGMMMMRQDPPMMPPAPHINGPPPROMMPVGPAPCMRP ORLIMGIMUSELKOHPLIRILQCVEKKLEQWILDYIESLLDLIC HIVBTINNEKINILSWULHPINSRGSAAPFAVFHIMTRILBATISL HIVBTINNEKINILSWULHPINSRGSAAPFAVFHIMTRILBATISL HIVBTINNEKINILSWULHPINSRGSAAPFAVFHIMTRILBATISL HIVBTILQNIKKGPRSMITINSSFSVEFLIPLIYFIEILITDIESS NQALYPPEGHINVDAEPVERAALKHTAMILGI.  6197 3 619 ADPEGTESAVMSRYTRPPRWTSLFIRIVADATRPROLRREFGRYG PIVDVYIPLDPYTRRPRGFAYQPEDVRDARBALYNILMRKWVCG RQIKHQFAQGDRTTPCQMKSKRRHDCSPSDHRRSBSPSORRTRS RSSWGRNRRSDSLKESSHRPFSYSQEKSSKSLPRSTSTARQ RSTYRRMFGSRGREKSKSLQKRSKIGKSQSSSPQKTTSS RSHGRHSDSIARSPCKSPRGYTNFETKVQTAKHSHFRSHSRSRS RSHGRHSDSIARSPCKSPRGYTNFETKVQTAKHSHFRSHSRSRS RSHGRHSDSIARSPCKSPRGYTNFETKVQTAKHSHFRSHSRSRS RSHGRHSDSIARSPCKSPRGYTNFETKVQTAKHSHFRSHSRSRS RHIRNSW  6198 111 1912 SEAALSPSFISPACFILRKLPALEDGTLPHPDTICMNYEGARSE RENHADDSESGALIMCCSBRLPGLPQFIVMFALDBAGTW GVPSLILLVFLSGGIVLVTTLVWHLLRTPPRPPTPLPPERRRGSV REMPPPPPPSPSPDSPDAQKPPPRESSCHSITVRSSLCLFAASQFI LACGVLWFSGYGHIWSQNATNIVSSLCLFLASGEFTKMPRESS AREYLLSASRVLQABELHEKALDPFLLQAEPFREIPMNFVDPKEY JEPGLVRRNYKTTLENPRISRVCLTSPPDDDDPLSSYINANYIRG YGGEKVYIATQGPIVSTVADPWRWWQBTFIIVMTINTBEMM EKCTEYWPEBQVAYDGVEITVQKVHTEDYRLRLISLKSGFERF GLKHYWFTSWPDQKTDDRAPPLLHLVRVERRAQQGGFHCAPII VHCSAGIGRTGCFIASICCQQLRGGGVUDLKTTCQLRQDRGG KHYWFTSWPDQKTDDRAPPLLHLVRVERRAQQGGFHCAPII VHCSAGIGRTGCFIASICCQQLRGGGVUDLKTTCQLRQDRGG HIQHEGQYQPVHHWMSLYKRQLSRGSPE MIQHEGQYQPVHWMSLYKRQLSRGSPE 6199 144 1211 MARENGESSSSWKKAREDKRIFEKSTIGTGAPSEVVLAEERA				
AKKERTKIEFYTGYKKGTTINATSTTTTASTAVADAQKERSKM DSAIPYTIIAQPTILITTATLPAVVTVTYSAGSKTYTSAVGT TVKKAKQ  6195 736 235 VANGLQSMMPKPYCDYCDTYLTHDSPSVRKTHCSGRKHKENVKO YYQKMMERAQGSLIDKTTAAFQOGKIPPTPFSAPPPAGAMIPPP PSLEGPPROMMPAPHINGGPPMMPMMGPPPRGMPVCPAPCMRP PMGGHMPMMPGPPMMPPPRGMPVCPAPCMRP PMGGHMPMMPGPPMMPPPRGMPPVGPAPCMRP PMGGHMPMMPGPPMMPPPRGMPPVGPAPCMRP PMGGHMPMMPGPPMMPPPRAMPPPR 6196 1512 623 KTGKRRSAVVRNILDNAEQVISNLEARNISPRITPLIQUEDSH CRILMGIMVSELKDHFILRIQCVEKKKIEQWIDYISKLLDLIC HIVSTNWRKINLISWULHFNSKSSAAEPAVFHIMTRILEATNSL FILPPPGPHTIHTILGVQCLPLHNILHCIDSGVLLITEATVIRL MKOLDNTEKNEKKKFSILVRLPPLIGGKICRLMDHPMSSNIISK NHVTRLLQNYKKQPRSSMINKSSFSVEFIPINYFIELITDIESS NQALYPPEGHDNVDAEFVERAALKHTAMLLGL  6197 3 819 ADPEGTERAVMSKYTEPPHTSELFIRNVADARTPRDLRREFGRYG PIVDVYIPLDFYTRRERGFAYVQFRUNDAEDALYNLINKKWCG RQIEIQFAQGDRETPCQMKSKERHPSSVEGEKSKESEPSQRTRS RSSSGRNRRRSDSLESSHRFPSVEGEKSKESEPSDRRTSSR RSSSGRNRRRSDSLESSHRFPSVEGEKSKESLPRSTSARQ SRTYRRMFGSRGRSRSKSLQRESGSSCRKGKSSPSDRKOTSSGTKS RSHGRHSDBIARSPCKSPRGYTNPETKVQTAKHSHFRSHSRSR SRHGRHSDBIARSPCKSPRGYTNPETKVQTAKHSHFRSHSRSR KRHKINSW  6198 111 1912 SEAALSFSFISPACFLIRKLPALEGTTJPPDTILGNVEGARSE REMIHADDSEGGALDMCCSBRLPGGLPDFULGABEGLDGSQ REMPPPPPSPSPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGULMFSGGGLVLVTTJUHFLRTPPPPTFIPPEPRRQSV SRQPSFTYSEMMEKLEDDFULDLDFVPBTPVPCCVMDIKPEADP TSILTVESMGLQERRGSNUSLTLDMCTPGCURSGGGYLMSPRBSS AREYLLSASRVLQABELHEKALPLLQEETTLPMPVDPKEY GGGEKVYIATQGPIVSTVADDWRNWGGRTFILTVMTTNIEDMN EKCTEVMPERQVAPWGBETTUGVKTHTDVHLRILIGLKSGFER GLKHYWFTSWPDQKTPDRAPFLLHLVREVEBAAQQEGPHCAPII WHCSAGIGRTGCFIATSICCQQLRGGGVDLLKTTCQLRQDRGG GLKHYWFTSWPDQKTPDRAPFLLHLVREVEBAAQQEGPHCAPII WHCSAGIGRTGCFIATSICCQQLRGGGVDLLKTTCQLRQDRGG MIQHEGQYQFVHHWSLYERQLSHQSSPE			ļ	
DSAIPVTIAQPTILTTATLPAVUTVTTSASGSKTTVISAVGT TUKKAKQ  1 VANGLQSIMPKPYCDYCDTYLTHDSPSVRKTHCSGRRHKENVKD YYQKMMBQAQSLIDKITAAPQQGKIPPTPFSAPPPAGAMIPPP PSLEGPPRGMMPAPHMG9PPMMPPPMMPPPPGMPPPGMPVGPAPGMP PSLEGPPRGMMPAPHMG9PPMMPPPMMPPPPGMPPPGAPAPMMPP PSLEGPPRGMMPAPHMG9PPMMPPPMMPPPPGMPPGAPAPMMPP 6196  1512 623 KTGKRSSAYVRNILDBAEQVISHLBARNISPRLTPLLQBEDSH KTGKRSSAYVRNILDBAEQVISHLBARNISPRLTPLLQBEDSH MKDLDNTEKNEKKHSILVHPNSRGSAARFAVPHIMTRILGATINSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTBTAVIRL MKDLDNTEKNEKKKFSILVHPLLGQKICLMDHPMSSNILSR MKDLDNTEKNEKKKFSILVHPLLGQKICLMDHPMSSNILSR NHVTRLLQNYKKQPRNSMINKSSPSVEFLPLNYPFIELITDIESS MQALYPPEGHDNVDABFVERALKHTAMLLGL  6197 3 619 ADPSSTESAVMSKRIKTPSTSTELTRIVADATRPEDLEREFGRYG PIVDVYIPLDFYTRRPGFAYVQFEDVRDAEDALYNLNRKWVCG RQIELQPAQGDRKTTCQMKSKERHDCSPSDHRBSBSSGRRTBS SSWGRNRRSDSLRSSRIFRFSYSGG KERKSLPBRSTSARQ SRTPRRN-GGRGRSKSLQKESKSICKSQSSSPQKQTBSGTSS RSHGRHSDBIARSPCKSPKGTTHFETTVQTAKHSHFRSHSRSS YRHKNSW SRCHERSSDSLARSFCKSPKGTTHFETTVQTAKHSHFRSHSRSS YRHKNSW 1912 SEAALSPSFISPACFLLRKLPALEDGTLPHPDTIGMNYBGARSE REMPPPPPSPSPSPPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGULWSGGGHUNGCSSRLPGLPQLPQFUVMALDBAEGLQDSQ REMPPPPPSPSPSPPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGULWSGGGHUNGCSSRLPGLPQLPQLTWPHALDGGTW GVPSLLLVPLSGGLVLVTTLVWHLRTPPPPPTPLPPEDRRQSV SRQPSFTYSEMMBEKIEDDPLDLDPVPETVPPCVMDIKPEADP TS:TVPSMGLQERGSNSUTLDLDCTTGCNEEGFGTIMSPRBS ARBYLLSASRVLQABELHEKALDPFLLQAEFFRIPMMPVDPKEY DIPGLVRRNRYKTLEPRPBERVCLTSBDDDPLSSYINANYIRG YGGEKVYIATQGFIVSTVADPWMWWQRHTPILVAITNIENM EKCTEYWPESWPDQRYDGVSTVADPWMWWQRHTPILVAITNIENM EKCTEYWPESWPDQRTSPRAPPLLHLVREVERAAQGEGPHCAPII VHCSAGIGRTGCYIATSICCQQLRQGSWVDILKTTCQLRQGRG MQHCEQYQFVHVMSLYEKQLSQSPE				
TVKKAKQ  195 195 196 197 197 198 198 199 199 199 199 199 199 199 199	1			
6195 736 235 VANGLQSMMPKPYCDYCDTYLTHDSPSVRFTHCSGRRHKENVKD YYQKWMEBQAQSLIDKTTAAFQQGKLIPTFPSAPPPAGANIPPP PSLEOPPREGMMPAPHNGSPPPEGMPVGFAPCMRP PMGGHMPMMPQPPMMRPPPRGMPVGFAPCMRP PMGGHMPMMPQPPMMRPPARPMWVPTRPGMTRPDR 6196 1512 623 KTGKRESAAYVRNILDBAEQVISHLERARNISPRLTPLLQUEDSH RTGKRESAAYVRNILDBAEQVISHLERARNISPRLTPLLQUEDSH RTGKRESAAYVRNILDBAEQVISHLERARNISPRLTPLLQUEDSH RKIGHLSWLKHFISHRULDFYSHLERINGVYBEKKKIEGMVLDYISKLLDLIC HIVSTINREKINIHSWVLHFBSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVILLITETAVIRI, MKDILDNTEKNEKLKFSILVRLPPLIQQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVBFLPLNYYFIELITDIESS NQALYPPEGHINVDABEVERAALKHTAMLLGL ADPEGTEZAVMSKYTRPHTSLFIRNVADATRPBDLREFGRYG PIVDVYIPLDPYTRPREGFAYVQPEDVRDAEDALYNLINRKWVCG RQIELQPAQGDRKTPCGMKSKERPDCSPSDHRRSRSFSQRRTRS RSSWCRNRRRSDSLESSRHRRPSYSQSKSRGKSLPRRSTSARQ RSTYRRHSGSRGKRSKSLQARSKSLGKSGSSFPQKQTSSGTKS RSHGRHSDBIARSPCKSPKSTUKSGSSSFPQKQTSSGTKS RSHGRHSDBIARSPCKSPKSTUKSGSSSFPQKQTSSGTKS RSHGRHSDBIARSPCKSPKSTUKSGSSSFPQKQTSSGTKS RSHGRHSDBIARSPCKSPKSTUKSGLENGTHSGLAGG REMPPPPPPSPSPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGGIVLWSQNATHLVSSLLTLLKQLEPTAALDSGTW GVPSLLLVFSGGIVLWTTLVWHLLRTPPBPPTPLPPBCRQSV SRQPSFTYSEMMBEKIEDDFLDDLDPVBTFVPDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPRESS ARBYLLSASRVIQAELHERKLDPFLLQAEFFELPMNFVDPKEY DIPGLVRRNRYKTILPMPERRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQHTPIIVNTINIEMN EKCTTEVPBPEQVADGWEITTVQKVIHTEDVRLKLIGLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEBAAQQEGPHCAPII VHCSAGIGRTGCTTATSICCQQLRQBGVVDILKTTCQLRQDRGG MIQHCGVQVPHHWMSLIKELGHGSPSE	1			
YYQKWMEBQAQSLIDKTTAAPQQGKIPPTPFSAPPPAGAMIPPP PSLSCPPREGMMPAGPPWMSGPPPKAMMYCGAPPAGAMIP PSLSCPPREGMMPAGPPWMSGPPPKAMMYCGAPPAGAMIP PMGGMPMMMQPPWMSPPPARMWVPTRPGMTRDR  6196 1512 623 KTGKRSAAYVRILDNAEQVISNLEARNLSPRLTPLLQEEDSH QRLLMGLMVSELKUHFLRHLGCVEKKLEQMVLDYLSKLLDLIC HIVBTNNKKRHLKHSWLKHSBGSAARFAVFHIMTILEATNSI, FLPLPPGPHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTKKNEKLKESLIVRLPPLLGQKLCRLMDHFMSSNIISR NHVTRLLQNYKKQPRASHNKSSFSVEPLIMYPTEILTIDESS NQALYPPEGHDNVDAEFVERAALKHTAMLLGL  6197 3 819 ADPESTESAVMSRYTRPDNTSLFIRNVADATRPBDLRREFGRYG PIVDVYIPLDFYTRRPGAYVGFBVNTDAEDALYNLRNKWVCG RQIBIQFAQGDRKTPCMKSKSRHDCSPSDHRRSRSPSQRRTRS RSSWGRNRRSDSLKESRHRRFSVQSKSRSKEFRRSTSARQ SRTWRNFGSRGRGRSKSLQKRSKSIGKSSSSPQKOTSSGTKS RSHGRHSDSIARSPCKSRKGJSRSFLGKSSSSPQKOTSSGTKS RSHGRHSDSIARSPCKSRKGTTNFETKVQTAKHSHFRSHSSRS YRHKNISW  6198 111 1912 SEAALSPSTISPACFILRKLPALEDGTLPHPDTLCMNYEGARSE RENHAADDSEGGALDMCCSKRLPGLPGPIVMRALDEAEGLQDSQ RKMPPPPPSPPSDPAQKPPPRGASSHSLTVRSSLCLFAASQVI, LACGVLWFSGYCHIWSQNATNLVSSLLITLLKQLEPTAWLDGGTW GVPSLLLVFLSGGIVLVTTLWHLLKTPPRPTPUPP PEDRRGSV SRQPSPTYSEMMBEKIEDDFLDLDPVPSTPVFDCVMDIKPBADP TSLTVKSMGLQERGGSNVSLTLDMCTPGCNEEGFGYLMSPRESS AREVILLSASRVLQARELHEKALDPFILQAEFFEIPMNFVDPKSY DIPGLVRKNYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG RGGEKYTAATQGPIVSTVADFWRWWQEHTPIIVMITNIEMN EKCTFYMPEGEQVATOGSTTVQKVIHTEDYRIRLLELKSGTERR GLKHYWFTSWPDQKTPDRAPPLLHLVREVBEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRGGGVVDILKTTCQLRQDRGG MIQHCBQVQFVHHWNSLVEKQLSHQSPE 6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAREKA	6195	736	235	
PSLPGPPRFGMPAPHMGGPPMMPMGPPPGMRPVGPAPGMRP PMGGHMPMMGQPPMMPMRPARPMMPVTRCMTRPDR 6196 1512 623 KTGKRSASAVVENILIANDAGVISNILARNKISPRITPLLQEEDSR QRLLMGLMVSELKDHFLRHLQEVEKKKIEQMVLDYISKLLDLIC HIVSTINWEKHNILKSWLHFNSRGSABFAVFHIMTRILBATNSL FLPLPPGPHTLHTILGVQLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNERLKFSILVRLPPLLTQKICRLMDHFMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLHYYFIEILTDIESS NQALYPFEGHDNVDAEFVERAALKHTAMLLGL 6197 3 819 ADPESTEEAVMSRYTTPPNTSLFIENVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFBUVRDAEDALYNLINKRWCCS RQIEIQFAQGDRKTFCQMKSKRHHCSPSDHRRSRSPSQRRTRS RSSWCHMRRSPSSLKESFHRPFSVEGGKSRGKSLFRFSTSARG SRTPRNFGSRGGRSKSLQKSKSGGKSKSFRSSPSRTRS SRYRKNSWS RSHGRHSDSIARSPCKSPRGTTNFETKVQTAKHSHFRSHSRSS YRHKNSW 6198 111 1912 SEAALSPSFISPACFLLKKLPALEDGTLPHPDTLCMNYHGARSE RENHAADDSEGGALDMCCSBRLPGIPQPTVMRALDEAEGLQDSQ REMPPPPPPSPDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYCHLWSQMATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPBPPTPLPPEDRRQSV SRQPSFTYSEMMBEKIEDDFILDDPVPETTYPTCVWDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGGCMESGFGTLMSFRESS AREYLLSASRVIQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRRNYKTILPNPBSRVCLTSPDPDDPLSSVINANYIRG YGGEKVYIATGGPIVSTVADFWRWWQEHTPIIVMITNIEMN EKCTTYWPECQVAYDGVSITTVQKVIHTEDYRRLESLKSGTERR GLKHYWFTSWPDQKTPDRAPPLLHLVREVBEAAQQEGPHCAPII VHCSAGIGRTCCFIATSICCQQLRGGGVVDLLKTTCQLRQDRGG MIQHCBQVGVYHHWMSLVKKQLSHQSPS	1 0175	750	1 233	
FMGGHMPMMPQPPMMRPPARPMMVPTRPGMTRPDR  6196  1512  623  KTGKRRSAAYVINILDNABGUJISMLEARNILSPRLTPLIQEEDSH QRLLMGLMVSELKDHPLRHLQGVEKKKLEQMULDYISKLLDLIC HIVSTIMKRGHILSWULHFNISGSAAFFAUFHIMTRILEATINSL FLPLPPGPHTLHTILGVQCLPLINILHCIDGSULLLTBTAVIRL MKOLDNTEKNBRLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRISMINKSSFSVEFLPLNYPIEILTDIESS NQALYPPEGHDNVDAEFVBEAALKHTAMLLGL  6197  3  819  ADPESTESAVMSRYTRPPHTSELTIRNVADATRPBDLREEFGRYG RQIEIQFAQGDRRTPCOMKSKRHDCSPSDHRRERSPSGRRTBS RSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ RQIEIQFAQGDRRTPCOMKSKRHDCSPSDHRRERSPSGRRTBS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTYRRN-GSSRGSRSKSLQKRSKSIGKSGSSPQKQTBSGTKS RSHGRHSDBIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS SRTHRHNSW  6198  111  1912  SRAALSPSFISPACFILRKLPALEDGTLPHPUTLGMNYKGARSE RENHAADDSEGGALDMCCSERLPGLPQP IVMEALDEAEGLQDSQ REMPPPPPSPSPDPADAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHILKTPPRPPTPLPPEDRRGSV SRQPSFTYSEWMBEKIEDDFLDLDPVPETPVFDCVMDIKPEADP TSJTVKSMGLQERRGSNVSLTLDMCTFGCNEEGFGYLMSPRRSS ARBYLLSASRVLQARELHEKALDPFLLQAEFFEIPMNYVDPKRY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDFLSSYINANYIRG GGEKVYITATGGPIVSTVADFWRWQBRTPIIVMTTNIEBMN EKCTEYWPEEQVAYDGVBITVQKVIHTEDYRLRLISLKSGTEER GLKHWFTSWPDQKTPDRAPPLLHLVREVERAAQOEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQBGVVDILKTTCQLRQDRGG MIQHCGQTQFVHHWMSLYKKQLSHQSPB	ł			
QRLLMGLMVSELKDHPLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVBTNMRKHINLHSWULHPNISRGSAABFAVFHINTRILEATINSL FLPLPPGPHTLHTILGVQCLPLHNLHCTDSGVLLLTBTAVIRL MKDLDNTEKNEKLKFSIIVRLPPLLGQKICRLWDHPMSSNIISR NHVTRLLQMYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDABFVERAALKHTAMLLGL 6197 3 619 ADPEGTEEAVMSRYTRPPNTSLFIENVADATRPEDLRREFGRYG PIVDVYIPLDFYTRPREGFAVVQFEDVRDAEDALYNLNRKWVCG RQIBIQFAQGDRTPCQMKSKERHPCSPSDHRRSRSPSGRRTES RSSWGRNRFGSRGKSLQKRSKSIGKSGSSSPQKOTBSGTTSS RSHGRHSDBIARSPCKSPKGYTNYETKVQTAKHSHFRSHSRSS YRHKNSW 6198 111 1912 SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSB RSHGRHSDBIARSPCKSPKGYTNYETKVQTAKHSHFRSHSRSS YRHKNSW 6198 111 1912 SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSB RSHGRHSDBIARSPCKSPKGYTNYETKVQTAKHSHFRSHSRSS YRHKNSW 6198 111 1912 SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSB REMPPPPPSPSPSDPAQKDPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFGSVGHIWSQNATNIVSSLITLLKQLEPTAMLDSGTW GVPSLLLVFGSGLVLVYTLVWHLLRTPPRPPPTPLPPEDRRQSV SRQPBFTYSEWMBEKISDDPLDLDPVPETTPPDCPMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEGFGYLMSPRESS ARBYLLSASRVLQABELHEKALDPFILQABFFRIPMNVDPKSY DIPGLVRKNYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADPWRNWQRHTPIIVMITNIERMN EKCTEYWPEEQVAYDGVETTVQKVIHTEDYRLRLISLKSGTEER GLKHWFTSWPDQKTPDRAPPLLHLVRBVBEAAQQGGPHCAPII VHCSAGIGRTGPIATSICCQQLRQEGVVDLKTTCQLRQDRGG MIQHCEGYQQFVHHWMSLYEKQLSHQSPE				· ·
QRLLMGLMVSELKDHPLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVBTNMRKHINLHSWULHPNISRGSAABFAVFHINTRILEATINSL FLPLPPGPHTLHTILGVQCLPLHNLHCTDSGVLLLTBTAVIRL MKDLDNTEKNEKLKFSIIVRLPPLLGQKICRLWDHPMSSNIISR NHVTRLLQMYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDABFVERAALKHTAMLLGL 6197 3 619 ADPEGTEEAVMSRYTRPPNTSLFIENVADATRPEDLRREFGRYG PIVDVYIPLDFYTRPREGFAVVQFEDVRDAEDALYNLNRKWVCG RQIBIQFAQGDRTPCQMKSKERHPCSPSDHRRSRSPSGRRTES RSSWGRNRFGSRGKSLQKRSKSIGKSGSSSPQKOTBSGTTSS RSHGRHSDBIARSPCKSPKGYTNYETKVQTAKHSHFRSHSRSS YRHKNSW 6198 111 1912 SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSB RSHGRHSDBIARSPCKSPKGYTNYETKVQTAKHSHFRSHSRSS YRHKNSW 6198 111 1912 SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSB RSHGRHSDBIARSPCKSPKGYTNYETKVQTAKHSHFRSHSRSS YRHKNSW 6198 111 1912 SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSB REMPPPPPSPSPSDPAQKDPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFGSVGHIWSQNATNIVSSLITLLKQLEPTAMLDSGTW GVPSLLLVFGSGLVLVYTLVWHLLRTPPRPPPTPLPPEDRRQSV SRQPBFTYSEWMBEKISDDPLDLDPVPETTPPDCPMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEGFGYLMSPRESS ARBYLLSASRVLQABELHEKALDPFILQABFFRIPMNVDPKSY DIPGLVRKNYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADPWRNWQRHTPIIVMITNIERMN EKCTEYWPEEQVAYDGVETTVQKVIHTEDYRLRLISLKSGTEER GLKHWFTSWPDQKTPDRAPPLLHLVRBVBEAAQQGGPHCAPII VHCSAGIGRTGPIATSICCQQLRQEGVVDLKTTCQLRQDRGG MIQHCEGYQQFVHHWMSLYEKQLSHQSPE	6196	1512	623	KTGKRRSAAYVRNILDNAEQVISNLEARNLSPRLTPLLQEEDSH
FIPLPPGPHTIHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKOLDNTEKNEKLKFSIIVRLPPLIGGKICRLMDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILITDIESS NQALVPFEGIDNYDAEFVERAALKHTAMILGL  6197 3 819 ADPEGTESAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIBIQFAQGDRITPCQMKSKERHDCSPSDHRRERSPSQRRTRS RSSGCRNRRRSDGLKESRHRRFSYGGEKGRSLPRRSTSARQ SRTPRRNFGSRGRGRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDBAEGLQDSQ REMPPPPPSPPSDPSDPAQKPPPRGAGSHSLTVRSSLCLFAASGFL LACGVLWFSGYGHIWSQNATNLVSSLITLLKQLEPTAWLDGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPRPPPPPLPEDRRGSV SRQPSFTYSEWMBEKIEDDFLDLDPVPETPVPCVMDIKPBADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNESGFGYLMSPRBES ARBYLLSASRVIQABELHEKALDPFLLQAEFFEIPMNFVDPKRY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG WGGEKVYIATQGFIVSTVADFWRMVWQBHTPIIVMITNIBEMN EKCTEYWPBEQVAYDGVBITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLHLVRSVBRAAQQEGPHCAPII VHCSAGIGRTGCPIXTSCQQIRQEGVVDILKTTCQIRQDRGG MIQHCBQQVVPHWMSLVEKQLSHQSFE 6199 144 1211 MARENGESSSSWKKQAEDIKKIFFKETLGTGAFSEVVLAREKA				
MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRILQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGDDNVDAEFVERAALKHTAMLLGL ADPEGTESAVMSRYTRPPRTSLFIRNVADATRPEDLEREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPCQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWCBRRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRRNFGSRGSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW  111 1912 SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLCMNYBGARSE REMPPPPPSPSPDAPQKPPPRGASHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATMLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPRPPTPLPPEDRRQSV SRQPSFTYSEMMBEKIEDDFLDLDVPETPVDCVMDIKPBADP TSLTVKSMGLQERRGSNVSLTLDMCTFGCNEGFGYLMSPRRES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQRHTPIIVMITNIEMN EKCTEYWPEEQVAYDGVBITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVBBAAQQEGPHCAPII VHCSAGIGRTGCPIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCBGYQFVHHVMSLYERQLSHQSPE  6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAREKA			į	HIVBTNWRKHNLHSWVLHFNSRGSAARFAVFHIMTRILEATNSL
NHVTRLLQNYKKQPRNSMINKSSPSVEFLPLNYFIEILTDIESS NQALYPPEGHDNVDAEFVERAALKHTAMILGI.  6197 3 819 ADPEGTEEAVMSRYTRPPNTSLFIENVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQPEDVRDAEDALYNLNRKWVCG RQIBIQFAQGDRKTFGQMKSKERHPCSPSDHRRSRSFSQRRTRS RSSWCRNRRSDSLKESRHRRFSYEQSKSRSKSLPRRSTSARQ SRTPRRNFGSRGRSKSLQKRSKSIGKSQSSSPQKQTBSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNBW  6198 111 1912 SEAALSPSFTISPACFILRKLPALEDGTLPHPDTICMNYKGARSE REMHAADDSEGGALDMCCSRRLPGIPQPIVMFALDRAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPRPPTPLPPEDRRQSV SRQPSFTYSEWMBEKIEDDPLDLDPVPBTPVFDVDVDLKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTFGCNESGFGYLMSPRRES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRWWQRHTPLIVMITNIERMN EKCTEYWPEEQVAYUGVEBTVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEBAAQQEGPHCAPII VHCSAGIGRTGCPIATSICCQQLRQBGVVDILKTTCQLRQDRGG MIQHCBQYQFVHHVMSLYERQLSHQSPE  6199 144 1211 WARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAREKA	1			FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL
NQALYPPEGHDNVDAEFVERAALKHTAMLIGL  6197 3 819 ADPEGTEZAVMSRYTRPPNTSLFIRNVADATRPEDLEREFGRYG PIVDVYIPLDFYTREPRGFAYVQFEDVEDAEDALYNLINKWVCG RQIBIQFAQGDRKTPCQMKSKERHCSPSDHRRSRSPSQRRTRS RSSSWGENRRSDSLKESRHRFFSYSGSKSRSKSLPRRSTSARQ SRTPRRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQRQTBSGTKS RSHGRHSD8IARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW  6198 111 1912 SEAALSPSFTSPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSRRLPGLPQPIVMKALDRAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPRPPTPLPPEDRRQSV SRQYSFTYSEWMBEKIEDPLDLDPVPETPVPVCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPRESS ARBYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRWWQRHTPIIVMITNIERMN EKCTEYWPEEQVAYDGAVBITVQKVIHTEDVRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVBEAAQQEGPHCAPII VHCSAGIGFTGCPIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCBQYQFVHHWMSLYEKQLSHQSPE  6199 144 1211 WARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAREKA	1			
6197 3 619 ADPEGTERAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRERGFAYVQFEDVRDAEDALYNLINKWVCG RQIRIQFAQGDRKTPGQMKSKERHPCSPSDHRERSEPSQRRTRS RSSWGRNRRSDSLKESRHRFSYSQSKSRGKSLPRRSTSARQ SRTPKRNFGSRGSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSD81ARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSS YRHKNSW  6198 111 1912 SEAALSPSTSPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHARDSDEGGALDMCCSERLPGLPQPIVMEALDRAEGLQDSQ REMPPPPPSSPSDPAQKPPRGASSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPBPPTPLPPEDRRGSV SRQPSFTYSEWMBEKIEDDFLDLDFVPETFVFDCVMDIKPEADP TSLTVKSMGLQERGSNVSLTLDMCTFGCNESGFGYLMSPRESS AREYLLSASRVLQAEELHEKALDPFLLQAFFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEMN EKCTFYWPEGQVAYDGVBITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVBBAAQQEGPHCAPII VHCSAGIGRTGCFYIATSICCQQLRQGGVVDILKTTCQLRQDRGG MIQHCBQYQFVHHWMSLYEKQLSHQSPE  6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAREKA				
PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIBIQFAQGDRKTFCQMKSKRRHPCSPSDHRRRSPSSQRTRS RSSWGRNRRSDSLKESRHRRFSYSQSKERSKSLPRRSTSARQ SRTPRRNFGSRGSRSKSLOKESKSLGKSQSSSPQKQTBSGTRS RSHGRHSDBIARSPCKSPKGYTNFETRVQTAKHSHFRSHSRSRS YRHKNSW  111 1912 SEAALSPSISPACFILLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDEGGALDMCCSBRLPGLPQFIVMFALDBAEGLQDSQ REMPPPPPSPSPPSDPAQKPPPRGASHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPRPPTPLPPEDRRQSV SRQPSFTYSEWMBEKIEDDFLDLDVPFTFVPDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNESGFGYLMSPRRES AREYLLSASRVLQAEBLHEKALDPFLLQAFFEIPMNFVDPKRY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRWVWQEHTPIIVMITNIEMN EKCTFYWPEGQVAYDGVBITVQKVIHTEDYBLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVBBAAQQEGPHCAPII VHCSAGIGRTGCFJIATSICCQQLRQBGVVDILKTTCQLRQDRGG MIQHCBQYQFVHHWMSLYEKQLSHQSPE  6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAREKA			<u> </u>	
RQIBIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSMCBNRRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRRNFGSRGRSRSKQKRSKSIGKSQSSSPQKQTBSGTKS RSHGRHSD8IARSPCKSPKGYTNFBTKVQTAKHSHFRSHSRSRS YRHKNSW  111 1912 SEAALSPSFISPACFILRKLPALEDGTLPHPDTICMNYBGARSE RENHAADDSEGGALMCCSRRLPGHPQPIVMRALDERABGLQDSQ REMPPPPPSPPSDPAQKPPPRGASSHSLTVRSSLCLFAASQFL IACCULWFSGGGHIWSQNATMLVSSLLITLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPRPPTPLPPEDRRQSV SRQPSFTYSEWMBEKIEDDFLDLDPVPETPVPCVMDIKPBADP TSLTVKSMGLQERRGSNVSLTLDMCTFGCNESGFGYLMSPRESS AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQRHTPIIVMITNIEMN EKCTEYWPEQVAYDGVBITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVRBVBBAAQQEGPHCAPII VHCSAGIGRTGCPIATSICCQQLRQBGVVDILKTTCQLRQDRGG MIQHCBGYQFVHHWMSLYERQLSHQSPE  6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAREKA	6197	3	819	
RSSSWGRNRRSDSLKESRHRRFSYSQSKERSKSLPRRSTSARQ SRTPRNFGSRGRSRSKSLOKRSKSIGKSQSSSPQKQTBSGTKS RSHGRHSDBIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW  6198 111 1912 SEAALSPSFTSPACFILRKLPALEDGTLPHPDYTLGMNYBGARSE RENHAADDSEGGALDMCCSBRLPGLPQP IVMEALDBAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGULWFSGGALIWSQNATMLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTLVWHLLRTPPBPPPPPLPPDEDRQSV SRQPSFTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPBADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNESGFGYLMSPRRBS ARBYLLSASRVLQABELHEKALDPFLLQAEPFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEKRVIATQGPIVSTVADFWRWWQRHTPLIVMITNIEMN EKCTEYWPEDQVAYGBVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVBBAAQQEGPHCAPII VHCSAGIGRTGCPIATSICCQQLRQBGVVDILKTTCQLRQDRGG MIQHCBQYQFVHHVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAREKA	j			
SRTYRRNFGSRGSRSKSLQKRSKSIGKSQSSSPQKQTBSGTKS RSHGRHSD81ARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS XRHKNSW  6198  111  1912  SEAALSPSFTSPACFLLRKLPALEGTLPHPDTLGMNYEGARSE REMHAADDSEGGALDMCCSRRLPGLPQPTVMRALDRAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPRPPTPLPPEDRRQSV SRQPSFTYSEWMBEKLEDDPLDLDPVPETPVPVDCVMDLKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPRRES ARBYLLSASRVLQAERLHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRWWQRHTPIIVMITNIERMN EKCTEYWPEEQVAYDGAVBITVQKVIHTEDYKLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVBBAAQQEGPHCAPII VHCSAGIGRTGCPIATSICCQQLRQEGVVDLKTTCQLRQDRGG MIQHCBQYQFVHHWMSLYEKQLSHQSPE  6199  144  1211  MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAREKA				
RSHGRHSD81ARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW  111  1912  SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEABGLQDSQ REMPPPPPPSPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPBPPTPLPPEDRRGSV SRQPSFTYSEWMBEKIEDDFLDLDPVPETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTFGCNESGFGYLMSPRESS AREYLLSASRVLQAEELHEKALDPFLLQAFFFEIPMNYDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN EKCTFYWPEGQVAYDGVBITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPGPPLTHLVREVBEAAQQEGPHCAPII VHCSAGIGRTGCPIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCBQYQFVHHWMSLYEKQLSHQSPE  6199  144  1211  MARENGESSSSWKKQAEDIKKIFFFKETLGTGAFSEVVLAREKA				
TRHKNSW  111  1912  SEAALSPSTISPACFILIRKLPALEDGTLPHPDTICMNYRGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDBAEGLQDSG REMPPPPPSPPSDPAQKDPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATMLVSSLLITLLXQLEPTAWLDEGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPRPPTPLPPEDRRQSV SRQPSFTYSEMMBEKIEDDFLDLDVPFTPVPCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEGFGYLMSPRRES ARBYLLSASRVLQARELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYLRG YGGEEKVYIATQGPIVSTVADFWRMVWQRHTPIIVMITMIEMN EKCTEYWPEEQVAYDGVBITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVRBVBBAAQQEGPHCAPII VHCSAGIGRTGCPIATSICCQQLRQEGVVDLKTTCQLRQDRGG MIQHCBGYQFVHHWMSLYEKQLSHQSPE  6199  144  1211  MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAREKA			Į.	
6198 111 1912 SEAALSPSTISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQP IVMEALDEAEGLQDSQ REMPPPPPPSPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFGYGHLWSQNATNLVSSLLITLLKQLEPTAWLDSGTM GVPSLLLVFLSGGLVLVTTLVWHLLRTPPRPPPTPLPPEDRRQSV SRQPSFTYSEMBEKIEDDPLDLDPVPETTVPDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES ARBYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQRHTPIIVMITNIEMM EKCTEYWPEEQVAYDGVBITVQKVIHTEDYRLKLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEBAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCBQYQFVHHVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAREKA			!	P and the second
RENHAADDSEGGALDMCCSERLPGLPQP IVMEALDEAEGLQDSQ REMPPPPPPSPSDPAQKPPPRGAGSHSLTTRSSLCLFAASQFL IACGVLWFSGYGHIWSQNAYMLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPRPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	6198	111	1912	
REMPPPPPPSDPAQKPPPRAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPRPPTPLPPEDRRQSV SRQPSFTYSEWMBEKIEDDPLDLDPVPBTPVFDVDVDLKPBADP TSLTVKSMGLQERRGSNVSLTLDMCTFGCNESGFGYLMSPRRES ARBYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRWWQBHTPLIVMITNIEFMN EKCTFYWPEQVAYUGVJETVQKVIHTEDYRLLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVBBAQQEGPHCAPII VHCSAGIGFTGCPIATSICCQQLRQBGVVDLKTTCQLRQDRGG MIQHCBQYQFVHHVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAREKA	32,90	-44	1	
LACGULWFSGYGHIWSQNATNLVSSLITLLKQLEPTAWLDSGTW GVPSLILVFLSGGLVILVTLVWHLLKTPPBPPTPLPPEDRRGSV SRQPSFTIYSEWMBEKIEDDFLDLDPPETPVFDCVMDIKPEADP TSLTVKSMGLQERGSNVSLTLDMCTFGCNESGFGYLMSPREBS ARBYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEMN EKCTEYWPEEQVAYDGVBITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVBBAAQQEGPHCAPII VHCSAGIGRTGCFJIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCSQYQFVHHWMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGYGAFSEVVLAEEKA				
GVPSLLLVFLSGGLVLVTTLVWHLLRTPPRPPTPLPPEDRRQSV SRQPSFTYSEWMBEKIEDDFLDLDVPSTPVPDCVMDIKPBADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQABELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYLRG YGGEEKVYIATQGPIVSTVADFWRMVWQRHTPIIVMITNIBEMN EKCTEYWPEEQVAYDGVBITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVBBAAQQEGPHCAPII VHCSAGIGRTGCPIATSICCQQLRQEGVVDLKKTCQLRQDRGG MIQHCBQYQFVHHVMSLYEKQLSHQSFE 6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGYGAFSEVVLAREKA			1	
SRQPSFTYSEWMBEKIEDDPLDLDPVPETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREBS ARBYLLSASRVLQAEBLHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPMPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRNVWQRHTPIIVMITNIEMN EKCTEYWPPEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWPTSWPDQKTPDRAPPLLHLVREVBERAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQBGVVDLLKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA	]			
TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES ARBYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYLRG YGGEEKVYIATGGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVBITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWDPQKTPDRAPPLLHLVREVEBAAQQEGPHCAPII VHCSAGIGRTCCFIATSICCQQLRQBGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA	1		<b>!</b>	
ARBYLLSASRVIQABELHEKALDPFILQAEPFRIPMNFVDPKEY DIPGLVRKNRYKTILENPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQRHTPIIVMITNIBEMN EKCTEYWPEEQVAYDGVBITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVBEAAQQEGPHCAPII VHCSAGIGRTCCYIATSICCQQLRQBGVVDILKTTCQLRQDRGG MIQHCBQYQFVHHVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA	1		1	
DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEBRUYIATQGPIVSTVADFWRWWQRHTPLIVMITNIBEMN EKCTEYWPEDQVAYDGVBITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVBBAAQQEGPHCAPII VHCSAGIGRTGCPIATSICCQQLRQBGVVDILKTTCQLRQDRGG MIQHCBQYQFVHHVMSLYERQLSHQSPE 6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAREKA			1	
BKCTEYWPEEQVAYDGVBITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVBBAAQQEGPHCAPII VHCSAGIGRTGCPIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCBQYQFVHHVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSWKKQAEDIKKIFEFKBTLGYGAFSEVVLAEEKA	1		ĺ	
GLKHYWFTSWPDQKTPDRAPPLLHLVREVBBAAQQEGPHCAPII VHCSAGIGRTGCPIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSWKKQAEDIKKIFEFKETLGYGAFSEVVLAEEKA	1			
VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSWKKQAEDIKKIFEFKETLGYGAFSEVVLAREKA	1		(	
MIQHCEQYQFVHHVMSLYERQLSHQSPE 6199 144 1211 MARENGESSSWKKQAEDIKKIFEFKETLGYGAFSEVVLAREKA			1	
6199 144 1211 MARENGESSSWKKQAEDIKKIFEFKETIGTGAFSEVVLAREKA			i	··
	l		l	
TGKLFAVKCI PKKALKGKESSI KNE I AVLRKI KHENI VALEDI Y	6199	144	1211	
				TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY
BSPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV	Į.	}	i	
YYLHRMGIVHRDLKPKNLLYYSQDEESKIMISDFGLSKMEGKGD	}		Į.	
VMSTACGTPGYVAPRVLAQKPYSKAVDCWSIGVIAYIILCGYPP	1		I	VMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPP

	•	•	The state of the s
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ł	residue of	amino acid	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	l sagecines	\=possible nucleotide insertion)
<b></b>			FYDENDSKLFEQILKAEYBFDSPYWDDISDSAKDFIRNLMEKDP
1	·		NKRYTCEQAARHPWIAGDTALMKNIHESVSAQIRKNFAKSKWRQ
1		j	AFNATAVVRHMRKLHLGSSLDSSNASVSSSLSLASOKDCASGTP
F			HAL*
6200	702	96	LPEVPHSLRPRVKPHLCCAQPAVRVMARLPKLAVFDLDYTLWPF
ì			WVDTHVDPPFHKSSDGTVRDRRGQDVRLYPEVPEVLKRLQSLGV
1			PGAAASRTSEIEGANQLLBLFDLFRYFVHREIYPGSKITHFERL
		1	QQKTGIPFSQMIFFDDERRNIVDVSKLGVTCIHIQNGMNLQTLS
L		<u>i</u>	QGLETFAKAQTGPLRSSLERSPFEA
6201	2809	2383	GQTPRVRWKMRRSLRAGKRRQTAGRKSKSPPKVPIVIQDDSLPA
		1	GPPPQIRILKRPTSNGVVSSPNSTSRPTLPVKSLAQREAEYARA
1		İ	RKRILGSASPRERQEKPILDRPTRISQPEDSRQPNNVIRQPLGP
			DGSQGFKQRR
6202	2	426	INADRAAVASSLLSRPTRKMAPQKDRKPKRSTNRFNLDLTHPVE
		5	DGIFDSGNFEQFLREKVKVNGKTGNLGNVVHIERFKNKITVVSE
1			KQFSKRYLKYLTKKYLKKNNLRDWLRVVASDKETYBLRYFQISQ   DEDESESED
6203	419	2550	RCPRPPATAGAAASRPDRSPPSGISGSEAAAGAGAAAAAASOHPA
1 5203	417	2330	TGTGAVQTEAMKQILGVIDKKLRNLEKKKGKLDDYOERMNKGER
			LNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIQKTIKKTA
			RREQLMREBAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLNGV
			PILSEEELSLLDEFYKLVDPERDMSLRLNEQYEHASIHLWDLLE
		,	GKEKPVCGTTYKVLKEIVERVFQSNYFDSTHNHQNGLCEEZEAA
	•		SAPAVEDQVPRAEPEPAREYTEQSEVESTEYVNRQFMARTQFTS
			GEKEQVDEWTVETVEVVNSLQQQPQAASPSVPEPHSLTPVAQAD
l :			PLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAQPM
1			NPTQNMDMPQLVCPPVHSBSRLAQPNQVPVQPEATQVPLVSSTS
	,		EGYTASQPLYQPSHATEQRPQKBPIDQIQATISLNTDQTTASSS
			LPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFXMNAPVP
i i			PVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVG
1			TYHGSPDQSHQVTGNHQQPPQQNTGFPRSNQPYYNSRGVSRGGS RGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQSQPSAP
			RDYSGYQRDGYQQNFKRGSGQSGPRGAPRGRGGPPRPNRGMPQM
1			NTOOVN
6204	2933	787	CTHNLISLLGGRALIHFNRFLNLKIQEGRAHNIFCPAYDCFOLV
1 . 1			PGDIIKSVVSKEMDKRYLQFDIKAFVENNPAIKWCPTPGCDRAV
			RLTKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFCWBCLGRAHEP
i I			CDCQTWKNWLQKITEMKPBELVGVSRAYEDAANCLWLLTNSKPC
1 1			ANCKSPIQKNEGCNHMQCAKCKYDFCWICLEEWKKHSFVHWEVI
			YRCTRYEVIQHVEEQSKEMTVEAEKKHKRFQELDRFMHYYTRFK
			NHEHSYQLEQRLLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV
			HVLLKTRRILKCSYPYGFFLEPKSTKKEIFELMQTDLEMVTEDL
j l			AQKVNRPYLRTPRHKI IKAACLVQQKRQEPLASVARGVAPADSP
į		İ	EAPRRSFAGGTWDWEYLGPASPEEYAEFQYRRRHRQRRRGDVHS
			LLSNPPDPDEPSESTLDIPEGGSSSRRPGTSVVSSASMSVLHSS
{			SURDYTPASRSENQDSLQALSSLDEDDPNILLAIQLSLQESGLA
j			LDEBTRDFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE LLELGDSLMRLGAENDPFSTDTLSSHPLSEARSDFCPSSSDPDS
			AGQDPNINDNLLGNIMAWFHDMNPQSIALIPPATTEISADSQLP
J			CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLKENI
			PGGGKOHPQAW
6205	1	1200	RAHRGKMALEVGDMEDGQLSDSDSDMTVAPSDRPLQLPKVLGGD
	-		SAMRAPONTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR
			KROKCFNPPPKPBPFOFGOSSOKPPVAGGKKINNIWGAVLOBON
		İ	QDAVATELGILGMEGTIDRSROSETYNYLLAKKLRKESQEHTKD
			LDKELDBYMHGGKKMGSKBEBNGQGHLKRKRPVKDRLGNRPBMN
			*

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
١	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
			YKGRYBITAKDSQEKVADBISFRLQBPKKDLIARVVRIIGNKKA
	ì		ISLIMETABUEQNGGLFIMNGSRRRTPGGVFLNLLKNTPSISEE
	]		QIKDIFYIENQKEYENKKAARKRRTQVLGKKMKQAIKSLNFQED
l	Ì		DOTSRETFASDTNEALASLDRSQEGHAEAKLEAEEAIEVDHSHD
			LDIF
6206	10	1442	ITSERRERSCLHLVCIRCSCDVVEMGSVLGLCSMASWIPCLCGS
		Ī	APCILCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQ LNKIPGFCBNEKGVVPCNILVGYKAVYRLCFGLAMPYLLLSILM
		i	IKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIPEGTFTTVW
			PYVCMAGAFCFILIOLVLLIDFAHSWNESWVEKMEEGNSRCWYA
Į		1	ALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLC
1		1	VGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTWSAMTNEPE
i			TNCNPSLLSIIGYNTTSTVPKEGQSVQWWHAQGIIGLILFLLCV
i	į.		FYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
		ļ	RAVDNERDGVTYSYSFFHFMLFLASLYIMMTLTNWYRYBPSREM
			KSQWTAVWVKISSSWIGIVLYVWTLVAPLVLTNRDFD
6207	2924	1471	TVMARAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG
1		İ	GGGGGSDGSGGGWTKQVTCRYFNHGVCKEGDNCRY8HDLSDSPY
l	j	}	SVVCKYFQRGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLAA
			SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEFVP
		İ	GQPYCGRTAPSCTBAPLQGSVTKESSEKEQTAVETKKQLCPYAA VGBCRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
		1	HEKDMELSFAVORSKDMVCGICMEVVYEKANPSERRFGILSNCN
	·		HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVBE
1			KEEKOKLILKYKBAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
1			GRRESPOROKVGTSSRYRAQRRNHFWELIEERENSNPFDNDEEE
1			VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDL
6208	2924	1471	TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPIVTAPSLGAG
1			GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSPY
1			SVVCKYFQRGYCIYGDRCRYEHSKPLKQBEATATELTTKSSLAA
		1	SSSLSSIVGPLVEMNTGRARSRNSNFATVGAGSEDWVNAIEFVP
ļ			GOPYCGRTAPSCTEAPLOGSVTKKESEKEQTAVETKKQLCPYAA
l	ĺ		VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERRFGILSNCN
1		]	HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSKYWVEK
İ	}	1	KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
!		1	GRREEPORQKVGTSSRYRAQRRNHFWELIEERENSNPFDNDEEE
]			VVTFELGENLLMLLAAGGDDELTDSEDEWDLFHDRLEDFYDLDL
6209	1758	829	ERLCFPCMQSKIYSYMSPNKCSGMRFPLQEBNSVTHHBVKCQGK
	1		PLAGIYRKREEKRNAGNAVRSAMKSEEQKIKDARKGPLVPFPNQ
ļ			KSEAAEPPKTPPSSCDSTNAAIAKQALKKPIKGKQAPRKKAQGK
1			TQQNRKLTDFYPVRRSSRKSKABLQSRERKRIDELIBSGKBEGM
1	1	1	KIDLIDGKGRGVIATKQFSRGDFVVEYHGDLIBITDAKKRBALY
İ			AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ
	İ		TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIKAHPWL
	<u> </u>		KH
6210	3761	387	IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT
1.		1	SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMRAV
	1		SVICHQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD
1	1	1	CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE
l	1	1	IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHABDAGVICSKG
1		İ	ADLSLELVDGVTECSGELEVEFOGEWGTICDDGWDSYDAAVACK
1		1	QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHE
ł	1 .	•	WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEIQRL
1	1		LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWL
L	<u> </u>	<u> </u>	moti. community to the property of the party

SEQ Predicted predicted end beginning nucleotide location nucleotide location corresponding to first amino acid residue of residue of amino acid sequence predicted end human acid sequence sequence should be predicted end human acid segment containing si (A=Alanine, C=Cysteine, D=Aspart Glutamic Acid, F=Phenylalanine, Glutamic Acid, F=Phenylalanine, H=Histidine, I=Isoleucine, K=Lystellocation in the sequence sequence sequence sequence sequence sequence sequence sequence Amino acid segment containing si (A=Alanine, C=Cysteine, D=Aspart Glutamic Acid, F=Phenylalanine, M=Aspart H=Histidine, I=Isoleucine, M=Aspart Glutamic Acid, F=Phenylalanine, M=Aspart Glutamic Acid, F=Phenylalanine, M=Aspart Glutamic Acid, F=Phenylalanine, M=Aspart Glutamic Acid, F=Phenylalanine, M=Aspart Glutamic Acid, F=Phenylalanine, M=Aspart Glutamic Acid, F=Phenylalanine, M=Aspart Glutamic Acid, F=Phenylalanine, M=Aspart M=Histidine, I=Isoleucine, M=Histidine, I=Isoleucine, M=Histidine, I=Isoleucine, M=Histidine, I=Is	ic Acid, B= G=Glycine, ine, agine, ne, own, *=Stop etion,
MO: nucleotide location corresponding to first amino acid residue of amino acid sequence sequence location corresponding to first amino acid sequence location corresponding to first amino acid w=Tryptophan, Y=Tyrosine, X=Own (>=possible nucleotide insertion)	G=Glycine, ine, agine, ne, own, *=Stop etion,
location corresponding to first amino acid residue of amino acid sequence  location corresponding to first amino acid residue of amino acid sequence  location corresponding to first amino acid w=Tryptojane, M=Methionine, N=Aspar P=Proline, Q=Glutamine, R=Aryini S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unkn defined sequence  location corresponding to first W=Leucine, M=Methionine, N=Aspar P=Proline, Q=Glutamine, R=Aryini S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unkn defined	ine, agine, ne, own, *=Stop etion,
corresponding to first L=Leucine, M=Methionine, N=Aspar to first amino acid residue of sequence L=Codon, /=possible nucleotide insertion)  L=Leucine, M=Methionine, N=Aspar P=Proline, Q=Glutamine, R=Argini S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unkn Codon, /=possible nucleotide del \=possible nucleotide insertion)	agine, ne, own, *=Stop etion,
to first amino acid p=Proline, Q=Glutamine, R=Argini amino acid residue of sequence P=Proline, Q=Glutamine, R=Argini S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unkn Codon, /=possible nucleotide del \=possible nucleotide insertion)	own, *=Stop etion,
amino acid residue of S=Serine, T=Threonine, V=Valine, residue of amino acid w=Tryptophan, Y=Tyrosine, X=Unkn amino acid sequence Codon, /=possible nucleotide del \=possible nucleotide insertion)	own, *=Stop etion,
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unkn amino acid sequence Codon, /=possible nucleotide del \=possible nucleotide insertion)	etion,
amino acid sequence Codon, /=possible nucleotide del sequence (=possible nucleotide insertion)	etion,
sequence   \=possible nucleotide insertion)	
I DOCKONDIODING CRANQUO O DI CENTE BERRO	TTCCAUDRODIA
GGDIPCSGRVEVKHGDTWGSICDSDFSLEAAS	
SILGGAHFGEGNGQIWAEBFQCEGHESHLSLC	-
SRDVGVVCSRYTBIRLVNGKTPCEGRVELKTL	
IEDAHVLCOOLKCGVALSTPGGARFGKGNGQI	
HMGDCPVTALGASLCP8EQVASVICSGNQSQT	_
RPTIPERSAVACIESGOLRLVNGGGRCAGRVE	
DSWDLSDAHVVCRQLGCGEAINATGSAHFGEG	
GKESRIWOCHSHGWGOONCRHKEDAGVICSEF	
	i
ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCR ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSP	
WITCONKIRLOEGPTSCSGRVBIWRGGSWGTV	
VCOOLGCGPALKAPKRAEPGOGTGPIWLNEVK	
ARRWGHSECGHKEDAAVNCTDISVQKTPQKAT VGILGVVLLAIFVALFFLTKKRRQRQRLAVSS	
· VGILGVVELALFVALFFLIKKRQRQRLAVSS - EMNSCLNADDLDLMNSSGGHSEPH	WORKTAWARK
	TURIT T. C. A.C. LAND
6211 3761 387 IFGMSKLRMVLLKDSGSADFRRHFVNLSPFTI SSLGGTDKELRLVDGRNKCSGRVEVKVOREWG	
SSIGGIDAEGRIVAGENACSGRVAVAVAGENG	
CKHDGWGKHSNCTHOODAGVTCSDGSNLEMRL	
IKFOGRWGTVCDDNFNIDHASVICRQLBCGSA	
SGPIWFDDLICNGNESALWNCKHQGWGKHNCD	
ADLSLRLVDGVTECSGRLEVRFQGRWGTICDD	
OLGCPTAVTAIGRVNASKGFGHIWLDSVSCOG	
WGKHYCNHNEDAGVTCSDGSDLELELEGGGSR	
LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQ	
FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAK	
GGDIPCSGRVEVKHGDTWGSICDSDFSLEAAS	
SILGGAHFGEGNGQIWARBFQCEGHESHLSLC	
SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTL	
IEDAHVLCQQLKCGVALSTPGGARPGKGNGQI	
HMGDCPVTALGASLCPSRQVASVICSGNQSQT	
RPTIPERSAVACIESGOLRLVNGGGRCAGRVE	
DSWDLSDAHVVCRQLGCGEAINATGSAHFGEG	
GKRSRIWOCHSHGWGQQNCRHKBDAGVICSBR	
ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCR	
ACASKIBSVFINOAROTVOIDANTOVO	•
WITCDNKIRLQEGPTSCSGRVBIWHGGSWGTV	
VCQQLGCGPALKAFKRAKFGQGTGPIWLNEVK	
ARRWGHSECGHKKDAAVNCTDISVQKTPQKAT	
VGILGVVLLAIFVALFFLTKKRRQRQRLAVSS	
EMNSCLNADDLDLMNSSGGHSEPH	
	GPPSSLPRAFRE
6212 1 1134 LKWBLRPGGAVWGTGRGAGTGAPRSCCCQINP RELPFPACHEIGLGABAGSGPPPAPARESRS	
GCSKPHLEKITIGITRILESSPGVTEVTIIEK	
QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDBH	
SKLTQLTQSSMYSLPNAPTLADLEDDTHRASD	
VIPELDSCNGSCKVCLVYKSGKPALARDTRIM	
DTFTAYYRLLITHLGLPOWOYAFTSYGISPQA	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPK	wwa.s.A.Ks.HPP/K
GPSGPSGPSTSSTSKSSSGSGNPTRK	CDDGGG TOV TOV
6213 1 1134 LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNP	
RELPFPACHBIGLGARAGSGPPPAPAARESRS	
GCSKPHLEKLTLGITRILESSPGVTEVTIIEK	
QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDBH	
SKLTQLTQSSMYSLPNAPTLADLEDDTHRASD	DOOPERPHEDSRS

			· · · · · · · · · · · · · · · · · · ·
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT
ł			DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY
	Ì		NTNLLTBETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK
			GPSGPSGPSTSSTSKSSSGSGNPTRK
6214	2	460	HELAPSAIRRAARLGIGPARWQSRAAAFYFVRGFRTGWSFVGWV
		Į.	VLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRESKRFSAYN
		•	YRTYAVRRIRDAFRENKNYKDPVEIQTLVNKAKRDLGVIRRQVH
		·	IGQLYSTDKLIJENRDMPRT
6215	2	1849	FVAGGPRGSGSAARTMPRIRVTPLGAGQDVGRSCILVSLAGKNV
	1	1	MLDCGMHMGFNDDRRFPDFSYITQNGRUTDFLDCVIISHFHLDH
	j		CGALPYPSENVGYDGPIYMTHPTQAICPILLEDYRKIAVDKKGE
	{		ANPFTSQMIKDCMKKVVAVHLHQTVQVDDBLBIKAYYAGHVLGA
ļ		I	AMFQIKVGSESVVYTGDYNMTPDRHLGAAWIDKCRPNLLITEST
	1		YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGRAQELC
	[		ILLETFWERMNLKVPIYPSTGLTEKANHYYKLFIPWTNQKIRKT
	1	ł	FVQRNMFBFKHIKAFDRAFADNPGPMVVPATPGMLHAGQSLQIF
		Ĭ	RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRQVLEVK
	}	ļ	MOVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKMEPLKQ
'	ł	i	KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKREMAQGL
			LPRAKKPRLLHGTLIMKDSNFRLVSSEQALKBLGLABHQLRFTC
		]	RVHLHDTRKBQETALRVYSHLKSVLKDHCVQHLPDGSVTVESVL
			LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLPQAPS
6216	11	393	QTTRPEPRNSALRQSRSKMAVVGVSSVSRLLGRSRPQLGRPMSS
		ł	GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGKHERPE
			FIAYPHLRIRTKPFPWGDGNHTLPHNPHVNPLPTGYEDE
6217	9	1178	TRVGRGESGLKMEVKPPPGRPQPDSGRRRRRGEEGHDPKEPEQ
			LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQTKRSRG
	ļ		PGFVTYSCVEBVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA
		1	HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEDRQSGK
		1	KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSKQEMQS
	1		AGSQRGRGGGSGNFMGRGGNFGGGGGFGRGGYGGGG GGSRGSYGGGDGGYNGFGGDGGNYGGGPGYSSRGGYGGGPGYG
		1	NQGGGYGGGGGYNEGGNYGGGNYGGGGNYNDFGNYSGQQQS
		1	NYGPMKGGSFGGRSGSPYGGGYGSGGGGGGGGGGRRF
		906	
6218			
	1305	300	SCERRGFIMADDLKRFLYKKLPSVEGLHAIVVSDRDGVPVIKVA
	1305	308	NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV
			NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELRQVVEVS
6219	2	890	NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIAŞSSANTGLIVSLBKELAPLFEELRQVVEVS AGPGEGAGAGTRCAGAKABMASAGGEDCESPAPKADRPHQRPFL
6219			NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIAŞSSANTGLIVSLEKELAPLFEELRQVVEVS AGPGEGAGAGTRCAGARAEMASAGGEDCESPAPBADRPHQRPPL IGVSGGTASGKSTVCEKIMELLGQNEVBQRQRKVVILSQDRFYK
6219			NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIAŞSSANTGLIVSLEKELAPLFEELRQVVEVS AGPGEGAGAGTRCAGAKAEMASAGGEDCESPAPBADRPHQRPPL IGVSGGTASGKSTVCBKIMELLGQNEVBQRQRKVVILSQDRFYK VLTABQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP
6219			NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLIVVSFIASSSANTGLIVSLBKBLAPLFBELRQVVEVS AGPGEGAGAGTRCAGAKAEMASAGGBDCESPAPEADRPHQRPFL IGVSGGTASGKSTVCBKIMELLGQNEVEQRQRKVVILSQDRFYK VLTABQKAKALKGGYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFBGILVFYSQBIRDMFHLRLP
6219			NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIA;SSANTGLIVSLEKELAPLFEELRQVVEVS AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPERDRPHQRPFL IGVSGGTASGKSTVCEKIMELLGQNEVBQRRKVVILSQDRFYK VLTABQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTESRLPETTVVYYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEPCLP
6219			NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIA;SSANTGLIVSLEKELAPLFEELRQVVEVS AGPGEGAGAGTRCAGAEABMASAGGEDCESPAPBADRPHQRPFL IGVSGGTASGKSTVCEKIMELLGQNEVBQRRKVVILSQDRFYK VLTABQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYYPADVVLFEGILVFYSQBIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQLLTQYTTFVKPAFEBPCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG
	2	890	NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIA;SSANTGLIVSLEKELAPLFEELRQVVEVS AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADRPHQRPFL IGVSGGTASGKSIYCEKIMELLGQNEVEQRQRKVVILSQDRPYK VLTABQKAKALKQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQBIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEBPCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTPSEPGDHPGMLTSGKRSHLESSSRPH
6219 6220			NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIA;SSANTGLIVSLEKELAPLFEELRQVVEVS AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADRPHQRPFL IGVSGGTASGKSTYCEKIMELLGQNEVRQRQRKVVILSQDRFYK VLTABQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVY TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQBIRDMFHLRLP VDTDSDVRLERRVLRDVRRGRDLEQILTQYTTFVKPAFEBPCLP TKKYADVIIPRGVDNMVAINLIVQHTQDILMGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH EQNISLEMSCTIEKALADAKALVERLRDHDDAABSLIEQTTALN
	2	890	NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLIVVSFLASSSANTGLIVSLBRELAPLFBELRQVVEVS AGPGEGAGAGTRCAGARAEMASAGGBDCESPAPEADRPHQRPFL IGVSGGTASGKSTVCBKIMELLGQNEVEQRQRKVVILSQDRFYK VLTABQKAKALKGGYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFBGILVFYSQBIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVRPAFBBPCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH EQNISLEMSCTIBKALADAKALVERLRCHDDDARSLIEQTTALN KRVEANKQYQEBIQELNEVARHPRSTLVMGIQQBNRQIRELQQ
	2	890	NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIASSSANTGLIVSLBKBLAPLFBELRQVVEVS AGPGEGAGAGTRCAGAKAEMASAGGEDCESPAPEADRPHQRPFL IGVSGTTASGKSTVCEKIMELLGQNEVEGRQRKVVILSQDRFYK VLTABQKAKALKGQYNFOHPDAFONDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQBIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFBEPCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILMGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSRPH EQNISLEMSCTIEKALADAKALVERLRDHDAAESLIEQTTALN KRVEANKQYQEKIQELNEVARHRPRSTLVMGIQQEMRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMPRLLMASKKDDPGIIMK
	2	890	NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIASSSANTGLIVSLERELAPLFEELRQVVEVS AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADRPHQRPFL IGVSGGTASGKSTVCEKIMELLGQNEVEGRQRKVVILSQDRFYK VLTABQKAKALKGQYNFOHPDAFONDLMIRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQBIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEPCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILMGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSRPH EQNISLEMSCTIEKALADAKALVERLRDHDDABSLIEQTTALN KRVEAMKQYQERIQELNEVARHRPRSTLVMGIQQEMRQIRELQQ ENKELRTSLERHQSALELIMSKYREQMPRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANO
6220	2 227	890 764	NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIA;SSANTGLIVSLEKELAPLFEELRQVVEVS AGPGEGAGAGTRCAGAEABMASAGGEDCESPAPBADRPHQRPFL IGVSGGTASGKSTVCEKIMELLGQNEVBQNGRKVVILSQDRFYK VLTABQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYYPADVVLFEGILVFYSQBIRDMFHLRL; VDTDSDVRLSRRVLRDVRRGRDLEQLLTQYTTFVKPAFEBPCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEANKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLBEHQSALELIMSKYREQMPBLLMASKNDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH
	2	890	NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELRQVVEVS AGPGEGAGATRCAGAEABMASAGGEDCESPAPBADRPHQRPFL IGVSGGTASGKSTVCEKIMELLGQNEVBQRKVVILSQDRFYL VLTABQKAKALKQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQBIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEBPCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEANKQYQESQGLURVARHRPRSTLVMGIQQENQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMPRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP
6220	2 227	890 764	NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLIVVSFLASSSANTGLIVSLBRELAPLFBELRQVVEVS AGPGEGAGAGTRCAGARAEMASAGGBDCESPAPEADRPHQRPFL IGVSGGTASGKSTVCBKIMELLGQNEVEQRQRKVVILSQDRFYK VLTABQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVBGKTVEVP TYDFVTHSRLPBTTVVYPADVVLFBGILVFYSQBIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVRPAFBBPCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH EONISLEMSCTIBKALADAKALVERLRCHDDAAESLIEQTTALM KRVEAMKQYQEBIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLBEHQSALELIMSKYREQMFRLIMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH RNIWDLMPVSDGLBLRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG
6220	2 227	890 764	NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLUVSFIASSSANTGLIVSLBRELAPLFBELRQVVEVS AGPGEGAGAGTRCAGAKAEMASAGGBDCESPAPEADRPHQRPFL IGVSGGTASGKSTVCEKIMELLGQNEVEQRQRKVVILSQDRFYK VLTABQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFBGILVFYSQBIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFBEPCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH EQNISLEMSCTIEKALADAKALVERLRDHDDAARSLIEQTTALN KRVEANKQYQEKIQELNEVARHPRRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMPRLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH RWIWDLMPVSDGLBLRPKYNGILHCLTTIWKLDGLRGLYQGVTP NINGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCTINPLWVTKTRLMLQYDAVVNSPHRQYKGMPDTLVKIYK
6220	2 227	890 764	NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIA;SSANTGLIVSLERELAPLFEELRQVVEVS AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADRPHQRPFL IGVSGGTASGKSTVCEKIMELLGQNEVEGPRORRKVVILSQDRFYK VLTABQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQBIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFBEPCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILMGDICKWHRGGSNG RSYKRTTSEPGDHPGMLTSGKRSHLESSSRPH EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEBIQELNEVARHRPRSTLVMGIQQEMRQIRELQQ ENKELRTSLBEHQSALELIMSKYREQMPRILMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NINGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMPDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE
6220	2 227	890 764	NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIA;SSANTGLIVSLEKELAPLFEELRQVVEVS AGPGEGAGAGTRCAGAEARMASAGGEDCESPAPEADRPHQRPFL IGVSGTTASGKSTVCEKIMELLGQNEVEQRQRKVVILSQDRFYK VLTABQKAKALKGQYNFDHPDAFDNDLMIRTLKNIVEGKTVEVP TYDFVTISRLPETTVVYPADVVLFEGILVFYSQBIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEPCLP TKKYADVIIPRGVDNMVAINLIVQHTQDILMGDICKWHRGGSNG RSYKRTTSEPGDHRGMLTSGKRSHLESSSRPH EQNISLEMSCTIEKALADAKALVERLRDDDAAESLIEQTTALN KRVEANKQYQEBIQELNEVARHRPRSTLVMGIQQEMRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRILMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH RWIWDLNPVSDGLBLRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFUFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKCMPDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNCHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI
6220	2 227	890 764	NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIA;SSANTGLIVSLERELAPLFEELRQVVEVS AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADRPHQRPFL IGVSGGTASGKSTVCEKIMELLGQNEVEGPRORRKVVILSQDRFYK VLTABQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQBIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFBEPCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILMGDICKWHRGGSNG RSYKRTTSEPGDHPGMLTSGKRSHLESSSRPH EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEBIQELNEVARHRPRSTLVMGIQQEMRQIRELQQ ENKELRTSLBEHQSALELIMSKYREQMPRILMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NINGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMPDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE

		•	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ī	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
6222	2	2116	MARELRALLLWGRRLRPLLRAPALAAVPGGKPILCPRRTTAQLG
Į		}	PRRNPAWSLQAGRLFSTQTARDKEEPLHSIISSTESVQGSTSKH
I	j	1	efqaetkkildivarslysekevfirelisnasdalrkirhklv
1	1		SDGQALPEMEIHLQTNAEKGTITIQDTGIGMTQEELVSNLGTIA
l			RSGSKAPLDALQNQAEASSKIIGQFGVGFYSAFMVADRVEVYSR
i			SAAPGSLGYQWLSDGSGVFETABASGVRTGTKIITHLKSDCKEF
l .			SSEARVRDVVTKYSNFVSFPLYLNGRRMNTLQAIWMMDPKDVRE
ł	ł	[	WQHEBFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKPSM
1	1	!	PDVSRELGSSVALYSRKVLIQTKATDILPKWLRFIRGVVDSEDI
1	l	i	PLNLSRELLQESALIRKLRDVLQQRLIKFFIDQSKKDABKYAKF
Į.	i	<b>!</b>	FEDYGLPMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTSLS
]	ł		EYASRMRAGTRNIYYLCAPNRHLAEHSPYYKAMKKKDTEVLFCF
	1	Į.	ROFDELTILHLREFDKKKLISVETDIVVDHYKEEKFEDRSPAAE
}	ł	1	CLSEKETBELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLENG
Į.	i		AARHFIRMQQLAKTQEERAQLIQPTLEINPRHALIKKINQLRAS
			EPGLAQLLVDQIYENAMIAAGLVDDPRAMVGRLNELLVKALERH DAWARTMAGMVDFQDEEQVKSYLENMEVECNYHCYHEKDPDGCY
6223	3	715	RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDSCYKLGAYYVTGK
i			GGLTODLKAAARCFLMACEKPGKKSIAACHNVGLLAHDGQVNED
1	İ		GOPDLGKARDYYTRACDGGYTSSCFNLSAMPLQGAPGFPKDMDL
ł	1	ļ	ACKYSMKACDLGHIWACANASRMYKLGDGVDKVEAKAEVLKNRA
ì			OOVHKEOOKGVOPLTFG
6224	1	133	LRTISSMAWGPLLLTLLAHCTGSWAQSVLTQPPSVSGARIPHEK
6225	3259	938	LISCHRIAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT
0223	3437	,,,,,	OKENRILSPAGRALYREVTLENYSHLVSLGILHSKPELIRRLEG
i	1	[	GEVPWGEERRRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD
1	ł	1	OSFOSDTARGOEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES
1	1	1	SOGORENPTEIDKVLKGIENSRWGAFKCAKRGQDFSRKMMVIIH
1		i	KKAHSROKLFTCRECHQGPRDESALLLHQNTHTGEKSYVCSVCG
1	1		RGPSLKANLLRHORTHSGEKPFLCKVCGRGYTSKSYLTVHERTH
	1	· ·	TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT
1	1	1	NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK
1	1	1	PPACROCKOSPSVKGSLLRHORTHSGEKPFVCKDCERSFSQKST
1	1	1	LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEXPFVC
			KOCGRGFIQKSTFTLHQRTHSEKKPYGCRECGRRFRDKSSYNKH
1	Ī .	1	LRAHLGEKRFYCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE
1		1	KSFSLKANLLRHOWTHSGERPFNCKDCGRGFILKSTLLFHQKTH
1	1		SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN
1			WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE
	1	1	KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS
L	<u> </u>	L	YYSKHLKRHLREKRFCTGSVGEASS
6226	29	266	TKVSELLGGSQRLPFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS
L_	<u> </u>	<u> </u>	IMBGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA
6227	2581	890	MSASSLIEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP
1	1	1	NNAYTAMSDSYLPSYYSPSIGFSYSLGBAAWSTGGDTAMPYLTS
İ	ŀ	1	YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS
	ŀ	j	AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL
1	J	<u> </u>	nkapgmntidqgmaalklgstevasnvpkvvgsavgsgsitsni
Ι ,		[	VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL
[	1	Į.	PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG
1	1	1	QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQQAAQPTRWV
1	1	1	APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLBKLRSIN
1	l	l .	NYNPKDFDWNLKHGRVFIIKSYSKDDIHRSIKYNIWCSTBHGNK
1	]		RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVABMKSAVDYNTCAG
i	Ī	[	VWSQDKWKGRFDVRWIFVKDVPNSQLRHIRLENNENKPVTNSRD
1		1	TQEVPLEKAKQVLKIIASYKHTTSIPDDFSHYEKRQ

			· ·
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6228	47	1978	GRCCRRGAVMELAQEARELGCWAVEEMGVPVAARAPESTLERL
			CLGQGADIWAYILQHVHSQRTVKKIRGNLLWYGHQDSPQVRRKL
1			ELEAAVTRLRAEIQELDQSLELMERDTEAQDTAMEQARQHTQDT
ł	1		QRRAILLRAQAGAMRRQQHTLRDPMQRLQNQLRRLQDMERKAKV
	ł	]	DVTPGSLTSAALGLEPVVLRDVRTACTLRAQFLQNLLLLPQAKRG
		[	
1		ĺ	SLPTPHDDHFGTSYQQWLSSVETLLTNHPPGHVLAALEHLAAER
1		ļ	EABIRSLCSGDGLGDTBISRPQAPDQSDSSQTLPSMVHLIQEGW
	Į.	Ì	RTVGVLVSQRSTLLKERQVLTQRLQGLVEEVERRVLGSSERQVL
	1		ILGLRRCCLWTKLKALHDQSQELQDAAGHRQLLLRELQAKQQRI
1			LHWRQLVEBTQEQVRLLIKGNSASKTRLCRSPGEVLALVQRKVV
1			PTFEAVAPQSRELLRCLEEEVRHLPHILLGTLLRHRPGELKPLP
İ			TVLPSIHQLHPASPRGSSFIALSHKLGLPPGKASELLLPAAASL
1		1	RQDLLLLQDQRSLWCWDLLHMKTSLPPGLPTQELLQIQASQRKQ
1	-		QKENLGQALKRLEKLLKQALERIPELQGIVGDWWEQPGQAALSE
			BLCQGLSLPQWRLRWVQAQGALQKLCS
6229	1571	560	GPSLLGTRGTPNPARTLQIPFLIIGRRLTGRMAAVDDLQFEEFG
	İ		NAATSLTANPDATTVNIEDPGETPKHQPGSPRGSGREEDDELLG
İ			NDDSDKTELLAGQKKSSPFWTFEYYQTFFDVDTYQVFDRIKGSI,
			LPIPGKNFVRLYIRSNPDLYGPPWICATLVFAIAISGNLSNFLI
			HLGEKTYHYVPEFRKVSIAATIIYAYAWLVPLALWGFLMWRNSK
i			VMNIVSYSPLEIVCVYGYSLPIYIPTAILWIIPHKAVRWILVMI
			ALGISGSLLAMTFWPAVREDNRRVALATIVTIVLLHMLLSVGCL
			AYFFDAPEMDHLPTTTATPNQTVAAAKSS
6230	1723	600	SKMSGRSGKKKMSKLSRSARAGVIFPVGRLMRYLKKGTFKYRIS
			VGAPVYMAAVIEYLAAEILELAGNAARDNKKARIAPRHILLAVA
i			NDEELNQLLKGVTTASGGVLPRIHPELLAKKRGTKGKSETILSP
i			PPEKRGRKATSGKKGGKKSKAAKPRTSKKSKPKDSDKEGTSNST
			SEDGPGDGPTILSSKSLVLGQKLSLTQSDISHIGSMRVEGIVHP
1			TTABIDLKEDIGKALEKAGGKEFLETVKELRKSQGPLEVAEAAV
			SQSSGLAAKFVIHCHIPQWGSDKCEEQLEBTIKNCLSAABDKKL
			KSVAFPPFPSGRNCFPKQTAAQVTLKAISAHFDDSSASSLKNVX
6231	149	870	FLLFDSRSIGIYVQEMAKLDAK
0231	143	870	LIFSSSTMDRSLRNVLVVSFGFLLLFTAYGGLQSLQSSLYSEEG
i			LGVTALSTLYGGMLLSSMFLPPLLIERLGCKGTIILSMCGYVAF
1			SVGNFFASWYTLIPTSILLGLGAAPLWSAQCTYLTITGNTHARK
			ACKRGKDMVNQYFGIPFLIFQSSGVWGNLISSLVFGQTPSQETL
1	ľ		PEEQLTSCGASDCLMATTTTNSTQRPSQQLVYTLLGIYTGSGVL
6232	3679	1477	AVIMIAAFIQPIRDVQRESE
0434	30/9	1476	PVAGTTMAGFWVGTAPLVAAGRRGRWPPQQIMLSAALRTLKHVL
1			YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC
	1		KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA
			IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA
			IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDABKAVRIARBIGY
1			PVMIKASAGGGGKGMRIAWDDEBTRDGFRLSSQEAASSFGDDRI.
]	,		LIEKFIDNPRHIBIQVLGDKHGNALWLNERECSIQRRNQKVVEE
			APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY
	ļ		FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR
			INGWAVECRVYAEDPYKSFGLPSIGRLSQYQEPLHLPGVRVDSG
<u> </u>			IQPGSDISIYYDPMISKLITYGSDRTBALKRMADALDNYVIRGV
			THNIALLREVIINSRFVKGDISTKFLSDVYPDGFKGHMLTKSEK
1	ĺ		NQLLAIASSLFVAFQLRAQHFQENSRMPVIKPDIANWELSVKLH
, !			DKVHTVVASNNGSVFSVEVDGSKLNVTSTWNLASPLLSVSVDGT
	İ		QRTVQCLSREAGGNMSIQFLGTVYKVNILTRLAABLNKFMLEKV
[	.		TEDTSSVLRSPMPGVVVAVSVKPGDAVAEGQBICVIEAMKMQNS
			MTAGKTGTVKSVHCQAGDTVGEGDLLVELE
6233	1	2654	HSTRENLNAGNFNFPSEGHLVRSTGPGGSFAKHMVAQCVSPKGP

		No. 11/04	The second state of the second second states and
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	Bequence	sequence	\=possible rucleotide insertion)
	Bequence		LACSRTYFFGATHVPYLGGDSKLPKKTBOIRLLSQIYAAVIEAV
	}		
			LAGIACYAKTSSLTKAKEVAEQTLGSGLDSFELIPFKAALRSKM
l		ľ	TFHIHAVNNOGRIVPLDSEDSLSFVKTACMAVYDIPDLLGGNGC
		ŀ	LGSVVFSESFLTSQILVKEKDGTVTTETSSVVLTAAVPRFCSWL
		<u> </u>	VEDNEVKLSEKTHQAVRGDESFLGTYLTGGEGAYLYSSNLQSWP
			REGNVHFFSSGLLFSHCRHGSIIISKDHMNSISFYDGDSTSTVA
	•		ALLIDFKSSLLPHLPVHFHGSSNPLMIALFPKSKIYQAFYSEVF
	1		SLWKQQDNSGISLKVIQKDGLSVBQKRLHSSAQKLFSALSQPAG
			EKRSSLKLLSAKLPELDWFLQHPAISSISQEPVMRTHLPVLLQQ
		1	ABINTTHRIBSDKVIISIVTGLPGCHASELCAFLVTLHKECGRW
	I	I	MVYRQIMDSSECFHAAHFQRYLSSALKAQQNRSARQSAYIRKKT
	1	1	RLLVVLQGYTDVIDVVQALQTHPDSNVKASFTIGAITACVBPMS
	I		CYMEHRFLFPKCLDOCSOGLVSNVVFTSHTTEQRHPLLVOLQSL
1	I	1	IRAANPAAAFILAENGIVTRNEDIELILSENSFSSPEMLRSRYL
	1	I	MYPGWYEGKLNAGSVYPLMVQICVWFGRPLEKTRFVAKCKAIQS
	İ		SIKPSPPSGNIYHILGKVKPSDSERTMEVCYNTLANSLSIMPVL
		į.	RGPTPPPDSKSVSQDSSGQQECYLVFIGCSLKEDSIKDWLRQSA
			KQKPQRKALKTRGMLTQQEIRSIHVKRHLEPLPAGYFYNGTQFV
	ì		MFFGDKTDFHPLMDQFMNDYVERANREIBKYNQELEQQEYHDLF
			BPKb
6234	1731	404	PRVREDMDHKSPGNKGSLVYAGIKSIVKSSLGMVESSRHNWSGL
	!		DKQSDIQNLNBERILALQLCGWIKKGTDVDVGPFLNSLVQEGEW
	i .		PRABAVALFNLDIRRAIQILNEGASSEKGDLNLNVVAMALSGYT
ľ			DEKNSLWRENCSTLRLQLNNPYLCVMFAFLTSETGSYDGVLYEN
		1	KVAVRDRVAFACKFLSDTQLNRYIEKLTNEMKEAGNLEGILLTG
ì	1	1	LTKDGVDLMESYVDRTGDVQTASYCMIQGSPLDVLKDERVQYWI
1		1	ENYRNLLDANRFWHKRAEFDIHRSKLDPSSKPLAQVFVSCNFCG
1			KSISYSCSAVPHQGRGFSQYGVSGSPTKSKVTSCPGCRKPLPRC
			ALCLINMGTPVSSCPGGTKSDEKVDLSKDKKLAQFNNWFTWCHN
			CRHGGHAGHMLSWFRDHABCPVSACTCKCMQLDTTGNLVPAETV
İ			OP
	ļ		EKRDHRLPSWPRAALKYPGRGGRYGTTPELAACGIMATRNPPPQ
6235	1	571	•
			DYESDDDSYEVLDLTEYARRHQWWNRVFGHSSGPMVEKYSVATQ
1	1		
	ł	ļ	IVMGGVTGWCAGFLFQKVGKLAATAVGGGPLLLQIASHSGYVQI
ł			DWKRVEKDVNKAKRQIKKRANKAAPEINNLIREATEFIKQNIVI
			DWKRVEKDVNKAKRQIKKRANKAAPEINNLIREATEFIKQNIVI SSGFVGGFLIGLAS
6236	1	703	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIREATEFIKQNIVI SSGFVGGFLLGLAS WDQNKGAAAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF
6236	1	703	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIREATEFIKQNIVI SSGFVGGFLIGLAS
6236	1	703	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIREATEFIKQNIVI SSGFVGGFLLGLAS WDQNKGAAAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF
6236	1	703	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIREATEFIKQNIVI SSGFVGGFLLGLAS WDQNKGAAAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAAKELSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAE
<b>6236</b>	i	703	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIREATEPIKQNIVI SSGFVGGFLIGLAS WDQNKGAAAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAAKBLSRSAKKCDKEBKAEKAKIKKAIQKGNMEVARIHAE NAIRQKNQAVNFLKMSARVDAVAARVOTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISALMDKFEHQFETLDVQTQOMRDTMSSTTT
<b>6236</b>	1	703	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIREATEPIKQNIVI SSGFVGGFLIGLAS WDQNKGAAAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAAKELSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAE NAIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK
			DWKRVEKDVNKAKRQIKKRANKAAPEINNLIEEATEPIKQNIVI SSGFVGGFLIGLAS WDQNKGAAAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAAKELSRSAKKCDKEEKAEKAKIKKALQKGNMEVARIHAE NAIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISALMDKFEHQFETLDVQTQQMEDTMSSTTT LTTPQNQVDMLLQEMADRAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLRDQV
6236	312	703	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIEEATEPIKQNIVI SSGFVGGFLIGLAS WDONKGARAGSGITIDPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAAKBLSRSAKKODKEEKAEKAKIKKAIQKGNMEVARIHAE NAIRQKNQAVNFLKMSARVDAVAARVQTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISAIADDKFHQFETIDVQTQOMEDTMSSTTT LTTPQNQVDMLLQEMADBAGLDLNMELPQGQTGSVGTSVASAEQ DBLSQRLARLRDQV PTAMAEEGIAAGGVMDVNTALQEVLKTALIHDGLARGIREAAKA
			DWKRVEKDVNKAKRQIKKRANKAAPEINNLIERATEPIKQNIVI SSGFVGGFLIGLAS WDQNKGAAAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAAKELSRSAKKCDKEKKAEKAKTKKALQKGNMEVAR IHAE NALRQKNQAVNFLKMSARVDAVAARVQTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISALMDKFEHQFETLDVQTQQMEDTMSSTTT LTTPQNQVDMLLQEMADRAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLRDQV PTAMAEGGIAAGGVMDVNTALQEVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCAEHQINLIKVDDNKKL
			DWKRVEKDVNKAKRQIKKRANKAAPEINNLIERATEPIKQNIVI SSGFVGGFLIGLAS WDQNKGAAAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAAKELSRSAKKCDKEEKAEKAKTKKALQKGNMEVAR IHAE NALRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISALMDKFEHQFETLDVQTQQMEDTMSSTTT LTTPQNQVDMLLQEMADRAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLRDQV PTAMAEEGIAAGGVMDVNTALQBVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCAEHQINLIKVDDNKKL GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK
6237	312	720	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIREATEPIKQNIVI SSGFVGGFLIGLAS WDONKGARAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFARKBLSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAE NAIRQKRQAVNFLKMSARVDAVAARVOTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISALMDKPEHQFETLDVQTQOMEDTMSSTTT LTTPQNQVDMLLQEMADRAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLRDQV PTAMAEEGIAAGGVMDVNTALQEVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCAKHQINLIKVDDNKKL GEWVGLCKIDREGKPRKVVGCSCVVVKOYGKESQAKDVIERYFK CKK
			DWKRVEKDVNKAKRQIKKRANKAAPEINNLIERATEPIKQNIVI SSGFVGGFLIGLAS WDONKGARAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAKKLSKKCDKEEKAEKAKIKKAIQKGNMEVARIHAE NAIRQKNQAVNFLKMSARVDAVAARVOTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISALMDKFEHQFETLDVQTQOMEDTMSSTTT LTTPQNQVDMLLQEMADBAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLRDQV PTAMAEEGIAAGGVMDVNTALQEVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCAKHQINLIKVDDNKKL GBWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIERYFK CKK ERVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI
6237	312	720	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIERATEPIKQNIVI SSGFVGGFLIGLAS WDONKGARAGSGITIPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAAKBLSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAE NAIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISAIMDKFEHQFETLDVQTQOMEDTMSSTTT LTTPQNQVDMLLQEMADBAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLRDQV PTAMAEGIAAGGVMDVNTALQBVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCAEHQINLIKVDDNKKL GBWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEBYFK CKK EKVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLF
6237	312	720	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIEEATEPIKQNIVI SSGFVGGFLIGLAS WDONKGARAGSGITTDPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAAKKLSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAE NAIRQKNQAVNFLKMSARVDAVAARVQTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISAIADDKFHQFETLDVQTQQMEDTMSSTTT LTTPQNQVDMLLQEMADBAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLRDQV PTAMAEEGIAAGGVMDVNTALQBVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVBALCARHQINLIKVDDNKKL GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIERYFK CKK ERVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLF YQTTQKGTDPQVIDMSVKSLTLKVSSVIINTMITITSALYTTKE
6237	312	720	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIERATEPIKQNIVI SSGFVGGFLIGLAS WDONKGARAGSGITIPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAAKBLSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAE NAIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISAIMDKFEHQFETLDVQTQOMEDTMSSTTT LTTPQNQVDMLLQEMADBAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLRDQV PTAMAEGIAAGGVMDVNTALQBVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCAEHQINLIKVDDNKKL GBWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEBYFK CKK EKVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLF
6237	312	720	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIEEATEPIKQNIVI SSGFVGGFLIGLAS WDONKGARAGSGITTDPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAAKKLSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAE NAIRQKNQAVNFLKMSARVDAVAARVQTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISAIADDKFHQFETLDVQTQQMEDTMSSTTT LTTPQNQVDMLLQEMADBAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLRDQV PTAMAEEGIAAGGVMDVNTALQBVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVBALCARHQINLIKVDDNKKL GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIERYFK CKK ERVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLF YQTTQKGTDPQVIDMSVKSLTLKVSSVIINTMITITSALYTTKE
6237	312	720	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIREATEPIKQNIVI SGGFVGGFLIGLAS WDONKGAAAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAAKBLSRSAKKCDKEBKABKAKIKKAIQKGMMEVARTHAB NAIRQKNQAVNFLKMSARVDAVAARVOTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISALMDKFEHQFETLDVQTQQMEDTMSSTTT LITTPQNQVDMLLQEMADBAGLDLNMELPQGQTGSVGTSVASABQ DELSQRLARLRDQV PTAMAREGIAAGGVMDVNTALQBVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVBALCABHQLNLIKVDDNKKL GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIERYFK CKK ERVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLF YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMTTITSALTTKE TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP
6237	312	720	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIREATRPIKQNIVI SSGFVGGFLIGLAS WDQNKGARAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFARKBLSRSAKKCDKEBKABKAKIKKAIQKGNMEVARIHAE NAIRQKRQAVNFLKMSARVDAVAARVOTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISALMDKPEHQFETLDVQTQOMRDTMSSTTT LTTPQNQVDMLLQEMADRAGLDLNMELPQGQTGSVGTSVASABQ DELSQRLARLRDQV PTAMAEEGIAAGGVMDVNTALQBVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCABHQINLIKVDDNKKL GBWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIERYFK CKK ERVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRGKITTVLQPCDLF YQTTQKGTDPQVIDMSVKSLTLKVS?VIINTMITITSALYTTKE TIPEETASSTAHLWEKKDTKTLKMWFLEESNETKLAPTTELVP KGEMIKMNIDSIPIVLEAGIGHRTVPMLLAKSRFSGEGKNNSSL
6237	312	720	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIEEATEPIKQNIVI SSGFVGGFLIGLAS WDONKGARAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAAKBLSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAE NAIRQKNQAVNFLKMSARVDAVAARVOTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISALMDKFEHQFETLDVQTQOMEDTMSSTTT LTTPQNQVDMLLQEMADBAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLRDQV PTAMAEEGIAAGGVMDVNTALQBVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCAKHQINLIKVDDNKKL GBWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIERYFK CKK EKVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLF YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALTTKE TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP KGEMIKMNIDSIPIVLEAGIGHRTVPMLLAKSRFSGEGKNNSSL INIHCQLELEVHYYNEMFGWWEPLLEPLEIDQTEDFRPWNLGIK MKKKAKMAIVESDPEERNYKVPRYKTVISFHSKDQLNITLSKCG
6237	312	720	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIEEATEPIKQNIVI SSGFVGGFLIGLAS WDQNKGARAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAAKBLSRSAKKCDKEEKAEKAKIKKALQKGNMEVAR IHAE NAIRQKNQAVNFLKMSARVDAVAARVOTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISALMDKFEHQFETLDVQTQOMEDTMSSTTT LTTPQNQVDMLLQEMADBAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLRDQV PTAMAEGIAAGGVMDVNTALQBVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCAKHQINLIKVDDNKKL GBWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEBYFK CKK EKVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLP YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMTITSALTTKE TIPEETASSTAHLWEKKDTKTLKWFLEESNETBKIAPTTELVP KGEMIKMNIDSIFIVLKAGIGHRTVPMLLAKSRFSGEGKNNSSL INLHCQLELEVHYNNEMFGVWEPLLEPLEIDOTEDFRPWNIGIK MKKKAKMAIVRSDPRERNYKVPRYKTVISFHSKDQLNITLSKCG
6237	312	720	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIEEATEPIKQNIVI SSGFVGGFLIGLAS WDONKGARAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAAKBLSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAE NAIRQKNQAVNFLKMSARVDAVAARVOTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISALMDKFEHQFETLDVQTQOMEDTMSSTTT LTTPQNQVDMLLQEMADBAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLRDQV PTAMAEEGIAAGGVMDVNTALQBVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCAKHQINLIKVDDNKKL GBWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIERYFK CKK EKVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLF YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALTTKE TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP KGEMIKMNIDSIPIVLEAGIGHRTVPMLLAKSRFSGEGKNNSSL INIHCQLELEVHYYNEMFGWWEPLLEPLEIDQTEDFRPWNLGIK MKKKAKMAIVESDPEERNYKVPRYKTVISFHSKDQLNITLSKCG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1.	corresponding	to first	L=Leucine, M=Methlonine, N=Asparagine,
Į.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			DTVEGSKKVTIRSPVQIRNHFSVPLSVYBGDTLLGTASPBNEFN
ľ			IPLGSYRSF1FLKPEDENYQMCEGIDFEE11KNDGALLKKKCRS
l			KNPSKESFLINIVPEKDNLTSLSVYSEDGWDLPYIMHLWPPILL
	}		RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQLGKARLHLKL
		•	LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT
ł			YNTGQTVVAFHSPYWMVNKTGRMLQYKADGIHRKHPPNYKKPVL
			PSFQPNHFFNNNKVQLMVTDSBLSNQFSIDTVGSHGAVKCKGLK
1			MDYQVGVTIDLSSFNITRIVTFTPFYMIKNKSKYHISVAEEGND
			KWLSLDLEQCIPFWPKYASSKLLIQVERSEDPPKRIYFNKQENC
1	,		ILLRLDNBLGGIIARVNLAEHSTVITFLDYHDGAATFLLINHTK
	1		NELVQYNQSSLSEIRDSLPPGKAVFYTWADPVGSRRLKWRCRKS
	İ		HGRVTQKDDMMMPIDLGEKTIYLVSFFEGLQRIILFTKDPRVFK
(			VTYESEKAELAEQEIAVALQDVGISLVNNYTKQEVAYIGITSSD
}	1		VVWETKPKKKARWKPMSVKHTEKLEREFKBYTESSP9EDKV1QL
Ì	, ,		DTNVPVRLTPTGHNMKILQPHVIALRRNYLPALKVEYNTSAHQS
l			SFRIQIYRIQIQNQIHGAVFPFVFYPVKPPKSVTMDSAPKPFTD
1			VSIVMRSAGHSQISRIKYFKVLIQEMDLRLDLGFIYALTDLMTR
•			ABVTENTEVELPHKDIRAFKERYKTASLVDQSQVSLYEYFHISP
<u> </u>	}		IKLHLSVSLSSGREKAKDSKONGGLIPVHSLNLLLKSIGATLTD
1			VQDVVFKLAFFELNYQFHTTSDLQSEVIREYSKQAIKQMYVLIL
i			GLDVLGNPFGLIREFSEGVEAFFYEPYQGAIQGPEEFVEGMALG
	<u>}</u>		LKALVGGAVGGLAGAASKITGAMAKGVAAMTMDEDYQQKRREAM
ľ	· ·	İ	NKQPAGFREGITRGGKGLVSGFVSGITGIVTKPIKGAQKGGAAG
l			FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR
			PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD
<u> </u>	l		DDDDDDDDBSDLNH
6239	2108	634	KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEBSFNLQA
ŀ			THOLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL
		į	SLLEMSKFYSQLIVRGVIGLGVIFGLWTLQKEVRRHFGAMVATM
i	1		FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI
	ŀ	Į	WLSAFAIIVFRV3LCLFLGLLLLLALGNRKVSVVRALRHAVPAG
ŀ			ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL
1			WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL
	}		PHKELRFIIYAF?MLNITAARGCSYLLNNYKKSWLYKAGSLLVI
	1		GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI
1			DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA
ļ	i		PGLLALYROTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL
			ERLPRPS
6240	2202	1176	HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF
[	1		DPLSSGSRSSSLKSAQGTGF3LGQLQSIRSEGTTSTSYKSLANQ
1	1		TRNGSLSYDSLLTPSDSPDFESVQAGPRPDPPLGYTSPFLSARL
ļ	1		AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL
1			LRQSPPLPGREERPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP
1	I		LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS
[	1		SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS
			ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV
6241	3	1341	RNABEKKRISLQREKITARVSIDNRTRALVQALRRTTDPKLCIT
l	1		RVEELTFHLLBPPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR
'	1		EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ
			KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV
1	l	ļ	FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIBTARNP
1			TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM
Ì	1	}	WQAIRASSAAPGYFAKYALGNDLHQDGGLLLINNPSALAMHECKC
1			LWPDVPLECIVSLGTGRYRSDVRNTVTYTSLKTKLSNVINSATD
[	l		TERVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLR
1	1		GLKYIBRNEQKMKKVAKILSQEKTTLQKINDWIKLKTDMYEGLP

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alarine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, P-Phenylalanine, G-Glycine.
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
I	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	seguence		\=possible nucleotide insertion)
			PFSKL.
6242	198	1310	QHPLPGAETWSPGAAVCTARRFPGRSLAAFPRPAAPRRAVEMGE
		Į	SSEDIDOMFSTLLGEMDLLTQSLGVDTLPPPDPNPPRAEFNYSV
ı	Ĭ	<b>[</b>	GFKDLNESLNALEDQDLDALMADLVADISRAEQRTIQAQKESLQ
1	[		NQHHSASLQASIFSGAASLGYGTNVAATGISQYKDDLPPPPADP
ì		·	VLDLPLPPPPPEPLSQEREEAQAKADKIKLALEKLKRAKVKKLV
	ŀ		VKVHMNDNSTKSLMVDERQLARDVLDNLPBKTHCDCNVDWCLYB
	ŀ		IYPELQIBRPFEDHENVVEVLSDWTRDTENKILFLEKEEKYAVF
ì	ļ	<b>{</b>	KNPQNFYLDNRGKKESKETNEKMNAKNKESLLEVRLILQSGRKE
6243	1509	614 .	KDVCSIFKSPASENNGKI
0243	1509	674	RSASRFSGCWSRDSTCCCCPSTCWSRSSASCPRARWPPSSAPAT TSRASSRRLACGPOTRAGAETRSTAMIRANSAARDTRRATCRSA
			AGTPSPTIMTCLTDVPTGCAAVEPTARLPAAAMASTITTGCCPA
!			MGQAGAGPAGRKGSEAGGGPGRAHHAHPSPLPREPRVRTGPPAH
ì			SPTPGSIDPSPELSWGSAGVTQESPLLDPVDFLLFRTRAVDPLR
1	]		RVFFFFYOHLTFFSIOPOPPPCHAFHPRDPPAGTKROLILVPLK
1	İ		GPPILAPILSLTPILSRWSCYFPRSRIAQGWHLS
5244	2119	1745	FEHAYASQFGTFLGNNESERCKLKLQQKTMSLWSWVNQPSELSK
	1		FINPLFRANNLVIWPSVAPQSLPLWEGIFLRWNRSSKYLDRAYE
l			EMVNIIEYNKELQAKVNILRRQLAELETEDGMQBSP
6245	81	1148	LSLRNAKYSFPQKLISLFSMTDLNDNICKRYIKMITNIVILSLI
]			ICISLAFWIISMTASTYYGNLRPISPWRWLFSVVVPVLIVSNGL
1	ļ		KKKSLDHSGALGGLVVGPILTIANFSFFTSLLMFFLSSSKLTKM
1			KGEVKKRLDSEYKEGGQRNWVQVFCNGAVPTELALLYMIENGPG
1	•		BIPVDFSKQYSASWMCLSLLAALACSAGDTWASBVGPVLSK\$SP
	ļ <sup>i</sup>	, i	RLITTWEKVPVGTNGGVTVVGLVSSLLGGTFVGLAYFLTQLIFV NDLDISAPQWPIIAFGGLAGLLGSIVDSYLGATMQYTGLDESTG
1			MVVNSPTNKARHIAGKPILDNNAVNLFSSVLIALLLPTAAWGFW
	ļ		PRG
6246	1177	359	SLWPWILMODSLMQISLOLLCVYTANFPNGCSSLCWSSCGOHPV
			QATHRGAVSNSLMLCILKLASQMPLENTTVQQMVPMLLSNLALS
			HDCKGVIOKSNFLONFLSLALPKGGNKHLSNLTILWLKLLLNIS
l			SGEDGQQMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCFS
			PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ
			KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN
			LVQLLNSS
6247	3	1678	NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP
			PGPGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL
			YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV
ĺ			SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS
1			LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSIG
		1	QVTAIFICIGVFTGQLIGLPELLGKRSTWPYLFGVIVVPAVVQL
1			LSLPFLPDSPRYLLLEKHNEARAVKAPQTFLGKAHVSQEVREVL
1			ABSRVQRSIRLVSVLEILRAPYVRWQVVTVIVTMACYQLCGLNA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIRHI
]			GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI
1			IASFCSGPGGIPPILTGEFFQQSQRPAAFIIAGTVNWLSNPAVG
1			LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI
		•	SOAFSKRNKAYPPEEKIDSAVTDGKINGRP
6248	56	1773	VPPPRMMAAVPPGLE?WNRVRIPKAGNRSAVTVONPGAALDLCI
1			AAVIKECHLVILSLKSOTLDAETDVLCAVLYSNHNRMGRHKPHL
[		•	ALKQVBQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP
			SQPVVBLVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII
1			LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP
	•		YFKDFTFPSDITEFLGQPYFRAFKKKMPIAFAAKGINKLLNKLF
1			LINEQSPRASEETLIGISKKAKOMKINVONNVDLGQPVKNKRVP

SEQ	Predicted	Predicted end	Drive poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=Glutamic Acid, F=Phenylalanine, G=Glycine,
""	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			KEBSSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
1		i	VIGTPHAKSFVQRFREAESFTQLSEBIQMAVVWCRSKKLKAQAI
1			FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
}	Ì		TSKHHLRORRSONKFLRRORKPORKLOSTLLRBIOOFSOGTRKS
1	<b>!</b>		ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKBKMI
1			HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6249	56	1773	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI
1			AAVIKECHLVILSLKSQTLDARTDVLCAVLYSNHNRMGRHKPHL
l			ALKOVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP
1			SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQBFII
1			LNLVMVGLVSRLWVLYKGVLKRLILLYBPLFGLLQEVARIQPMP
1			YPKDFTPPSDITEFLGQPYPRAFKKKMPIAFAAKGINKLLNKLF
			LINEQSPRASEBTLLGISKKAKQMKINVQNNVDLGQPVKNKRVF
			KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
J i			VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAQAI
1			FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
1			TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
1			ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
6250	232	1306	HENLEGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
1	232	1300	LAALHIMALPFRKDLEKYKOLDEDKLIGNISETELKQLETVLDD LDPENALLPAGFRQKNQTSKSTTGPFDREHLLSYLEKEALEHKD
			REDYVPYTGEKKGKIFIPKQKPVQTFTEEKVSLDPELEEALTSA
1			SDTELCDLAAILGMHNLITNTKFCNIMGSSNGVDQRHFSNVVKG
	·		EKILPVFDBPPNPTNVEESLKRTKENDAHLVEVNLNNIKNIPIP
			TLKDFAKALETNTHVKCFSLAATRSNDPVATAFAEMLKVNKTLK
			SLNVESNFITGVGILALIDALRDNETLABLKIDNQRQQLGTAVE
			LEMAKMLEENTNILKFGYQFTQQGPRTRAANAITKNNDLVRKRR
			VEGDHQ
6251	62	972	TPGSGPMSAWAAASLSRAAARCLLARGPGVRAAPPRDPRPSHPE
1 3			PRGCGAAPGRTLHFTAAVPAGHNKWSKVRHIKGPKDVBRSRIFS
1 1			KLCLNIRLAVKEGGPNPEHNSNLANILEVCRSKHMPKSTIRTAL
	l l		KMEKSKDTYLLYEGRGPGGSSLLIEALSNSSHKCQADIRHILNK
}			NGGVMAVGARHSFDKKGVIVVEVEDREKKAVNLERALEMAIEAG
	1		AEDVKETEDBEBERNVFKFICDASSLHQVRKKLDSLGLCSVSCAL EFIPNSKVQLAEPDLEQAAHLIQALSNHEDVIHVYDNIR
6252	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
]		2031	BTVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPOV
	· 1		PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR
	į		KLPHSKAKTRSRLEVARAREERTSIKAARSELLLAREPGFLEGE
	I		DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG
	i		RHLAFGGRRGHVAALDWYTKKLMCBINVMBAVRDIRFLHSEALL
j i	l		AVAQNRWLHIYDNQGIBLHCIRRCDRVTRLEFLPFHFLLATASE
	)		TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
	ŀ		TVSLWSPAMKKPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
1 1	ſ		KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA
į j			GQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT
			SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPARLIC
	I		LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
	i		SSTASLVKRKRKVMDEKHRDKVRQSLQQQHHKRAKAKPTGARPS
J		·	ALDRFVR
6253	27	1897	EEFCTWIAVRVGEMETAPKPGKOVPPKKDKLQTKRKKPRRYWEE
]	j		ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
	1		PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR
			KLPHSKAKTRSRLEVARABEBETSIKAARSELLLAEBPGFLEGE
		l	DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG
LL			RHLAFGGRRGHVAALDWVTKKLMCBINVMBAVRDIRFLHSRALL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F≂Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
[			AVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFLLATASE
ŀ	4	1	TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
	ļ		TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
ļ.			KIPDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA
1	j .	ļ	GQGKASPPSLEQPYLTHRLSGPVHGLQFCPPEDVLGVGHTGGIT
1		<b>,</b>	SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPAELIC
1	1	1	LDPRALAEVDVISLEQGKKEQIBRLGYDPQAKAPFQPKPKQKGR
ł			SSTASLVKRKRKVMDBEHRDKVRQSLQQQHHKBAKAKPTGARPS
			ALDREVR
6254	155	. 1139	HALGREGGSQELSAAACGCFALELEAPGSGEPALAPGAAAFAGL
1	1		GGAPRFPPRGSAAGRTMLLKEYRICMPLTVDEYKIGQLYMISKH
1	<b>(</b>	1	SHEQSDRGEGVEVVQNEPFEDPHHGNGQFTEKRVYLNSKLPSWA
1	1	1	RAVVPKIFYVTEKAWNYYPYTITEYTCSFLPKFSIHIETKYEDN
Į.	}	1	KGSNDTIFDNEAKDVEREVCFIDIACDEIPERYYKESEDPKHFK
1	I	1	SEKTGRGQLREGWRDSHQPIMCSYKLVTVKFEVWGLQTRVEQFV
ļ		1	HXVVRDILLIGHRQAPAWVDEWYDMTMDDVREYEKNMHEQTNIK
			VCNQHSSPVDDIRSHAQTST
6255	1	1444	PTRPQQRLLVSLATVI FVASQKALSVESKAVI KQQLESVSNGWT
i	<u> </u>	1	VYRIARQASRMGNHDMAKBLYQSLLTQVASKHFYFWLNSLKEFS
l			HABQCLTGLQEENYSSALSCIABSLKFYHKGIASLTAASTPLNP
ŀ		l	LSFQCEFVKLRIDLLQAFSQLICTCNSLKTSPPPAIATTIAMTL
l			GNDLQRCGRISNQMKQSMEEPRSLASRYGDLYQASFDADSATLR
f		l	NVELQQQSCLLISHAIEALILDPESASPQEYGSTGTAHADSEYE
	Į		RRMMSVYNHVLEEVESLNGKYTPVSYMHTACLCNAIIALLKVPL
		1	SFORYFFOKLOSTSIKLALSPSPRNPARPIAVONNOOLALKVEG VVOHGSKPGLFRKIQSVCLNVSSTLOSKSGODYKIPIDNMTNEM
Į.	Į.	Į.	BORVEPHNDYFSTOFLLNPAILGTHNITVESSVXDANGIVWKTG
ļ	ļ		PRTTIFVKSLEDPYSQQIRLQQQQQQQQQQQQQQRNAYTRF
6256	1	1542	CRGAGAEPAANPRSPRSLVPSLESTSTSVPFAPGTMATDSWALA
0250	<u> </u>	1342	VDEQEAAAESLSNLHLKEEKIKPDINGAVVKINANAEKIDEEK
Į			EDRAAQSILINKLIRSNIJONTNQVEVIQRDPNSPLYSVKSFEEL
1	ĺ		RLKPOLLOGVYAMGFNRPSKIOKNALPLMLAEPPONLIAOSQSG
1	ł	ł	TGKTAAFVLAMLSQVEPANKYPQCLCLSPTYELALQTGKVIEQM
1	İ	l	GKFYPELKLAYAVRGNKLERGOKISEQIVIGTPGTVLDWCSKLK
Į	l	l	FIDPKKIKVFVLDEADVMIATQGHQDQSIRIQRMLPRNCQMLLF
	1		SATFEDSVWKFAQKVVPDPNVIKLKREEETLDTIKQYYVLCSSR
1		l	DEKFQALCHLYGAITIAQAMIFCHTRKTASWLAARLSKEGHQVA
		[	LLSGEMMVBQRAAVIERPREGKEKVLVTTNVCARGIDVEQVSVV
1	ļ	l	INFOLPYDKOGNPONETYLHRIGRIGREGKRGLAVNMVDSKHSM
1		1	NILNRIOEHFNKKIERLDTDDLDEIEKIAN
6257	210	615	AFIPAMARLIOKKLOGEVEKYOOLOKDLSKSMSGROKLEAQLTE
	1		NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI
1		l	TAEIKRYESOLRDLEROSEQORETLAQLQQBFQRAQAAKAGAPG
1			KA
6258	210	615	AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE
	]	]	NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI
1			TAEIKRYBSQLRDLERQSBQQRBTLAQLQQBFQRAQAAKAGAPG
		]	KA KA
6259	2	1540	ILEKGFPSOCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV
		)	SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII
í I		1	SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDOKRNAI
i			NYHQDLSQPSFGQSFEYSKNGQGPHDBAAFFTNKRSQIGETVCK
			YNECGRIFIESI,KLNISQRPHLEMEPYGCSICGKSPCMNLRFGH
1	,	Ì	QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD
			QKALIKUNPYEYNEYGELPCUNSAFILHQAATIKALUKEIKVSU   KTWEKSALLKHQIVHMGGKSYDYNENGSNPSKKSHLTQLRRAHT
1			
1	L	Ī	GEKTFECGECGKTFWEKSNLTQHQRTHTGEKPYECTECGKAFCQ

WO 01/53312

SEQ	Predicted	Predicted end	The state of the s
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H-Histidine, I-Isoleucine, K-Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
!	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
<u> </u>	<del>                                     </del>	<del></del>	KPHLTNHQRTHTGEKPYECKQCGKTFCVKSNLTEHQRTHTGEKP
1			YECNACGKSFCHRSALTVHQRTHTGEKPFICNECGKSFCVKSNL
l	ļ		IVHQRTHTGEKPYKCNECGKTFCEKSALTKHQRTHTGEKPYECN
ŀ	1	ļ	ACGKTFSQRSVLTKHQRIHTRVKALSTS
6260	2081	1436	GTGPEIHACAHASARAPGSRAMALRELKVCLLGDTGVGKSSIVW
1			RFVEDSFDPNINPTIGASFMTKTVQYQNELHKFLIWDTAGQERF
ŀ			RALAPMYYRGSAAAIIVYDITKRETFSTLKNWVKELROHGPPNI
1	i		VVAIAGNKCDLIDVREVMERDAKDYADSIHAIFVETSAKNAINI
			NELFIEISRRIPSTDANLPSGGKGFKLRRQPSEPKRSCC
6261	3	1188	FWYRLGPGTRSRWPRRGSWAASLVPRGPSPAALVTSPCPPDPLR
			SPACEPCRPDFAPRPALLLRSGPRSAPAVTGKPALKGQPGPWPG
1			MAEVSIDQSKLPGVKEVCRDFAVLEDHTLAHSLQEQEIEHHLAS
1			NVQRNRLVQHDLQVAKQLQEEDLKAQAQLQKRYKDLEQQDCBIA
	i i		QEIQEKLAIKAERRRIQEKKDEDIARLLQEKELQEEKKRKKHFP
1			EFPATRAYADSYYYEDGGMKPRVMKBAVSTPSRMAHRDQBWYDA
1			BIARKLQBBBLLATQVDMRAAQVAQDBEIARLLMAEEKKAYKKA
1			KEREKSSLDKRKQDPEWKPKTAKAANSKSKESDEPHH9KNERPA RPPPPIMTDGBDADYTHFTNQQSSTRHFSKSESSHKGFHYKH
6262	2	1759	PRCHSOGLCSVHRPGKVPQARMSGLVLGQRDBPAGHRLSQRKIL
1	-	2,00	GSTRLVSQGLEALRSEHQAVIQSISQTIECLQQGGHEEGLVHEK
1			ARQLRRSMENTELGLSEAQVMLALASHLSTVESEKQKLRAQVRR
1			LCQENQWLRDELAGTQQRLQRSEQAVAQLEBEKKHLEFLGQLRQ
1			YDEDGHTSREKEGDATKDSLDDLFPNEEBBDPSNGLSRGQGATA
			AQQGGYEIPARLRTLHNLVIQYAAQGRYEVAVPLCKQALEDLER
ł			TSGRGHPDVATMLNILALVYRDQNKYKBAAHLLNDALSIRESTL
ł			GPDHPAVAATLNNLAVLYGKRGKYKEAEPLCQRALEIREKVLGT
			NHPDVAKQLNNLALLCQNQGKYBAVERYYQRALAIYEGQLGPDN
ı			PNVARTKNINLASCYLKQGKYABABTLYKBILTRAHVQEFGSVDD
		•	DHKPIWMHAEEREEMSKSRHHEGGTPYARYGGWYKACKVSSPTV
1 :			NTTLRNLGALYRROGKLKAAETLEECALRSRROGTDPISQTKVA
			ELLGESDGRRTSQEGPGDSVKPEGGEDASVAVEWSGDGSGTLQR SGSLGKIRDVLRR
6263	1	2408	RELDSLADLPERIKPPYANGLSTSHLRSSSVKDVKLIISEGRPT
			IEVRRCSMPSVICEHTKQFQTISERSNQGSLLTVPGDTSPSPKP
1			EVFSNVPERDLSNVSNIHSSFATSPTGASNSKYVSADRNLIKNT
1 .			APVNTVMDSPVHLEPSSQVGVIQNKSWEMPVDRLETLSTRDFIC
i i			PNSNIPDQESSLQSFCNSENKVLKENADFLSLRQTELPGNSCAQ
1 1			DPASFMPPQQPCSFPSQSLSDARSISKHMSLSYVANQBPGILQQ
<b>)</b>			KNAVQIISSALDTDNESTKDTENTFVLGDVQKTDAFVPVYSDST
1 1			IQEASPNFEKAYTLPVLPSEKDFNGSDASTQLNTHYAFSKLTYK
1			SSSGHEVENSTTDTQVISHEKENKLESLVLTHLSRCDSDLCEMN
!	į		AGMPKGNLNEQDPKHCPESEKCLLSIEDERSQQSILSSLENHSQ
)	į		QSTQPEMHKYGQLVKVKLRENARDDKTENQIPQRMTRNKANTMA
1 1	J		NQSKQILASCTLLSEKDSESSSPRGRIRLTEDDDPQIHHPRKRK
	1		VSRVPQPVQVSPSILQAKEKTQQSLAAIVDSLKLDEIQPYSSER
] [	]		ANPYFEYLHIRKKIEEKRKLLCSVIPQAPQYYDEYVTFNGSYLL
[	İ		DENPLSKICIPTITPPPSLSDPLKELFRQQBVVRMKLRLQHSIE RBKLIVSNEQEVLRVHYRAARTLANQTLPFSACIVLLDAEVYNV
]	l		PLDSQSDDSKTSVRDRFNARQFMSWLQDVDDKFDKLKTCLLMRQ
] [	ļ		
1 1	1		QHEAAALWAVQRLEWQLKLQELDPATYKSISIYKIQEFYVPLVD VNDDFKLTPI
6264	143	1960	KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI
			TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
j [	1		WMMCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL
] ]			SSTLVYNSMGTINQQAMDQLYYVTKLTHRIRSKSSPDENKNRDS
	1		ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT

·			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
<b>!</b>	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ı 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			SQKDKNFNLPRLCIRKFPPKKKCFVPDLPIHRRKLAQLEKLQD8
			BLDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
1			INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ
ı î			LPABTIQKLIDLHRVSEREATBVYMKNSPKDVDHLFQKKLAAQL
		,	DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEBVKAGIYSKPGG
			YCLFIQKLQDLEKKYYEEPRKGIQAEBILQTYLKSKESVTDAIL
			QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK
1 }	1	}	BKSYQEHVKQLTBKMERERAQLLEEQBKTLTSKLQEQARVLKBR
			CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6265	143	1960	KHRQENNALDMAPBIHMTGPMCLIENTNGELVANPEALKILSAI
1			TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGPSLGSTVKSHTKGI
į į			WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL
			SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS
			ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT
1 1			SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDB
			ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
		}	INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ
			LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLPQKKLAAQL
			DKKRDDPCKQNQBASSDRCSALLQVIFSPLBEEVKAGIYSKPGG
1			YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL
			QTDQILTEKEKEIBVECVKAESAQASAKMVBEMQIKYQQMMBEK
(			EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER
			COGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6266	. 276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE
			GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD
i I			ISSRGGLGVSSSTDGTMKIWQASNGBLRRVLEGHVPDVNCCRFF
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR
			GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN
		. '	SINIGSPEQMPSEREVGTEARMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH
; J			RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD
1			PVYKVATWEKQIYTCCRDGLVRRYQLSDL
6267	3	622	LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGRGIFREIWK
020,	•		NRYVVLKGDOLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS
			RSKKNHSKPTLAHSKQPGNTAPNLIFLAVSPKEKESWINALNSA
			ITRAKNRILDEVTVEEDSYLAHPTRORAKIQHSRRPPTRGHLMA
			VASTSTSDGMLTLDLIQEEDPSPERPTSLC
6268	160	1368	HRELCONLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV
0200			DESREEWGLIGPTORTEYRDVMLETFGHLVSVGWETTLENKELA
			PNSDIPEEPAPSLKVOBSSRDCALSSTLEDTLOGGVORVODTV
1			LKOMESAORKOLPOKKHPONRESQANSGALDTNOVSLOKIONPE
i I			SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ
			KSCEROKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK
			1FRNPRYFSVHKKIHTGBRPXVCQDCGKGFVQSSSLTQHQRVHS
			GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ
		1	SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR
			KKKQPTS
6269			\ \ \( \tau_{
	2886	1449	
1	2886	1449	HASAPTRRNMAAASPLRDCHAWKDÄRLPLSTTSNEACKLFDATL TOYVKWINDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT
0203	2886	1449	TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT
0203	2886	1449	TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKBLDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN
	2886	1449	TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKBLDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN FPKACBLWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR
	2886	1449	TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKBLDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN FPKACBLWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKRALSINP
	2886	1449	TQYVKWINDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKBLDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN FPKACBLWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKRALSINP TDAWSVHTVAHIHEMKABIKDGLBFMQHSBTLWKDSDMLACHNY
	2886	1449	TQYVKWINDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKBLDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN FPKACBLWBQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQABKLAKBALSINP TDAWSVHTVAHIHEMKABIKDGLBFMQHSBTLWKDSDMLACHNY WHWALYLIEKGEYRAALTIYDTHILPSLQANDAMLDVVDSCSML
	2886	1449	TQYVKWINDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKBLDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN FPKACBLWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKRALSINP TDAWSVHTVAHIHEMKABIKDGLBFMQHSBTLWKDSDMLACHNY

		¥ `	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
į	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
<u> </u>	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ì	sequence	1 -	\=possible nucleotide insertion)
	<del></del>		DENPDRVLELLLPIRYRIVOLGGSNAORDVFNOLLIHAALNCTS
l		l	SVHKNVARSLLMERDALKPNSPLTERLIRKAATVHLMO
6270	23	2086	SVTVTLGSEGDCRPPTYHLBEMEQEPONGRPAEIKIIREAYKKA
02.70	25	1	FLEVNKGLNTDELGQKERAKNYYKQGIGHLLRGISISSKESEHT
	Į.		GPGWESARQMQQKMKETLQNVRTRLEILEKGLATSLQNDLQEVP
			KLYPEFPPKDMCEKLPEPQSFSSAPQHAEVNGNTSTPSAGAVAA
	1		PASLSLPSQSCPAEAPPAYTPQAAEGHYTVSYGTDSGEFSSVGE
	i	1	BFYRNHSQPPPLBTLGLDADELILIPNGVQIFFVNPAGEVSAPS
		Į.	•
	l		YPGYLRIVRFLDNSLDTVLNRPPGFLQVCDWLYPLVPDRSPVLK
1	1	1	CTAGAYMFPDTMLQAAGCFVGVVLSSELPEDDRELFEDLLRQMS
ļ	[	!	DLRIQANWNRAREENBFQIPGRTRPSSDQLKEASGTDVKQLDQG
		1	NKDVRHKGKRGKRAKDTSSEEVNLSHIVPCEPVPEEKPKBLPEW
}	]	1	SEKVAHNILSGASWVSWGLVKGABITGKAIQKGASKLRERIQPE
	[		EKPVEVSPAVTKGLYLAKQATGGAAKVSQFLVDGVCTVANCVGK
1	Į	ł	BLAPHVKKHGSKLVPESLKKDKDGKSPLDGAMVVAASSVQGFST
		i	vwqglecaakcivnnvsaktvqtvrykygynageathhavdsav
ŀ	}		NVGVTAYNINNIGIKAMVKKTATQTGHTLLEDYQIVDNSQRENQ
	L	Ĺ	BGAANVNVRGEKDEQTKEVKRAKKKDK
6271	32	1058	GCGVKTAGMVGREKELSIHFVPGSCRLVEBEVNIPNRRVLVTGA
	Ì		TGLLGRAVHKBFQQNNWHAVGCGFRRARPKFBQVNLLDSNAVHH
1	1	1	IIHDFQPHVIVHCAAERRPDVVENQPDAASQLNVDASGNLAKEA
!			AAVGAFLIYISSDYVFDGTNPPYREEDIPAPLNLYGKTKLDGKK
Ì	] .	' '	AVLENNLGAAVLRIPILYGEVEKLEESAVTVMFDKVQFSNKSAN
1	· ·		MDHWQQRFPTHVKDVATVCRQLAEKRMLDPSIKGTFHWSGNEQM
ļ			TKYEMACAIADAFNLPSSHLRPITDSPVLGAQRPRNAQLDCSKL
Ì			RTLGIGQRTPFRIGIKESLWPFLIDKRWRQTVFH
6272	1136	528	CAVMEDAAAPGRTEGVLERQGAPPAAGQGGALVELTPTPGGLAL
ļ		1	VSPYHTHRAGDPLDLVALAEQVQKADEFIRANATNKLTVIAEQI
i	,		QHLQEQARKVLEDAHRDANLHHVACNIVKKPGNIYYLYKRESGQ
•			QYFSIISPKEWGTSCPHDFLGAYKLQHDLSWTPYEDIBKQDAKI
ì			SMMDTLLSQSVALPPCTEPNFQGLTH
6273	256	843	SCPRVSPECRSLGCQVMFSLPLNCSPDHIRRGSCWGRPQDLKIA
			SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV
1	]		HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS
<b>\$</b>	1		ITCFVRKWKBKVANPRLTKEDIKPVWLSVDFDNWRDWEGDBEME
Į.	1		LAHVEHYAEVRONTYCVLPT
6274	56	1142	AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT
}	1	1	VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL
ļ	1	1	LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR
1		l	DVFRPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS
1		l .	AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED
}	}	1	LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS
l	· ·	Į.	ELGNGIAAPESVPTAIYCFLRCMBPDPBIPSAFNSLQRTLIYSI
	1	1	SLGGDTDTIATMAGAIAGAYYGMDOVPRSWQQSCEGYEETDILA
1			OSLHRVFOKS
6275	20	565	SRRGRARCLARGSRRPVPRPAKTMAFMVKTMVGGOLKNLTGSLG
02/3		""	GGEDKGDGDKSAAEAQGMSREEYEEYOKQLVEEKMERDAOFTOR
1			KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRBLAKMI
1	}	1	RABRATERSHERDAT REPARETURSQLQMASGDVERPRELARMT BEDTBERERKASVLGQLASLPGLNLGSLKDKAQATLGDLKQSAE
ļ	1	(	
		<del> </del>	KCHVM
6276	797	97	TLLPLPPLPDTEGMILLNTGLEGTVAENPVPIVHTPSGNILTLE
02/0			SCLOOLATHPGHWGIHLOIAEPAALRPSLALLARLSSLGLLHWP
02/0		)	
52.70			VWVCAKISHGSPSVPGHVAGRELLTAVAEVFPHVTVAPGWPEEV
1 0270	5		VWVGAKISHGSPSVPGHVAGRELLTAVAEVFPHVTVAPGWPBEV LGSGYREQLLTDMLELCQGLWQPVSPQMQAMLLGHSTAGAIGRL
<b>3270</b>			VWVCAKISHGSPSVPGHVAGRELLTAVAEVFPHVTVAPGWPEEV

SEQ Predicted Predicted end hucleotide (A=Alanine, C=Cysteine, D=Aspartic flucation corresponding H=Histidine, I=Isoleucine, K=Lysine	
NO: nucleotide location Glutamic Acid, F=Phenylalanine, G=G location corresponding H=Histidine, I=Isoleucine, K=Lysine	
location corresponding H=Histidine, I=Isoleucine, K=Lysine	
I I I I I I I I I I I I I I I I I I I	
corresponding to first beleatine, M=Methionine, N=Asparagi	ne,
to first amino acid P=Proline, Q=Glutamine, R=Arginine, amino acid residue of S=Serine, T=Threonine, V=Valine,	
	tu Cham
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknown	
amino acid sequence Codon, /=possible nucleotide deleti	on,
sequence \=possible nucleotide insertion)	MANAGENE VET NOO
6277 4600 2744 MAPRIEMGLYYSYPKTIVEAPSFLNGVWMIMNDKL	
LKRPNLYPEVILASWYRIYTKIMDLIGIQTKICWT	
TESCEGLGDPACFYVAVIFILNGLMMALFFIYGTY	
VTVLCFFFNHGECTRVMWTPPLRESFSYPFLVLQM	
TKLYRGSLIALCISNVFFMLPWQFAQFVLLTQIAS	
IDICKLRXIIYIHMISLALCPVLMPGNSMLLTSYY	
ILAMKPHFLKINVSELSLWVIQGCFWLFGTVILKY	
NDAHIGNLLTSKFFSYKDFDTLLYTCAARFDFMRK	
LLLEPVVLVGFVAIVRKIISDMWGVLAKQQTHVRKH	
HALQLLAYTALGILIMRIKLFLTPHMCVMASLICS	
KVHPGAIVFAILAAMSIQGSANLQTQWNIVGEFSN	-
IKYSTKPDAVFAGAMPTMASVKISALRPIVNHPHY	
KIVYSNYSRKAAREVKRELIKLKVNYYILEESWCV	
PRIWDVEDPANAGKTPLCNLLVKDSKPHFTTVFQN	SALKAPEAA
KB KB	AVERTONIC TV
6278 3 823 ILFRLVILLSLVYLLNSVATEERKPABVLIVEGQQY IRIILEYCOGVDNIPSVTTDMLTRLSDLLKYFNSR	
ALOVVGLKTITTKNIALSSRCIOLIVHYIPVIRAH	
1 1	
YSMLRHFDHITKDYHDHIARISAKLVAINDSLFDK PVPSACFRNICKOMTKMHRAIFDLLPEBOTOMLFL	
LKKOLSHLNVINDGGPONGLVTADVAFYTGNLQAL	l.
MARINEQXR	MIGHTON
J I	EDDLT.UCTT.
6279 127 1687 GGAMASDGARKQFWKRSNSKLPGSIQHVYGAQHPP LRSTAKMPTTPVKAKRVSTFQEFESNTSDANDAGR	
ABSLINSEVVMETANRVLRNHSQRQGRPTLQEGPGL PPSPPSGDLRLVKSVSESHTSCPARSASDAAPLQR	
VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGE	
LSWSGIPKPVRPMTWKLLSGYLPANVDRRPATLQR	
EHYYDSRNDEVHODTYRQIHIDIPRMSPEALILQP	-
LFIWAIRHPASGYVQQINDLVTPPFVVPICEYIEA	
GVPABVLCNIEADTYWCMSKLLDGIQDNYTFAQPG	
BLVSRIDEQVHRHLDQHEVRYLQFAFRWMMNLLMR	
LWDTYQSEPDGFSHFHLYVCAAFLVRWRKBILEEK	
ONLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYK	
6280 857 2515 ECCDONMGSRNSSSAGSGSGDPSEGLPRRGAGLRR	
DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALL	
WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELAT	
OKHSFPRMLHORBRGLCHROSFSLGEOSRVISHFL	
YSQKAPCGIYSKDGQIFMSACQDQTIRLYDCRYGR	
RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYG	
LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFD	
IBSHBDDVNAVAFADISSQILFSGGDDAICKVWDR	
PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKL	
BGMEASRQAATQONWDYRWQQVPKKAWRKLKLPGD	
GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYD	The state of the s
LITNHKACVRDVSWHPFKEKIVSSSWDGNLRLWQYR	
PESRECASAPAPVPQSSTPFSSPQ	
6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLER	SKEREFEDE
DVDLAOVLAYLLRRGOVRLVOGGGAANLOFIQALL	
WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELAT	
OXHSFPRMLHORERGLCHRGSPSLGEQSRVISHFL	
VSOKAFCGIYSKDGQIFMSACODOTIRLYDCRYGR	
RDVGWSVLDVAFTPDGNHFLYSSWSDYTHICNIYG	
RDVGWSVDDVAF IPDGNRFDISSWSDI IRICAIIG LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFD	
IRPDERRFAVESTAVSSIGREV LGGANDALITYFD IRSHEDDVNAVAFADISSOILFSGGDDAICKVWDR	
PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKL	
LANGUTATATATATATATATATATATATATATATATATATATA	***************************************

		134.14	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
)	amino acid	sequence	Codon, /-possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH
	1		GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK
1	[		LINHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM
	1		PESEECASAPAPVPQSSTPFSSPQ
6282	125	906	RMAACRALKAVLVDLSGTLHIBDAAVPGAQBALKRLRGASVIIR
İ	<b>,</b>	ļ	FVTNTTKESKQDLLERLRKLEFDISEDEIFTSLTAARSLLERKQ
	İ		VRPMLLVDDRALPDPKGIQTSDPNAVVMGLAPEHFHYQILNQAF
1	1		RLLLDGAPLIAIHKARYYKRKDGLALGPGPFVTALEYATDTKAT
ļ		ł	VVGKPEKTFFLEALRGTGCEPERAVMIGDDCRDDVGGAQDVGML
1	İ		GILVKTGKYRASDEEKINPPPYLTCESFPHAVDHILQHLL
6283	140	1043	LSLFGIHVMNPFWSMSTSSVRKRSEGEEKTLTGDVKTSPPRTAP
			KKQLPSIPKNALPITKPTSPAPAAQSTNGTHASYGPFYLEYSLL
l	1	1	ABFTLVVKQKLPGVYVQPSYRSALMWFGVIFIRHGLYQDGVFKF
i	1	1	TVYIPDNYPDGDCPRLVFDIPVFHPLVDPTSGELDVKRAFAKWR
į		Į.	RNHNHIWQVLMYARRVFYKIDTASPLNPRAAVLYEKDIQLFKSK
i	İ		VVDSVKVCTARLFDQPKIEDPYAISFSPWNPSVHDEAREKMLTQ
ì	1	1	KKKPEEQHNKSVHVAGLSWVKPGSVQPFSKEEKTVAT
6284	1	2879	RSVIPGSTISSRNPGLSRPRFMAAHEWDWFQREELIGQISDIRV
l	<u> </u>		QNLQVERENVQKRTFTRWINLHLBKCNPPLEVKDLFVDIQDGKI
ì	)	1	LMALLEVLSGRNLLHEYKSSSHRIFRLNNIAKALKFLEDSNVKL
	ł.		VSIDAARIADGNPSLVLGLIWNIILPFQIKELTGNLSRNSPSSS
l			LAPGSGGTDSDSSFPPTPTAERSVAISVKDQRKAIKALLAWVQR
1		j	KTRKYGVAVQDPAGSWRSGLAFLAVIKAIDPSLVDMKQALENST
1		l .	RENLEKAPSIAQDALHIPRLLEPEDIMVDTPDEQSIMTYVAQFL
l	1		ERFPELKARDIFDSDKEVPIESTFVRIKETPSBQESKVFVLTEN
	]	1	CERTYTVNHETSHPPPSKVFVCDKPESMKEFRLDGVSSHALSDS
l	Į.	Į.	STEFMHQIIDQVLQGGPGKTSDISBPSPESSILSSRKENGRSNS
ŀ	ŀ		LPIKKTVHFEADTYKDPFCSKNLSLCFEGSPRVAKESLRQDGHV
<b>)</b>	1		LAVEVAEEKEQKQESSKIPESSSDKVAGDIFLVEGTNNNSQSSS
l		·	CNGALESTARHDEESHSLSPPGENTVMADSFQIKVNLMTVRALE
j		i ·	BGDYPEAIPLKASKFNSDLIDFASTSQAPNKVPSPHETKPDEDA
1	1		RAFENHARKLGKRSIKSAHKKKDSPEPQVKMDKHEPHQDSGREA
l	ł	l .	EGCPSAPEETPVDKKPEVHEKAKRKSTRPHYEEEGEDDDLQGVG
l		l	EKLSSSPPSSCVSLETLGSHSEEGLDFKP8PPLSKVSVIPHDLF
1	}	[	YPPHYEVPLAAVLEAYVEDPEDLKNEEMDLEBPEGYMPDLDSRE
l	l	[	ERADGSQSSSSSVPGESLPSASDQVLYLSRGGVGTTPASBPAP
		1	LAPHEDHQQRETKENDPMDSHQSQESPNLENIANPLEENVTKES
1	1	1	ISSKKKEKRKHVDHVESSLFVAPGSVQSSDDLEEDSSDYSIPSR
ł	_	l _	TSHSDSSIYLRRHTHRSSRSDHFSLCSVEERSRSG
6285	2157	1331	SCKTENLLEMWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHII
	1	1	IDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATIYVRYKQVH
l	l	ł	ALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVS
l	1	1	GAVLTFGMGSLYMFVQTILSYQMQPKIHGKQVFWIRLLLVIWCG
1	1	1	VSALSMLTCSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAA
l	Į.	ł	ENSMSFSFFGFFLTYIRDFQKISLRVBANLHGLTLYDTAPCPIN
1	J	1	NERTRILISRDI
6286	1619	276	KAGASCCGSANPYVSVGKSCVLLAMAQLQTRFYTDNKKYAVDDV
[		1	PFSIPAASEIADLSNIINKLLKDKNEFHKHVEFDFLIKGQFLRM
J	i	I	PLOKHMEMENISSBEVVBIEYVBKYTAPQPEQCMFHDDWISSIK
i	1	<b>.</b>	GAEBWILTGSYDKTSRIWSLEGKSIMTIVGHTDVVKDVAWVKKD
	i	1	SLSCLLLSASMDOTILLWEWNVERNKVKALHCCRGHAGSVDSIA
1	1	1	VDGSGTKFCSGSWDKMLKIWSTVPTDEBDRMEESTNRPRKKQKT
l	1	1	EQLGLTRTPIVTLSGHMEAVSSVLWSDABBICSASWDHTIRVWD
	l	1	VESGSLKSTLTGNKVFNCISYSPLCKRLASGSTDRHIRLWDPRT
}	1	Ì	KDGSLVSLSLTSHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDT
1	Į.	<b>,</b>	RSCKAPLYDLAAHEDKVLSVDWTDTGLLLSGGADNKLYSYRYSP
1	1	<u></u>	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
I	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	SESerine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
1			TESHVGA
6287	278	1482	MOFFPNFQIGLRSTSGKEKYSGDAGFLGDALQLFLQCLALDEDF
1 2.30 /			APAKLOVOKILCOLLLPENLKEGLKBSSWSSLPCTKNRPFDFHS
l .			VMEESQSLNEPSPKQSEEIPEVTSEPVKGSLNRAQSAQSINSTE
1			MPAREDCLKRYSSEPVLSVOEKGVLLKRKLSLLEODVIVNEDGR
}	•	}	NKLKKQGBTPNEVCMFSLAYGDIPBBLIDVSDFECSLCMRLFFE
i			PVTTPCGHSFCKNCLKRCLDHAPYCPLCKESLKBYLADRRYCVT
1		į	OLLEBLIVKYLPDELSERKKIYDEBTAELSHLTKNVPIFVCTMA
1			YPTVPCPLHVFEPRYRLMIRRSIQTGTKQFGMCVSDTQNSPADY
i	, i		GCMLQIRNVHFLPDGRSVVDTVGGKRFRVLKRGMKDGYCTADIE
			YLEDV
6288	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
5200	•	, , ,	MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM
1			HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM
1	:	İ	KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM
1		ł	PKVHWLRTQPPSLDIEVDGGVGPDTVHKCARAGANMIVSGSAIM
			RSEDPRSVINLLRNVCSBAAQKRSLDR
6289	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
		,	MLDSGADYLHLDVMDGHFVPNITFGHPVVKSLRKQLGQDPFFDM
<b>j</b>		[	HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRRNGM
i '		}	KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM
		Í	PKVHNLRTQFPSLDIEVDGGVGPDTVHKCAKAGANMIVSGSAIM
i		·	RSEDPRSVINLLRNVCSEAAQKRSLDR
6290	3	1856	TLGRWLLGVYETVAPTLACLPRPRLRRRRRRRRRRRRRMISRYTRKA
1			VPQSLELKGITKHALNHHPPPBKLEBISPTSDSHEKDTSSQSKS
,			DITRESSFTSADTGNSLSAFPSYTGAGISTEGSSDFSWGYGELD
1		1	QNATEKVQTMPTAIDELLYEQKLSVHTKSLQEECQQWTASFPHL
	•	Į.	RILGRQIITPSEGYRLYPRSPSAVSASYETTLSQERDSTIFGIR
			GKKLHFSSSYAHKASSIAKSSSFCSMERDERDSIIVSEGIIREY
	Ì		LAPDHIDIEEGFHGKKSRAATEKQKLGYPPIAPFYCMKEDVLAY
Į.		<b>,</b>	VPDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSBSSCV
		1	LSKLHPLVLPRVPQSKVLYITENPMSLCQASRHQPNVNDLLVHG
1	Ī	1	MPLQPRNLSIMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS
		l	TSSLSYTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEILRGA
		1	RVPVAPDSLSSPSPTPLSRNNLLPPIGTARVEHVSTVGPQRQMK
1		<u> </u>	PHODSSRAQSAVVDBPNYQQPQKRLLLPDFFPRPNTTQSFLLDT
		l	QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG
	<u> </u>	L	P
6291	1732	602	LVAKMASSASARTPAGKRVINQBELRRLMKEKQRLSTSRKRIES
	Į.	ļ	PFAKYNRLGQLSCALCNTPVKSBLLWQTHVLGKQHRBKVAELKG
ļ		1	AKRASQGSSASSAPQSVKRKAPDADDQDVKRAKATI.VPQVQPST
1	1	İ	SAWTINFOKIGKEFIRATPSKPSGLSLLPDYKDEBEEEEKEKGD
	ł	,	GERKREDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK
		I	APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV
1	ì	i	RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAREDEEGRLDRQ
ļ	1	1	IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN
L			ADSDDEGBLQDLLSQDWRVKGALL
6292	1835	1142	TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV
	ļ	(	LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI
1	i	1	LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN
	}	1	SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY
1	{	Į.	LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA
1	ł	!	AKEPPPPYVSA
6293	2382	1035	FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL
	ļ	1	VGSRTLPVDFHIKMVESMKYPFRQGMRLEVVDKSQVSRTRMAVV
	1		DTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIK
	<del></del>		

CRO	T Dundlet - 3		
SEQ	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Í	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence	<b></b>	\=possible nucleotide insertion)
1		i	MSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTBGGWFEEGMK LEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCY
	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \		HASSHAIFPATFCQKNDIKLTPPKGYEAQTFNWENYLBKTKSKA
	!	İ	APSRLFNMDCPNHGFKVGMKLEAVDLMBPRLICVATVKRVVHRL
1	•		LSIHFDGWDSRYDQWVDCBSPDIYPVGWCELTGYQLQPPVAAEP
1	1		ATPLKAKEATKKKKKQFGKKRKRIPPTKTRPLROGSKKPLLRDD
ĺ	ĺ		PQGARKISSEPVPGETIAVRVKEEHLDVASPDKASSPELPVSVE
6294	354	1814	NIKQETDD
0234	334	1914	AQLITRGRTVAGGVRWIPSPFPDLELYSCCLGTDRGFPELSHHC
1			KNVIATASDYDMABITNIRPSFDVSPVVAGLIGASVLVVCVSVT VFVWSCCHQQABKKHKNPPYKFIHMLKGISIYPETLSNKKKIIK
1			VRRDKDGPGREGGRRNLLVDAAEAGLLSRDKDPRGPSSGSCIDQ
			LPIKMDYGEELRSPITSLTPGESKTTSPSSPEEDVMLGSLTFSV
			DYNFPKKALVVTIQEAHGLPVMDDQTQGSDPYIKMTILPDKRHR
1			VKTRVLRKTLDPVFDETFTFYGIPYSQLQDLVLHFLVLSFDRFS
1			RDDVIGEVMVPLAGVDPSTGKVQLTRDIIKRNIQKCISRGELQV
			SLSYQPVAQRMTVVVLKARHLQKMDIAGLSGNPYVKVNVYYGRK
ļ	<u>l</u>		RIAKKKTHVKKCTLNPIFNESFIYDIPTDLLPDISIEFLVIDFD RTTKNEVVGRLILGAHSVTASGAEHWREVCESPRKPVAKWHSLS
1			EY
6295	2795	617	VSSALLTGATSGSDAAKSEGASASPLSCTNAVAMDRPDEGPPAK
			TRRLSSSESPORDPPPPPPPPPPLLRLPLPPPPQQRPRLQEETEAA
j i			QVLADMRGVGLGPALPPPPPYVILEEGGIRAYFTLGAECPGWDS
			TIESGYGRAPPPTRSLEALPTPRASGGSLRIDFQVVQSSSPGGE
			GALETCSAVGWAPQRLVDPKSKEEAIIIVEDEDEDERESMRSSR RRBRRRRKQRKVKRESRERNAERMESILQALEDIQLDLEAVNI
			KAGKAFLRLKRKFIQMRRPFLERRDLIIQHIPGFWVKAFLNHPR
			ISILINRRDEDIFRYLTNLQVQDLRHISMGYKMKLYFQTNPYFT
			NMVIVKBFQRNRSGRLVSHSTPIRWHRGQBPQARRHGNQDASHS
	,		FFSWFSNHSLPRADRIAEIIKNDLWVNPLRYYLRERGSRIKRKK
			QEMKKRKTRGRCEVVIMEDAPDYYAVEDIFSEISDIDETIHDIK
	Ì		ISDFMETTDYFETTDNBITDINENICDSENPDHNEVPNNBTTDN
1			NESADDHETTDNNESADDNNENPEDNNKNTDDNEENPNNNENTY GNNFFKGGFWGSHGNNQDSSDSDNEADEASDDEDNDGNEGDNEG
			SDDDGNEGDNEGSDDDDRDIEYYEKVIEDFDKDQADYEDVIEII
			SDESVEREGIEGIQQDEDIYEEGNYEEGSEDVWEEGEDSDDS
			DLEDVLQVPNGWANPGKRGKTG
6296	727	1199	RHCGCDAQGACDSLPPTGTSSPVTARNAIPRARCCVWLLDGTTV
( l			EAVRPARERLARKKLROKRMOOFSRDSAYSSNKDSTCLLTERDT
			LGTSLQFPSPFSGTISFGSPSDSGIFPLGSQCCLGFQQPSISGK
6297	1	922	KWALIHKRVRLSVFGARWGRIYFGK
/	-	742	QRAAAASPSSCGPRGABYGALMAMEGYWRPLALLGSALLVGFLS VIFALVWVLHYRBGLGWDGSALBFNWHPVLMVTGFVFIQGIAII
	į		VYRLPWTWKCSKLIMKSIHAGINAVAAILAIISVVAVPENHNVN
	<b>]</b>		NIANMYSLHSWVGLIAVICYLLQLLSGFSVFLLPWAPLSLRAPL
	. 1		MPIHVYSGIVIFGTVIATALMGLTEKLIFSLRDPAYSTFPPEGV
	t t		PVNTLGLLILVFGALIFWIVTRPQWKRPKBPNSTILHPNGGTRQ
			GARGSMPAYSGNNMDKSDSBLNNBVAARKRNLALDBAGQRSTM
6298	3	985	SVPLRRLSLSGTLQGAGTTTKMAVARLAAVAAWVPCRSWGWAAV
	ŀ	i	PFGPHRGLSVLLARI PQRAPRWLPACRQKTSLSFLNRPDLPNLA
			YKKLKGKSPGIIFIPGYLSYMNGTKALAIEEFCKSLGHACIRFD
]			YSGVGSSDGNSERSTLGKWRKDVLSIIDDLADGPQILVGSSLGG
ĺ			WLMLHAAIARPEKVVALIGVATAADTLVTKPNQLPVBLKKEVEM KGVWSMPSKYSBEGVYNVQYSFIKEAEHHCLLHSPIPVNCPIRL
			LHGMKDDIVPWHTSMQVADRVLSTDVDVILRKHSDHRMREKADI
	Ì		QLLVYTIDDLIDKLSTIVN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosins, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	-	\=possible nucleotide insertion)
6299	512	814	BCDLEGIMPNVTISLSLPTNGSPLQDILVHPCVTSLDSAILTSS
ŀ	1	ļ	SIDAMDDSAFSGPYKFPFTPPLESFNLCFYTSQVPVPPILGFYQ
1			MKEEVOLRNNH
6300	121	692	AAPSCWSQRGVPAAGTPSSPRLLVSRAAAPSAGPWGAWROGARA
			AQSP?SIPNSSSVPYGSQDSVHSSPBDGGGGRDRPVGGSPGGPR
Į.	<b>í</b>		LVIGSLPAHLSPHMFGGFKCPVCSKFVSSDEMDLHLVMCLTKPR
I	i		ITYNBDVLSKDAGBCAICLEBLQQGDTIARLPCLCIYHKGCIDB
1			
6301	616	204	WFEVNRSCPEHPSD
0301	0.10	284	GKFVPVNWEPPQPLPFPKYLRCYRCLLETKELGCLLGSDICLTP
1	]		AGSSCITLHKKNSSGSDVMVSDCRSKBQMSDCSNTRTSPVSGFW
6303	100		IFSQYCFLDFCNDPQNRGLYTP
6302	490	745	IPGFLHLFHMEHSFLLVCALFAHVFFSSSCGSSVALHSDPCLLS
			PVLLNCLPGDLRPLDELYAQKLKYKAISEKLDHALNDMTSL
6303	2	1961	YWNBYGGGLLWQSWQEKHPGQALSSEPWNFPDTKEEWEQHYSQL
1			YWYYLEQFQYWEAQGWTFDASQSCDTDTYTSKTEADDKNDEKCM
	{		KVDLVSFLSSPIMGDNDSSGTSDKDHSBILDGISNIKLNSERVT
	1		QSQLDSCTSHDGHQQLSEVSSKRECPASGQSEPRNGGTNEESNS
			SGNTNTDPPAEDSQKSSGANTSKDRPHASGTDGDESERDPPEHK
	1		PSKLKRSHELDIDENPASDFDDSGSLLGFKYGSGQKYGGIPNFS
1			HRQVRYLEKNVKLKSKYLDMRRQIKMKNKHIFFTKESEKPFFKK
1			SKILSKVEKFLTWVNKPMDEEASQESSSHDNGHDASTSCDSEEQ
			DMSVKKGDDLLETNNPEPEKCQSVSSAGELETENYERDSLLATV
			PDEQDCVTQEVPDSRQAETEAEVKKKNKKKNKKVNGLPPBIAA
			VPELAKYWAQRYRLFSRFDDGIKLDREGWFSVTPEKIARHIAGR
	-		VSQSFKCDVVVDAFCGVGGNTIQFALTGMRVIAIDIDPVKIALA
			RNNAEVYGIADKIEFICGDFLLLASFLKADVVFLGPPWGGPDYA
			TARTFDIRTMMSPDGFEIFRLSKKITNNIVYFLPRNADIDQVAS
			LAGPGGQVEIBQNFLNNKLKTITAYFGDLIRRPASET
6304	1	1438	HRARVDRSRESPGGDLRHPGRVRRDITLSGHPRLSTOHVVLLRE
			DEVGDPGTKDLGHPQHGSPIQETQSEVVTLVSPLPGSDMAALPA
			WRATSGLTLWPHTAEGROLLGAENRALTGGQQAEDPTLASGAYO
			WPGSVEKLQGSVWCDAETLLSSSRTGGQAPPWLTDHDVQMLRLL
l	- 1		AQGEVVDKARVPAHGQVLQVGFSTBAALQDLSSPRLSQLCSQGL
			CGLIKRPGDLPBVLSFHVDRVLGLRRSLPAVARRFHSPLLPYRY
			TDGGARPVIWWAPDVQHLSDPDEDQNSLALGNLQYQALLAHSCN
	j		WPGQAPCPGIHHTEWARLALFDFLLQVHDRLDRYCCGFEPEPSD
	]		PCVEERLREKCRNPAELRLVHILVRSSDPSHLVYIDNAGNLQHP
			EDKLNFRLLEGIDGF?BSAVKVLASGCLQNMLLKSLQMDPVPWE
			SQGGAQGLKQVLQTLEQRGQVLLGHIQKHNLTLFRDEDP
6305	99	420	NMIWRGRSTYRPRPRRSVPPPRLIGPMLEPGDEEPOOEEPPTES
			RDPAPGQEREEDQGAAETQVPDLEADLQELSQSKTGDECGDGPD
			VOGKILTKSEOPKMPRGR
6306	1	1874	
5500	_ [	10/4	PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC
			KFNCHKRCATRVPNDCLGRALINGDVPMEKATDPSBADKSALMD
			BSEDSGVIPGSHSENALHASBEBEGEGGKAQSSLGYIPLMRVVQ
	]		SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFQ
	i		NNTTNRYYKEIPLSEILTVESAQNPSLVPPGTNPHCFBIVTANA
'			TYFVGEMPGGTPGGPSGQGAEAARGWETAIRQALMPVILQDAPS
	Į.		APGHAPHRQASLSISVSNSQIQENVDIATVYQIPPDEVLGSGQF
			GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR
	İ		HPGIVNLECMFETPEKVFVVMEKLHGDMLKMILSSEKGRLPERL
	ĺ		TKFLITQILVALRHLHPKNIVHCDLKPENVLLASADPFPQVKLC
	1		DFGFAR1IGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG
	İ		vimyvslsgtfpfnededindqiqnaafmypaspwshisagaid
	l		LINNLLQVKMRKRYSVDKSLSHPWLQBYQTWLDLRELEGKMGER
<u> </u>	}		YITHESDDARWEQFAABHPLPGSGLPTDRDLGGACPPQDHDMQG

SEQ	Predicted	! Predicted end	Amino agid coment control in a
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
- 1	sequence	Doquesion	\=possible nucleotide insertion)
			LAERISVL
6307	2136	589	CFLLPRGRDPEPPEAGAAAPCAPGAPDMSFRKVVRQSKPRHVFG
		]	QPVKNDQCYEDIRVSRVTWDSTFCAVNPKFLAVIVEASGGGAFL
1			VLPLSKTGRIDKAYPTVCGHTGPVLDIDWCPHNDEVIASGSGRDC
[			TVMVWQIPENGLTSPLTEPVVVLEGHTKRVGIIAWHPTARNVLL
1			SAGCDNVVLIWNVGTABBLYRLDSLHPDLIYNVSWNHNGSLFCS
1			ACKDKSVRIIDPRRGTLVAEREKAHEGARPMRAIFLADGKVFTT
1	(		GFSRMSERQLALWDPENLEBPMALQELDSSNGALLPFYDPDTSV
			VYVCGKGDSSIRYFEITEEPPYIHFLNTFTSKEPQRGMGSMPKR
1			GLEVSKCEIARFYKLHERKCEPIVMTVPRKSDLFQDDLYPDTAG
1	]		PEAALEAEEWVSGRDADPILISLREAYVPSKQRDLKISRRNVLS
1			DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGEAGKLEEVM
I			QELRALRALVKEQGDRICRLEEQLGRMENGDA
6308	2	111B	GRPTRPEKMLLSLVLHTYSMRYLLPSVVLLGTAPTYVLAWGVWR
			LLSAFLPARFYQALDDRLYCVYQSMVLFFFENYTGVQILLYGDL
1	ĺ		PKNKENITYLANHQSTVDWIVADILAIRQNALGHVRYVLKEGLK
			WLPLYGWYFAQHGGIYVKRSAKFNEKEMRNKLOSYVDAGTPMYL
			VIFPEGTRYNPEQTKVLSASQAFAAQRGLAVLKHVLTPRIKATH
j l			VAFDCMKNYLDAIYDVTVVYEGKDDGGQRRESPTMTEPLCKECP
			KIHIHIDRIDKKDVPEEQEHMRRWLHERPRIKDKMLIEFYESPD
			PERRERFPGKSVNSKLSIKKTLPSMLILSGLTAGMLMTDAGRKL
			YVNTWIYGTLLGCLWVTIKA
6309	220	563	LVAEVKEPCSLPMLSVDMENKENGSVGVKNSMENGRPPDPADWA
1			VMDVVNYFRTVGFEEQASAFQEQEIDGKSLLLMTRNDVLTGLQL
1			KIGPALKIYEYHVKPLQTKHLKNNSS
6310	36	979	GPRCWKFLILSSVNCETLRIGKAWPQSSGQERYWTPRTHSSASE
}			AQRGSLABLNVAAAGLWADCDQPLYDCPMCGLICTNYHILOEHV
1 1			DLHLBENSFQQGMDRVQCSGDLQLAHQLQQEEDRKRRSEESRQE
1 1			IBEPQKLQRQYGLDNSGGYKQQQLRNMBIEVNRGRMPPSEFHRR
1			KADMMESLALGFDDGKTKTSGIIEALHRYYQNAATDVRRVWLSS
			VVDHFHSSLGDKGWGCGYRNFQMLLSSLLQNDAYNDCLKGMLIP
1 1			CIPKIQSMIEDAWKEGFDPQGASQLIIRLQGTKAWIGACEVYIL
1			LTSLRV
6311	1	675	PVWWNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL
1			ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLVKEVARLEANL
[·	l		PCTCKVHFPDPNKLHCFQLTVTPDEGYYQGGKFQFETEVPDAYN
1 1	[		MVPPKVKCLTKIWHPNITETGBICLSLLREHSIDGTGWAPTRTL
, I	J		KDVVWGLNSLFTDLLNFDDPLNIRAABHHLRDKEDFRNKVDDYI
L			KRYAR
6312	213	1400	GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW
	ţ		GKTEERAKQLAKEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT
1 1	l		RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN
į !	1		VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC
[ · ]			DELMGGGGLHTMGTYIVDLLTHLTGRRABKVHGLLKTFVRQNAA
] [			IRGIRHVTSDDFCFFQMLMGGGVCSTVTLMFNMPGAFVHEVMVV
j l	į		GSAGRI.VARGADLYGQKNSATQEKLLLRDSLAVGAGLPEQGPQD
	1		VPLLYLKGMVYMVQALRQSPQGQGDRRTWDRTPVSMAASFEDGL
L /		i	YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL
6313	2	2071	QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL
[ . {			FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQBFPEHHKMILD
			RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFOEF
}			TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEBEANDVWKAAE
			FLOMLEAIKALEVRNKENSAPLEENTIGKNEAKKRKIAETSNVI
		1	TESLPSAESEPVEIEVELAEGTIEVEDEGIKTLEEVASAKOSVK
	Í		YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK
[		ļ	QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE
			TICKERINA INTERNATIONAL INTERNATIONAL TOTA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, B-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
!	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence	_	\=possible nucleotide insertion)
<b></b>	<u> </u>	<del>-</del>	SPKCEICNKRYLRBSAWKOHLNCYHLEEGGVSKKQRTGKKIHVC
ŀ			QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH
1		1	LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQPKDHLVIHTGDK
		1	PNHCTLCDLWFMOGNELRRHLSDAHNISERLVTREVLSVETRVQ
		•	TEPVTSMTIJEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS
)		1	OVHDSHMSRLPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ
ł	Į.	i	MPVEVOTELLRADLDHVTPEIMNQEERESSQADAAEAAREDHED
1			AEDLETKPTVDSEAEKAENEDRTALPVLE
	<del> </del>	2071	ORSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL
6314	2	20/1	FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD
Ì	1	}	
l .			RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF
ľ		j.	TORPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE
ļ.			PLOMLEAIKALEVRNKENSAPLBENTTGKNBAKKRKIABTSNVI
i			TESLPSARSEPVEIEVRIAEGTIEVEDEGIETLEEVASAKQSVK
			YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK
		<u> </u>	QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE
ļ		1	SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC
ļ			QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH
}		1	LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK
			PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ
	<b>{</b>		TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS
			QVHDSHMSELPEQVQVSYLEVGRIQTEECTEVHVEELHVERVNQ
İ	j	1	MPVEVQTELLEADLDHVTPEIMNQBERESSQADAAEAAREDHED
ł			ARDLETKPTVDSRAEKARNEDRTALPVLE
6315	1	1015	LGLAVNVVTTLVLISYCPTATERAPYWTYLLCALGLFIYQSLDA
1		ł	IDGKQARRINSCSPLGBLFDHGCDSLSTVFMAVGASIAARLGTY
1			PDWFFSCSPIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI
ŀ		l	VFVLSAFGGATMWDYTIPILBIKLKILPVLGFLGGVIFSCSNYF
ŀ			HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
ĺ		ł	VFERHPCLYILMFGCVFAKVSQKLVVAHMTKSBLYLQDTVFLGP
i		i	GLLFLDQYFNNFIDBYVVLWMAMVISSFDMVIYFSALCLQISRH
i		·	LHLNIFKTACHQAPEQVQVLSSKSHQNNMD
6316	1503	792	VSAGAGTGIMGGTTSTRRVTFEADENENITVVKGIRLSENVIDR
İ			MKRSSPSGSKSQRYSGAYGASVSDEKLKRRVAERLALEQAKKES
			EDQKRLKQAKELDRERAAANEQLTRAILRERICSEEERAKAKHL
l			ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA
İ		1	BEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLKCSALATQY
1		1	MHCVNHAKQSMLEKGG
6317	102	839	PEACTSAVLARKKGHLPTMRHEAPMQMASAQDARYGQKDSSDQN
1			FDYMFKLLI IGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK
i	j	I	TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN
l	1		BESPNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG
l		i	OHLGEQLGPEFFETSAKDNINVKQTFBRLVDIICDKMSESLETD
1			PAITAAKONTRLKETPPPPQPNCAC
6318	1765	733	PWHPLRTLPLHHPHPRPPRAEGREGADSMSHLPGLELRREAPPL
0310	1/03	,33	LGPLLSPFPLPAGSWHROMLRSSLRFPITNSAGAPCKAAGRMNT
Ì	1 .	1	·-
l		1	LAPVRRDRVLARLPQCLRKBAALHGHKDFHPRVTCACQEHRTGT
l		1	VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFKM
1		1	ERFEVIGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN
l		1	DVASLRHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM
1			EKDALQVAQEMKAEYNAVSSLTGENVREFFFRVAALTFEANVLA
L	<u> </u>		KLEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP
6319	88	717	AATMRLNQNTLLLGKKVVLVPYTSBHVPSRYHEWMKSBBLQRLT
1			ASEPLITLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES
1	1		CMVGDVNLFLTDLKDLTLGBIEVMIAEPSCRGKGLGTEAVLAML
i			SYGVTTLGLTKPEAKIGQGNBPSIRMFQKLHFEQVATSSVFQEV

		·	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, B-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, +=Stop
· ·	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
			TLRLTVSESEHOWLLEOTSHVEEKPYRDGSAEPC
6320	90	1111	RPRTGRBKVAMAAVDSFYLLYRBIARSCNCYMEALALVGAWYTA
J			RKSITVICDFYSLIRLHFIPRLGSRADLIKQYGRWAVVSGATDG
ì			IGKAYABELASRGLNIILISRNEEKLQVVAKDIADTYKVETDII
ļ.			VADFSSGREIYLPIREALKDKDVGILVNNVGVFYPYPQYFTQLS
1	1	]	RDKLWDIINVNIAAASLMVHVVLPGMVERKKGAIVTISSGSCCK
	1	1	PTPQLAAFSASKAYLDHFSRALQYEYASKGIFVQSLIPFYVATS
ł	i		MTAPSNFLHRCSWLVPSPKVYAHHAVSTLGISKRTTGYWSHSIQ
ļ			FLFAQYMPEWLWVWGANILNRSLRKBALSCTA
6321	1418	341	HRKAALGALMAGRLLGKALAAVSLSLALASVTIRSSRCRGIQAF
		1	RNSFSSSWPHLNTNVMSGSNGSKENSHNKARTSPYPGSKVERSQ
1	1	1	VPNEKVGWLVEWQDYKPVEYTAVSVLAGPRWADPQISBSNF3PK
1			FNBKDGHVERKSKNGLYBIENGRPRNPAGRTGLVGRGLLGRWGP
ŀ	}		NHAADPIITRWKRDSSGNKIMHPVSGKHILQFVAIKRKDCGEWA
			IPGGMVDPGEKISATLKREFGERALNSLQKTSABKREIEBKLHK
}			LFSQDHLVIYKGYVDDPRNTDNAWMETEAVNYHDETGBIMDNLM
t	1		LEAGDDAGKVKWVDINDKLKLYASHSQFIKLVAEKRDAHWSEDS
i			RADCHAL
6322	2047	1083	NOBILKNVESSRTVQPHFLEFLLSLGWSVDVGRHPGWTGHVSTS
J			WSINCCDDGEGSQQBEVISSEDIGASIFNGQKKVLYYADALTEI
1			AFVVPSPVESLTDSLESNISDODSDSNMDLMPGILKOPSLTLEL
i .			FPNHTDNLNSSQRLSPSSRMRKLPQGRPVPPLGPETRVSVVWVE
			RYDDIENFPLSELMTRISTGVRTTANSSTSLRSTTLEKEVPVIF
l			IHPLNTGLFRIKIQGATGKFNMVIPLVDGMIVSRRALGFLVRQT
1			VINICRRKRLESDSYSPPHVRRKQKITDIVNKYRNKQLEPEFYT
	i		SLFQEVGLKNCSS
6323	1	656	PASTTDGAQBARVPLDGAFWIPRPPAGSPKGCFACVSKPPALOA
1			PAAPAPEPSASPPMAPTLFPMESKSSKTDSVRAAGAPPACKHLA
l ·			BKKTMINPTTVIEVYPDTTEVNDYYLWSIFNFVYLNFCCLGFIA
			LAYSLKVRDKKLLNDLNGAVEDAKTDRLINITRSGLAASCIMLW
1 .			MALSVIATHRGLRSSASILVAEPHDWNTERPQVTFRERCPAL
6324	1	2061	EGAGMRRCPCRGSLNEAEAGALPAAARMGLEAPRGGRRRQPGQQ
1			RPGPGAGAPAGRPEGGGPWARTEGSSLHSEPERAGLGPAPGTES
			POARFWTOGOTEPAAAGLGVETERPKOKTEPDRSSLRTHLEWSW
1 1			SELGTTCLWTETGTDGLWTDPHRSDLQFQPERASPWTQPGVHGP
			WTBLETHGSQTQPERVKSWADNLWTHQNSSSLQTHPEGACPSKE
1			PSADGSWKELYTDGSRTQQDIEGPWTKPYTDGSQKKQDTEAARK
[	ĺ		QPGTGGFQIQQDTDGSWTQPSTDGSQTAPGTDCLLGEPEDGPLE
			EPEPGELLTHLYSHLKCSPLCPVPRLIITPETPBPEAQPVGPPS
			RVEGGSGGFSSASSFDESEDDVVAGGGGASDPEDRSGSKPWKKL
	·		KTVLKYSPFVVSPRKHYPWVQLSGHAGNFQAGRDGRILKRFCQC
			EQRSLEQLMKDPLRPFVPAYYGMVLQDGQTFNQMEDLLADFEGP
			9IMDCKMGSRTYLERELVKARERPRPRKDMYBKMVAVDPGAPTP
			EEHAQGAVTKPRYMQWRBTMSSTSTLGFRIEGIKKADGTCNTNF
	ı		KKTQALEQVTKVLEDFVDGDHVILQKYVACLEBLREALBISPFF
	·		KTHEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPDHQTLSHRLP
			WAEGNREDGYLWGLDNMICLLQGLAQS
6325	165	944	GLRDPFRRKRRLKPQVKMSNYVNDMWPGSPQBKDSPSTSRSGGS
			SRLSSRSRSFSRSSRSHSRVSSRFSSRSRSRSRSRSRRRHO
			RKYRRYSRSYSRSRSRSRSRSRRYRERRYGFTRRYYRSPSRYRSRS
		•	RSRSRSRGRSYCGRAYAIARGORYYGFGRTVYPBEHSRWRDRSR
			TRSRSRTPFRLSEKDRMELLEIAKTNAAKALGTTNIDLPASLRT
6326	270	<u> </u>	VPSAKETSRGIGVSSNGAKPEVSILGLSEQNFQKANCQI
0326	238	680	GEPSPATQQKPSATGAGVLHQHFSSGHIYVLMGLLPPPWTISFT
			VQTTLQPPGGLPAAPVSGRMAFBPVGRDLARRMVPRAGKRTQTL
			GARRVAAQGARPLPEDRRPKSGERLHVTVAPCWEFVLPSVSLTA

Predicted   Pred				la financia de la composição de la compo
No:   location   corresponding   to first   mino acid   residue of	SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding to first amino acid residue of anino acid residue of anino acid residue of anino acid acquence and acquence and acquence acquence and acquence acquence and acquence acquence and acquence acquence and acquence acquence and acquence acquence and acquence	1			
Corresponding	NO:	1		
to first amino acid residue of amino acid am		location		
### anino acid		corresponding	to first	
menio acid adquence a		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
### ### ### ### ### ### ### ### ### ##		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
amino acid aequence  Codon, /-possible nucleotide deletion,	-	1	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
A-possible nucleotide insertion				Codon. /=possible nucleotide deletion.
1 1337 SLARILAPRIGESUMPTOPARPSTRAPPSRSLEGSLCALESDA DESSCONKABLPDOGRAVGERRYTCHERKIQLUKEKKQOKKERKER CARPSTRAPERSUL ALTERNAPE SUL ALTERNAPE SUL A			Doquesion	
1337   SLARILAPEGGSVVPPTQDPAPSTRAPEPSISLISGISCALES		sequence	ļ	l
DSGSSMKARLPPGGAVGRETKERKUQLKERKEK GARPETGAVBAGGGFTELPERGULGTFREKVQAKERKEK GARPETGAVBAGGGFTELPERGULGTFREKVRAFERSEA LPASERANGGAGGFTELPERGULGTFREKVRAFERSEA LPASERANGGAGFTELPERGULFTREKVRAFERGULFTREKVRAFERGAFTESTVAF RQBSLTQPMSIPSSVIHDMWTLGLQTSQGLWRGSBARCIALLE ALQQVIQDTTTEPREELSGULVKKLKYMSPILTQCRICAGAGAA ALQQVIQDTTTEPREELSGULVKKLKYMSPILTQCRICAGAGAA ALQAVIDTTTEPREELSGULVKKLKYMSPILTQCRICAGAGAA ALQAVIDTTTEPREELSGULVKKLKYMSPILTQCRICAGAGAA ALQAVIDTTTAARGUHAGVASTLITLPAASVULPESTEKDSKY GGKV  6328  1030  276  HABASVITAAARGUAMEERHITDAKIKAARGTGSSFRGIPGCSL RHFACEONILSRPDGASSIGGDTSVLAGVYGFASVAVSKULT KATLEVYLRPKULGPVARKSERGILTRITCCRVVLATLIPPETSI TVVLQVVSDBGSLJACCLMAACMALVDGSVYGFASVAVSKULT KATLEVYLRPKULGPVARKSERGILTRITCCRVVLATLIPPETSI TVVLQVVSDBGSLJACCLMAACMALVDGSVYGFASVAVSKULT SDGTULVLDPTSKORKARAVITTALDSVERILMSSTKGLVSDT ELQQCLAAAQAANSQHVYRYTRESLQRYYSKS  6329  3 2016  8EBVVAAGGGTRSRARBESGSUVVVSRTGAARSINGGGTSATT SNELSRALHERFVSIFKSVKEELGSISEDVQAMSNCCQMS SRICAGAACGAACHIVLTXTTLGASSKOKLEIRAVAADHACKSVDT SRICAGAACGAACHIVLTXTTLGASSKOKLEIRAVAADHACKSVDT SRICAGAACGAACHIVLTXTTLGASSKOKLEIRAVAADHACKSVDT GLEIMEMALALGETAVKRITTADDNIKMLEGGGGTTTAAT SRICAGAACGAACHIVLTXTTLGASSKOKLEIRAVAADHACKSVDT SRICAGAACGAACHIVLTXTTLGASSKOKLEIRAVAADHACKSVDT GLEIMEMALALGETAVKRITTACHINGGGGGTSATT SRICAGAACGAACHIVLTXTTLGASSKOKLEIRAVAADHACKSVDTATAA RGDIERMSLAGTRSGITTEDGARSTVVBGGTTAATGGGGGTSATT VHITTGGIVCORTATALLTTERSHILISKKIFFRISISLHASKIMD KYELPPPLEGPSSLANOTIMLIBRUVASHUSSVVPLDARQADHACKSVDTAACH VHITTGGIVCORTATALLTTERSHILISKKIFFRISISLHASKIMD KYELPPPLEGPSSLANOTIMLIBRUVASHUSSVVPLDARQADHACKSVTATUACH VYTYSGLTVKAGGTVKASNISTALLTSKTAATATSAADHACHIVTTAATA CRUTCATALQAHACHILATAAAACGAACAAANAPATINEKKROPENTIAGA KYELPPPLEGPSSLANOTIMLIBRUVASHUSSAADHATAACAACAAANAPATINEKKROPENTAATAAA A95 OQGGRVTTRGGRACAATPINSKYRIKATAANAPATNIKTAATAATAAAAAAAAAAAAAAAAAAAAAAAAAAAA				
GARPETGSAVSAAQCGGPTRALPESGUIGATFREKVPARGETSGAVE LPRYPOVODILLRELIVERSEGGVPPTRADSTFSGAVE LPRYPOVODILLRELIVERSEGGVPTRADSTGAVESGALTSGLIVERS ALGOVIGOTTTE PHEELSRDLVNKLKPYMSPLTOCEPICASMEN ALKOVIGOTTTE PHEELSRDLVNKLKPYMSPLTOCEPICASMEN ALKOVIGOTTTE PHEELSRDLVNKLKPYMSPLTOCEPICASMEN ALKOVIGOTTTE PHEELSRDLVNKLKPYMSPLTOCEPICASMEN ALKOVIGOTTTE PHEELSRDLVNKLKPYMSPLTOCEPICASMEN ALKOVIGOTTTE PHEELSRDLVNKLKPYMSPLTOCEPICASMEN ALKOVIGOTTTE PHEELSRDLVNKLKPYMSPLTOCEPICASMEN ALKOVIGOTTTE PHEELSRDLVNKLKPYMSPLTOCEPICASMEN ALKOVIGOTTTE PHEELSRDLVNKLKPYMSPLTOCEPICASMEN ALKOVIGOTTTE PHEELSRDLVNKLKPYMSPLTOCEPICASMEN ALKOVIGOTTTE PHEELSRDLVNKLKPYMSPLTOCEPICASMEN ALKOVIGOTTTE PHEELSRDLVNKLKPYMSPLTOCEPICASMEN RPHAGERITLASLUNGSVAPASYLLEPASTVLPEVSTEEKDSV GEKV  6328  1030 276 BASABYTTAAARGLAMAESSHHTDAKKIRAERGISSS PREPECSI RHAGEGORIJASPASSASPLGGTISULAGVYOPAKVUSKELIPN KATLEVILAPRKIGIPOVARSKERRELINTICERAVULGTLHPERSC KATLEVILAPRKIGIPOVARSKERRELINTICERAVULGTLHPERSC KATLEVILAPRKIGHPOVARSKERRELINTICERAVULGTLHPERSCASLIP TVULGVUSDASSASPLAGCISSEGVITASAGVITAGAGGGTSTAT TVULGVUSDASSASPLAGCISSEGVITASCASPAVESSELIPN KATLEVILAPRKIGHPOVARSKERRELINTICERAVULGTLHPERSCASLIP TVULGVUSDASSASPARGESGEVATVASTALAAGTVERSLLTERNIL RGDIERSLALAIRERFVS IPKSPKELESS ISEDVQAMSICCUMS SCHLARAERGIPTET LONDKRILLERALAALTSTPURSLLTERNIL RGDIERSLALAIRERFVS IPKSPKELESS ISEDVQAMSICCUMS SKLADARSGTOLLIPULTICERSCASPATIATICERSCOVS PVITOO MICHAELSCASPATIATICERS PRATESTATICERSCASPATIATICERSCOVS PVITOO MICHAELSCASPATIATICERS PRATESTATICERSCASPATIATICERSCOVS PVITOO MICHAELSCASPATIATICERS PRATESTATICERSCASPATIATICERSCOVS PVITOO HICKERSCASPATIATICERS PRATESTATICERSCASPATIATICERSCASPATIATICERS COMPANIA SCHOOLIPARATICERS PRATESTATICERSCASPATIATIC	6327	1	1337	
LARARRAKORARRALKORARRAKOROGGEPPEKASPSTARGETPSTVIKE LPPSPOVDOLLERENLKERPIKTORUTETSTVIKSTGLINGE ROSLITOFMSI PSSV IHPAMVPLELOZYSOGLVRGSKARCIALIA ALQOVIQOTITEPHEKSEDLVNIKAPYMSPLITOCURLSAMGIN AIKPINKE ITSUSSSRBEBERASSELRALTDETVQEKILVADADI SERAYQKI SIGDVILVYGCSSLVSRILQEANTEGRIPRIVUVDS PPHEGRETITELSLVBACVPASPLLI LPARSYULPSVITERKOSKV GGEKV  6328 1030 276 HASABYYTTARARGIGAMEBEHHTDAKIRABNGTGSSPROPGCSL RHYACGONLISRDOSASPIQODISVLAGVYGPABVVSVEKI IM KATLEVILRIPKIGLEVARKERSERLIENTCENKEKI IM KATLEVILRIPKIGLEVARKERSERLIENTCENKEKI IM KATLEVILRIPKIGLEVARKERSERLIENTCENKEKI IM KATLEVILRIPKIGLEVARKERSERLIENTCENKEKI IM KATLEVILRIPKIGLEVARKERSERLIENTCENCALD SDUTULDPTSKORKERARAVITALANGSVEKI IM KATLEVILRIPKIGLEVARKERSERLIENTCENCALDI SDUTULDPTSKORKERARAVITALANGSVEKI IM KATLEVILRIPKIGLEVARKERSERLIENTCENCALDI SDEWGLARGOGTRSARABSGEVVIVUSATURANGIGNAGGTSATT SNPLSRKHALIGITETALDNIKSRILGALKALSTFYVERSIRITRRIL RGDIERKSLAINERFVSI IYRBVKERLESSISEDVQAMSINCODMT SRCOJAKROGODILVIVETKIGASSKIKLIERAJANIANGLANGLEVARDI SERVARGOGTRSARABSGEVVIVUSATURANGIGNAGGTSATT SDEMSLLEGTRSPI TEDEFFKALGRVKQIHDVXVLLETNOQTA GLEHEMHALLEGTRSPI TEDEFFKALGRVKQIHDVXVLLETNOQTA GLEHEMHALLEGTRSPI TEDEFFKALGRVKQIHDVXVLLETNOQTA GLEHEMHALLEGTRSPI TEDEFFKALGRVKQIHDVXVLLETNOQTA GLEHEMHALLEGTRSPI TEDEFFKALGRVKQIHDVXVLLETNOQTA GLEHEMHALLEGTRSPI TEDEFFKALGRVKQIHDVXVLLETNOQTA GLEHEMHALLEGTRSPI TEDEFFKALGRVKQIHDVXVLLETNOQTA GLEHEMHALLEGTRSPI TEDEFFKALGRVKQIHDVXVLLETNOQTA GLEHEMHALLEGTRSPI TEDEFFKALGRVKQIHDVXVLLETNOQTA GLEHEMHALLEGTRSPI TEDEFFKALGRVKQIHDVXVLLETNOQTA GLEHEMHALLEGTRSPI TEDEFFKALGRVKQIHDVXVLLETNOQTA GLEHEMHALLEGTRSPI TEDEFFKALGRVKQIHDVXVLLETNOQTA GLEHEMHALLEGTRSPI TEDEFFKALGRVKQIHDVXVLLETNOQTA GLEHEMHALLEGTRSPI TEDEFFKALGRVKGHANGSCETLIKUTVTQOL GLEHEMHALLEGTRSPI TEDEFFKALGRVKALGERITALLER KYRLPPOLOGNISHALTITEDVCPI JAVARGATSHESSI SISHALKANGA GLEHEMHALLEGTRSPI TEDEFFKALGRVKALGEFTURALLEVAROMATASKERELIABLIKUTVAROQTATARICHTARAMATASKER FYTYTYETRIKTIFSREMVARGETLISHNIKARVENTEMDARAGATARICHTARAMATASKER FYTYTYTERIKTIFSREMVARGETLISHNIKARVENTEMDARAGATARICHTARAMATASKANGATARATARATARATARATARATARATA	ŀ		1	1
LPSTPOUDDILLIRELVIKEPRQOVPTRENTGSKYSLFSELLDYS RQMSILDPMS IPSSVITIPAMWISLGLYGGGUSKARCILLIK ALQQVIQDYTTPPNEKISEDSVIHIRAWSKIGLYGGGUSKARCILLIK ALQQVIQDYTTPPNEKISEDSVIHIRAWSKIGLYGGGUSKUVLARAQAI SRPRVQKISIGGENTLRSUVRACVPASYLLIPAASYVLPEVSTEEKDSKY GGKV GGKV  6328 1030 276 HASARYTTAARGGAAREBHHTDAKIRABSVLPEVSTEEKDSKY GGKV RHRACEGNILISRDOSASPIQODTSVLAGVGFBEVKVSKII KY KATLSVIHIRPKIGLPGVARKSERILIENTCERVVLSVEKII KY KATLSVIHIRPKIGLPGVARKSERILIENTCERVVLSTIHIPRTSI TVVLQVVSDAGSLACCIANAGAMLVTRACVPBEVKIKIST KY KATLSVIHIRPKIGLPGVARKSERILIENTCERVVLSTHFBYSI TVVLQVVSDAGSLACCIANAGAMLVTRACVPBEVKIKIST KY SDGTLVLDPTSKQEKRARAVLTPALDSVERKLIMSSTKGLYSDT ELQCLAAAQANSGRVPFYRRSIQARYSKS  6329 3 2016 SERVAGGGTSKARARUSTPALDSVERKLIMSSTKGLYSDT ELQCLAAAQANSGRVPFYRRSIQARYSKS RSVAGGGTSKARARUSTPALGSVERKLIMSSTKGLYSDT ELQCLAAAQANSGRVPFYRRSIQARYSKS RSVAGGGTSKARARUSTPALGSVERKLIMSSTKEVLTSDT SRPLSRKIHKLIETTLINDKERLIRENGI FRYDRASKITRNI. RGDISRKSLALIKERVS I FREVKERLES I SERVQAMSNINCQDWT SRLQAARSGTQDLIVKTTKLQSSSQKLIKTRAQVADAPISKROLT GLEIMEGMALLQETAYRRIJKRAGSECRTLTQSSCOVSPUTJOA MEALQDRPJLYKYTLDBEGTLARRIJKVRALISTULTROQTAT GLEIMEGMALLQETAYRRIJKRAGSECRTLTQSSCOVSPUTJOA MEALQDRPJLYKYTLDBEGTLARRIJKVRALISTULTROQTAT GLEIMEGMALLQETAYRRIJKRAGSECRTLTQSSCOVSPUTJOA MEALQDRPJLYKYTLDBEGTLARRIJKVRALISTULTROQTATIONE ENTGEVVGHITEGVCRPLKVRIGEVTAVANSPUTJATGGGGTFFR PIEMISHPDLRGVGTRLVKTRIJGEVTULTARGASVVLTRVQGLYY YNINKTTLALF EFTDRRLEMILQPGIERAHUTLINKGASVVLTRVCLSTYTIVTQQ HKPGGSLAMMPRILDSVTILARAMOVGPTVLSARDNILLIPQLINTI LSATVKEGIVKGTELVCRRYGEVTAAVNNPTNEYKOPENILHR SPQOVOTILS  6330 1151 333 PFYTYFYRIKFFSRMVARECETISINKCPDRAPRRFTLAGOOPL PVHQPHSLVSGGTTVKAMMKNSVVRGPPAAGAPTERPTTPTAFR KPYTSRGDPT JALLEHDSKRNTLAKVVRGPPAAGAPTERPTTPTAFR KPYTSRGDPT JALLEHDSKRNTLAKVVRGPPAAGAPTERPTTPTAFR KPYTSRGDPT JALLEHDSKRNTLAKVVRGPPAAGAPTERPTTPTAFR KPYTSRGDPT JALLEHDSKRNTLAKVVRGPPAAGAPTERPTTPTAFR KPYTSRGDPT JALLEHDSKRNTLAKVVRGPTARAGAPTERPTTPTAFR KPYTSRGDPT JALLEHDSKRNTLAKVVRGPPAAGAPTERPTTPTAFT KPYTSRGDPT JALLEHDSKRNTLAKVVRGPTAAGAPTERPTTPTAFT KYTSRCLIM  6331 3 495 CGGGRATHTULTGTLALLLASTVARSKSYNGSGLVAGA IPGPMITPLICMSTI	٠	1	l	
RQNSILIDPMSILSSVIHPAMVRLGIQYSGUVRGSNARCIALLIA. ALQOVIQUYTPPREISSBUINNIKAPYMSFLOPRISABMIN AIKFINKEITSUGSKRBEAKSELRAAIDRYVQEKIVLAQATI SERAYQKISMGDVILVYGUSSIVSRILQEANTBORREFRVVVVDS RPMLGGRETURELVHARVPASELLIPANSVILPEVSTEERUSKV GGEKV  6328 1030 276 HASARYTTAANGIGAMEBEHHTDAKIRABNGTGSSPRGPGCSL RHFACEQNILISRDGSASFIQODTSVLAGVFAPBKVUSKEIIPA KATLBYTLBPKIGDEVARSESBUILPANSVUJCFIHPETSI TVVLQVVSDAGSLLACCIANACMALVDASVPRALPCCVACALD SODTIVLIDPTSKQBKRARAVITFALDSVERKLIMSSTKGLYSDT ELQOCLAAAQAASQUVPEYATGAANAUNAGAGFTSATT RGDIERKSLAINEBFVSIYKBVKRELBSISBUQAMSNCOQMT SENDASKGGOTILVTTKUGSSSKKLERYAQAANAUNAGAGFTSATT RGDIERKSLAINEBFVSIYKBVKRELBSISBUQAMSNCOQMT SENDASKGGOTILVTTKUGSSSKKLERAQADANFLEKPQLIT SERVAGGOTESAANBESGGEVVTVSATGAANAUNAGAGFTSATT RGDIERKSLAINEBFVSIYKBVKRELBSISBUQAMSNCOQMT SENDASKGGOTILVTTKUGSSSKKLERAQADANFLEKPQLIT SENDASKGTODILVTKTVAGSSSKKLERAQADANFLEKPQLIT SENDASKGTODILVTKTVAGSSSKKLERAQADANFLEKPQLIT SENDASKGTODILVTKTVAGSSSKKLERAQADANFLEKPQLIT SENDASKGTODILVTKTVAGSSSKKLERAQADANFLEKPQLIT SENDASKGTODILVTKTVAGSSSKKLERAQADANFLEKPQLIT SENDASKATODILVTKTVAGSSSKKLERAQAVLIKKISINLERY RRITISGIVENSATALLTTIERRHILJSKKIFFNSLSLIARSKIMD KVELPPPLGFFARSTVARGFTODILVTROGPGGTPR PIEMISHDPLRYVGMITERGOVTSASRICATIONSCVVIDARQADFV VHITISGIVENSATALLTTIERRHILJSKKIFFNSLSLIARSKIMD KVELPPPLGPSSALANTMILITERSAVLITIKESVILIKNINGATYLITALE EPTDREBMIGPGIBALHDILITIKSQAVVLITAKISVITNILIKE PTDREBMIGPGIBALHDILITIKSQAVVLITALSVITNILIKE SPOQVOTILLE LSATVERGIVKOSTELIVCRAYGEVARAVNITIEKYKOPHILIP FYYTETRIKTFSRKWARECELISIANKCPDKMFKTKLLAQOPI- PVIQPHSILVSGETVKAMMINSVVRGEPAAGAFREPTTPTAFK KYERGDPPLABHDSKONKLAWKURISKIDPHHYDPLFPFOLC ENTFPYPEPRAGGETVKAMMINSVVRGEPAAGAFREPTTPTAFK KYERGDPPLABHDSKONKLAWKURISKIDPHHYDPLFPFOLC ENTFPYPEPRAGGETVKAMMINSVVRGEPAAGAFREPTTPTAFK KYERGDPPLABHDSKONKLAWKURISKIDPHHYDPLFFOLLC ENTFPYPEPRAGGETVKAMMINSVVRGEPAAGAFREPTTPTAFK KYERGDPPLABHDALFKCGTARSKILDPUNCHTURALLIKKANNO COGGREKTRORRACASATPLEGCVOLSFYRHAALLIKKANNO SOGGLIVSGOKRRENGENTOLDITACKMRRETE QILGRKVHLEY SOGLITAVLECLAAYDOKKSIKERINTSCAVURSFKERE KKNPS SVERPAMANILVHICHQTTDOLDIQITACKMRRETE QILGRKVHLEY SOGLITAV		1	1	
ALQOVIODYTTPPRETIS,SDLVNIKLEYMSFLTQCEPTISAMIN ALMFINKE IT SUCSSERBERASERLANDINGEVILVLAQAL SRFAYQKI SNGDVILVYGCSSLVSRILQEATTBERRIFRVUVDS RPWLEGRETTLRSLVHAGVPASYLLIPAASTVLPPEVSTEEKDSKV GGEKV GGEKV  6328  1030  276  HASARVITAARGIGAMEEBHETDAKIRABGIGSSFREDGCSL RHAGCENILSRPDGASSFIQDTSVLAGVIGAPBVKVEKEI KY KATLSVILRPKIGLEGVARKSBERLIRNTCEAVVLGTLHPRETSI TVVLQVUSDAGSLAACCIANAGALVINAGVPRABVKVEKEI KY KATLSVILRPKIGLEGVARKSBERLIRNTCEAVVLGTLHPRETSI TVVLQVUSDAGSLAACCIANAGALVINAGVPRABVKVEKEI KY SDGTIVLDPTSKORKRARAVITFALDSVERKLIMSSTKELVSDT ELQOCLAAAQAAOAQUVPREYMSELGRYSGES  6329  3 2016  SEEVAAGGGTRSAMAEGGGEVVTVSATGAANGIANAGGTSATT SNPLSRKHHILISTILDNKKBILBALAALSTFYVERSISTIRNL RGGIERKSLAIRBERYS I KREVKEELES ISEDVQANSINCOQDMI SRIQAAKGTQDLIVKTTKLGSBSQKLBTRAQVADAFISKRULT GIENEGMALLGETAYRRIJVRRAGSECRTLTQSSCOVSBYUTQA MRALODRFVLYKKTLDEGFTARRISTVURGF IDALTRIGGGGTFR PIEMISHDPLRYVGDMLAMHIQATASSKEBLEALLKRUTTGOVE BENTGEVVGHTEBOVCPLAVRI TEQVIVARPEGAVLIVKI SINLKE YHHTISGIVGNSATALLTTIEMHLLSKUI FPNSLSLIRASKIMD KVSLPPPDLGPSSALRGTTAMLREVLASHDSSVVPLDARQADDY QVLSCVLDPILGMCTVSASNICATAMATEVNSLIYMKKTTIALF EFTDRREBMLQFQIKATAMATEVNSLIYMKKTTIALF EFTDRREBMLQFQIKARAMOPDFNISAPINILI POLINT LSATVREQIVKGSTELIVCRAYGEVAAVANPI PINSYKOPENILIR SPQOVQTILLS  6330  1151  333  FFYYTTENRITTSRRWARRETISINKCPRAMPERTYTPTAFR KYPSRCJIN NSCOGIDVSQQKRENICOLIQUTURACHMPRIKALLAQOPL PVHQOPBLIVSBGTTVAMMINSVVUGEPHAAGAPERPTYPTAFR KYPSRCJIN NSCOGIDVSQQKRENICOLIQUTURACHMPRIKALLAQOPL PVHQOPBLIVSBGTTVAMMINSVVUGEPHAAGAPERPTYPTAFR KYPSRCJIN NSCOGIDVSQQKRENICOLIQUTURACHMPRITALLKVAQMVTL LSATVREQIVKGTELIANNSYSYSYEVYVICOLINILIPALINILIPR RQVICCTIKVQLQHUVSSAMVKALIVEYNGCIPULANI TEKNIMV NSCOGIDVSQQKRENICOLIQUTURACHMPRITALLKVAVP TYSSCILIN  6331  3 495  OGGGRVRTGGRRACASATPLEGCVDLSYPRHAALKVAVQF TYSSCILIN NLDVLIPBILDGLEQILIGIDNGKE IRKCEVVLOSFIKERIKNDS SVEYRAMANILVHICQTTDDLIQUTACHMPRITATILIPALRIP RVLICTSPPIGBELHYLIGTLILLILASIVASKSYNQSGIVAGA 1PCFMATPICLMSVINGYSTATISTYNGTASGSYSTETISTISTCROPEPP VIGVALGPHLSNODYFRVYTHTIVATORSSSSGSGSPPCRODTG KLSTMATHSQLVKTNTTGLRPROXASSSH  6333  3 1467  TRYPSERARGGEPGSCVSAARISDWT		İ	ı	LPBYPQVDDLLLRRLVKKPBRQQVPTRKDYGSKVSLFSHLPQYS
AIKFLINKETISVCSSKREBERASELRAAIDRYQGKIVLAQAI SRPAYOKI SKROWILIYVGCSLWSRILQGANTGGRFRWVVVDS RPWLEGRHTLRSLVHAGVPASYLLIPAASYVLPEVSTEEKDSKV GGRKV  6328 1030 276 HASARVYTTAARGLGAMEBEMETDAKIRAENGTGSSPRGPGCSL RHPACEQUILISRPDGSASPIJGDTSVLAGVYGFBEWKVEKEINY KATLSVILRFRIGLEVONBEKSRRILIRTGCAVUJGTHUPKTSI TVULQUVSDAGSILJACCLINAACHALVUAGVYGFBEWKVEKEINY SOCTULDPTSKORKKRARAVAUTTALDSVERLIMSSTKGLYSDT LOQCLAAAQAASQHVPRYTRSLQRYSKS  6329 3 2016 SEVARGGGTRSAMABGSGEVYTVSATGANKIINNOAGGTSATT SNELSRILLHKLISTIGLDKKNILBALKALSTFFVENSIGRTRIN RGDIEKKSLAINBEVVSIPKEUGSEISEDVQANKGCODMT RGDIEKKSLAINBEVVSIPKEUGSEISEDVQANKGCODMT SELOARKRONDLIVETKLAGSSKOKLIKRQVADAPISKFQLT GLEIMEQMALLQETAYRELKAGSSKOKLIKRQVADAPISKFQLT SDEMSLLAGTREGPTITEDFFKALGRVKQLIHNDVKVLLETNQQTA GLEIMEQMALLQETAYRELKAGSSKOKLIKRQVADAPISKFQLT SDEMSLLAGTREGPTITEDFFKALGRVKQLIHNDVKVLLETNQQTA GLEIMEQMALLQETAYRELKAGSSKOKLIKRQVADAPISKFQLT SDEMSLLAGTREGPTITEDFFKALGRVKQLIHNDVKVLLETNQQTA MRALODRPVLYKYTLDEFGTARBSTVVRGFIDLATRGGGGTFFR PIEMHSHDPLRYVGDMLAWILRQATASEKEHLEALIKHVYTOGVE ENIQEVVGHITEGVCRIKVRIGQVIVAEPGAVLLYKISNLLKF VHHTISGIVGNSATALLTITERHHILISKKIFFNSISLASKIMN KVSLPPPILGGESSAINQTHALBEVLASHVITTVGGVE ENIQEVGHITEGVCRIKVRIGQVIVAEPGAVLLYKISNLLKF VHENGESSLAMMPALDSVTILKANAVOPDRYLSAYTHYTVQQ HKSEQOSLAMMPALDSVTILKANAVOPDRYLSAYTHYTVQQ HKSEQOSLAMMPALDSVTILKANAVOPDRYLSAYTHYTVQQ HKSEQOSLAMMPALDSVTILKANAVOPDRYLSAYTHYTVQPFDGLC ENTFPYEFFRAGGIHMMEHGGKKLIDPVILIPKNALLKIN RQUICVTILKVLQHLUVSARMVGKKLINKUPSRMPKRYKILAQQFL PVHQPHSLYSGSFTVKARMKNSVVRGPFRAGAFKREPTYTTARR KYTERGDPFIALERHOGSKILDVLISTICHTIPKNALLKIN RQUICVTILKVLQHLUVSARMVGKKLINKUPSKYRGELIDIRIKTVNN NSGGGIDYSQQKRBNIGDLIQETLERAFRYGGBAPTINIKVVD TYSSCLIAM  6331 3 495 QGGGRVKTRGBRAGATPLEGCVDLSYPKTHAALLKVAQMVTL LIAPICVSRSSIMTNSAYSYFEVVTICOLINILAFVLEDELD FLEPHOTIFICHAGSHLISTKINGTORGSTAGGENFSPLHITTSCROPREP VIGYALGPHLSNGDYFMYVTTTTUARTCGROPSCHILTSCROPREP VIGYALGPHLSNGDYFMYVTTTTUARTCGROPSCHILTSCROPREP VIGYALGPHLSNGDYFMYVTTTTUARTCGROPSCHILTSCROPREP VIGYALGPHLSNGDYFMYVTTTTUARTCGROPSCHILTSCROPREP VIGYALGPHLSNGDYFMYVTTTTUARTCGROPSCHILTSCROPREP VIGYALGPHLSNGDYFMYVTTTTUARTCGRO				RONSLTOFMSIPSSVIHPAMVRLGLQYSQGLVRGSNARCIALLR
AIKFLINKETISVCSSKREBERASELRAAIDRYQGKIVLAQAI SRPAYOKI SKROWILIYVGCSLWSRILQGANTGGRFRWVVVDS RPWLEGRHTLRSLVHAGVPASYLLIPAASYVLPEVSTEEKDSKV GGRKV  6328 1030 276 HASARVYTTAARGLGAMEBEMETDAKIRAENGTGSSPRGPGCSL RHPACEQUILISRPDGSASPIJGDTSVLAGVYGFBEWKVEKEINY KATLSVILRFRIGLEVONBEKSRRILIRTGCAVUJGTHUPKTSI TVULQUVSDAGSILJACCLINAACHALVUAGVYGFBEWKVEKEINY SOCTULDPTSKORKKRARAVAUTTALDSVERLIMSSTKGLYSDT LOQCLAAAQAASQHVPRYTRSLQRYSKS  6329 3 2016 SEVARGGGTRSAMABGSGEVYTVSATGANKIINNOAGGTSATT SNELSRILLHKLISTIGLDKKNILBALKALSTFFVENSIGRTRIN RGDIEKKSLAINBEVVSIPKEUGSEISEDVQANKGCODMT RGDIEKKSLAINBEVVSIPKEUGSEISEDVQANKGCODMT SELOARKRONDLIVETKLAGSSKOKLIKRQVADAPISKFQLT GLEIMEQMALLQETAYRELKAGSSKOKLIKRQVADAPISKFQLT SDEMSLLAGTREGPTITEDFFKALGRVKQLIHNDVKVLLETNQQTA GLEIMEQMALLQETAYRELKAGSSKOKLIKRQVADAPISKFQLT SDEMSLLAGTREGPTITEDFFKALGRVKQLIHNDVKVLLETNQQTA GLEIMEQMALLQETAYRELKAGSSKOKLIKRQVADAPISKFQLT SDEMSLLAGTREGPTITEDFFKALGRVKQLIHNDVKVLLETNQQTA MRALODRPVLYKYTLDEFGTARBSTVVRGFIDLATRGGGGTFFR PIEMHSHDPLRYVGDMLAWILRQATASEKEHLEALIKHVYTOGVE ENIQEVVGHITEGVCRIKVRIGQVIVAEPGAVLLYKISNLLKF VHHTISGIVGNSATALLTITERHHILISKKIFFNSISLASKIMN KVSLPPPILGGESSAINQTHALBEVLASHVITTVGGVE ENIQEVGHITEGVCRIKVRIGQVIVAEPGAVLLYKISNLLKF VHENGESSLAMMPALDSVTILKANAVOPDRYLSAYTHYTVQQ HKSEQOSLAMMPALDSVTILKANAVOPDRYLSAYTHYTVQQ HKSEQOSLAMMPALDSVTILKANAVOPDRYLSAYTHYTVQQ HKSEQOSLAMMPALDSVTILKANAVOPDRYLSAYTHYTVQPFDGLC ENTFPYEFFRAGGIHMMEHGGKKLIDPVILIPKNALLKIN RQUICVTILKVLQHLUVSARMVGKKLINKUPSRMPKRYKILAQQFL PVHQPHSLYSGSFTVKARMKNSVVRGPFRAGAFKREPTYTTARR KYTERGDPFIALERHOGSKILDVLISTICHTIPKNALLKIN RQUICVTILKVLQHLUVSARMVGKKLINKUPSKYRGELIDIRIKTVNN NSGGGIDYSQQKRBNIGDLIQETLERAFRYGGBAPTINIKVVD TYSSCLIAM  6331 3 495 QGGGRVKTRGBRAGATPLEGCVDLSYPKTHAALLKVAQMVTL LIAPICVSRSSIMTNSAYSYFEVVTICOLINILAFVLEDELD FLEPHOTIFICHAGSHLISTKINGTORGSTAGGENFSPLHITTSCROPREP VIGYALGPHLSNGDYFMYVTTTTUARTCGROPSCHILTSCROPREP VIGYALGPHLSNGDYFMYVTTTTUARTCGROPSCHILTSCROPREP VIGYALGPHLSNGDYFMYVTTTTUARTCGROPSCHILTSCROPREP VIGYALGPHLSNGDYFMYVTTTTUARTCGROPSCHILTSCROPREP VIGYALGPHLSNGDYFMYVTTTTUARTCGROPSCHILTSCROPREP VIGYALGPHLSNGDYFMYVTTTTUARTCGRO	•	i	ĺ	
SRPAYOKISMOVILVYGCSSLIVERILORANTEGRRFERVUVUOS RPWLEGRITTASVHAGVPASYLIPAASYVLPEVSTEEKOSKV GGEKV  6328 1030 276 HASABVITTAARGUAMEBEMHITDAKTRAEMGTGSSPRGPGCSL RHPACEQUILISRPOSASPILGOTSVLAGVYGPABVKVEKEIPN KATLEVILRPKIGLIGVVABKSRERILIRTCEAVVLSTIHPRTSI TVVLQVVSDASSILACCLIANACVALUDBASVHRALECGVACALD SDGTLVLDPTSKOBKSARAVLTPALDSVERKLIMSSTKGLYSDT ELQOCLARAQDASQUVVFRYTRESLQRYYKSA  6329 3 2016 SERVARGGGTSAMAGSGEVVTVSATGANGUNMAGGTSATT SNELSRKLHKKLETILDADKENLEALKALSTFFVERSKERTERNI. RGDIERKSLAINERVUS IFRVVKEELSISEDVQAMSINCODMT SRIJAAKKOTQDLIVKTTKLQSESOKLKIRAOVADAPISKROLTS SDEMSLLAGFIREOPT TEDPEKALIGRVGUNASNICODMT SRIJAAKKOTQDLIVKTTKLQSESOKLKIRAOVADAPISKROLTS SDEMSLLAGFIREOPT TEDPEKALIGRVGUNASNICODMT SRIJAAKKOTQDLIVKTTKLQSESOKLKIRAOVADAPISKROLTS SDEMSLLAGFIREOPT TEDPEKALIGRVGUNASNICODMT SRIJAAKKOTQDLIVKTTKLQSESOKLKIRAOVADAPISKROLT SDEMSLLAGFIREOPT TEDPEKALIGRVGUNASVALIKAOVADAPISKROLT SDEMSLLAGFIREOPT TEDPEKALIGRVGUNASVALIKOOVADAPISKROLT SRIPAKREMILARVANILARVANICASSESEELBIALIKHVTTLGOTA MRALODREVIYKKTILDEGTTARRSTVVRGPIDALIKHVTTLGOTA MRALODREVIYKKTILDEGTTARRSTVVRGPIDALIKHVTTLGOTA MRALODREVIYKKTILDEGTTARRSTVVRGPIDALIKHVTLTGOTA MRALODREVUSHTITEGRVGUNASVALIKATIVAKSLIPMISLATINLIKE PITEMISHIDPLERVYOMLAMILGOATASEKEBILBALIKHVTTLGOTA MRALODREVUSHTITEGRVGUNASVALIKIPMISLAVIMITTILAL EFITORLIBMILOPTILARMISLAVIMISLIPMISLAVIMITTILAL EFITORLIBMILOPTILARMISLAVIMINEVILASHOSSVVELIAPOLITALIPOLIPHILIPOLIPHILIPOLIPHILIPOLIPHILIPHI	Ī		Į.	
8328 1030 276 HASAEVITAAARGLGAMEREMITTAKLIRARGGGSERRGCGLL RHPACEGRILLISREDGSASPIGGITSVLAGVYGPARVKVSKEI PN RATLEVILREKICLIGVURESRERILIRTICEAVULGTIHPRISI TVULQUVSDAGSILACCIANACHALVURGVPRARIFCCVACALD SDOTULDPISKQEKRARUKUTPALDSVEILMSSTKGLYSDT ELQOCLANAQASGHVPRYTRESLGRYSKS  6329 3 2016 SEVANGGGTISAMAGSGBEVVTVSATGAMAKIANIAGGTSATT SMPLGRKIHKILETRLDNDKEMLEALKALSTPPVENSLRTRRN, RGDIERKSLALINERVSIFYKEVERSELSIEEDQVSANGANGLANNGAGGTSATT SMPLGRKIHKILETRLDNDKEMLEALKALSTPPVENSLRTRRN, RGDIERKSLALINERVSIFYKEVERSELSIEEDQVSCOLOPUTOA MERLODRPVLYKYTLDERGTARRSTVVRGVIENDVKVLLETRQOTA GLEIMEGMALLGETAYRELKJASSGGKLEBLALKHVYTGGVE ENIGEVVGHITEGVCRPLKVVRIGQTVABEALLKHVYTGGVE ENIGEVVGHITEGVCRPLKVVRIGQTVABEALLKHVYTGGVE ENIGEVVGHITEGVCRPLKVRIEQVTVABCALLLKKTSILLKP YHHTISGIVONSATALLTIEERMHLLGKKIFFNALSLHASKLMD KVSLPPPDLAGPSSALNGTAMATHVNISLYMMATTIALE EPTDRIEMHDFLAVGTHALDGATSGERERLALKHVYTGGVE ENIGEVGHITEGVCRPLKVRIEQVTVABCALLLKKTSILLKP YHTISGIVONSATALLTTIERMHLLGKKIFFNALSLHASKLMD KVSLPPPDLAGPSSALNGTAMATHVNISLYMMATTIALE EPTDRIEMHLGPGIRAHLUTIINGAGSVLTRVGLSYTYNTVQQ HKPEQGSLAMPBLLDSVTLKAAMVOPDRYLSRYCHLASKLMD KVSLPPPDLAGPSSALNGTAMATHVNISLYMMATTIALFE EPTDRIEMHLGPGIRAHLUTIINGAGSVLTRVGLSYTYNTVQQ HKPEQGSLAMPBLLDSVTLKAAMVOPDRYLSRYDHILIFQLNPIL LSATVERGIVKGTERLVGRYGEVYAAVNNPINEYKOPENILHE SPQOVOTILLS FYYTYTYENKTFFREMVARKETILSLIKCPDRMPKRTKLLAQOPL PVHQPHSLVSGGFTVKAAMMASVVRGPPAAGAFKRRPYKPTAFK KYPERGDPFALLERINGGSKLDVHLIPTIPRILADLIN NSGGDIDVSGGKRINGGSKLLDVHTYRGILDIVINILKRVN NSGGDIDVSGGKRINGGSKLLDVHTYRGILDIVINILKRVN NSGGDIDVSGGKRINGDETLRAFRYGGRAFKRAPINIKYNV TYBSCLLIN  495 QGGRWRTRGRAGASATPLEGGVDLSYPKTHAALLKVAGNVTL LAPICVSSSLITNNSATSYFEVVTICOLINILAPFUHELFRPY RVITCISMPLSELHHVLIGTILLILISIVAASKSYNGGGLVAGA 1151 LAPICVSSSLITNNSATSYFEVVTICOLINILAPFUHELFRPY RVITCISMPLSELHULGGEDFILDRETYSSINGVARGFILDFILDERFRYLKEPS SGILTAVLPCLAYDDRKSTREVANVCNGSLIKKLVTESDDELD HLEPPGGRAGARPTPDDALKFRGGSTAGGSBFGGARKSEPPEDDALSH VIGWALGPHLSNODYFMYVTHTTUAATURGGSSGSSPPFCRODTG KLSTMATISGIVTTGTGGERGGRAGSGRASSISPTMEGGGGRAGG GLIFFBGGGGARGGARSLOWTAGGRAFKPROGLHTGGRERG	ļ			
6328 1030 276 HASAEVITAAARGLGAMEBEMHTDAKIRAENGTGSS PRGPGCSL RHPACEQRILISRPDGSASFIQGDTSVLAGYVGFASVKVEKEIN KATLEVILRPKIGLEVABKSRERILIRRTCEAVULGTHERTSI TVVLQVVSDASSILACCIARACHAUURGAVPMALPCGVACALD SDGTLVLDPTSKOBKRARAVILTPALDSVERKLIMSSTKGLYSDT ELOOCLAADAAASQN PYPYRBSLQRYRSJ 6329 3 2016 SSEVAAGGTRSAMAEGSGEVVTVSATGAANGLINNGAGGTSATT SNPLSRKIHKILETILDINDKRMLBALKALSTFFVENSKITKRNI. RGDIERKSLAINERVSI FREVVERELBSI SESDVQAMSNCCQDMY SRIQAAKRQTQDLIVKTTKLQSBSQKIKIRAQVADAPISKGQIT SDEMSLIKGTRREDP ITEDPKRVEKELBSI SESDVQAMSNCCQDMY SRIQAAKRQTQDLIVKTTKLQSBSQKIKIRAQVADAPISKGQIT GLSIMEQMALLQETAYBRLVRMAQSECRTLTQSSCDVSPULTOA MRALQDRPVILYKYTLDEPGTARRSTVURGFIDALTRGGFGGTPR PIEMISHDPLRYVGDMLAMLIQGATASEERILEALIKHVYTQGVE BNIGSVVGHITTEGVCRPLKVRI ISQVIVVABRGAULIX KISHLIKEY HHITISGI VGRSATALLITIERHILISKKI FINSISLIRASKIMD KVELPPPDLGPSSAINOTIMLLREVLASHDSSVVPLDARQDFV QVISCULDPLIQMCTVSASNIGTADMATFAWNSLYMMKTITLALF EFTDRRLEMLQFQIBAHLDTLINGASVULTRVGLSYTYNTVQQ HKDEQSSLAMMPALDSVILGAMUNDPRYLSAPDILLIPQLNFL LSATVKEQI VKQSTELLVCRAYGEV YAAWMPIENE KYDERNILHR SPQOVOTILLS SPQOVOTILS  6330 1151 333 FYYTYKSINFFSRKWABKGRKILDRIVGPPHAGAPKKRPTTPTAFR KYYRKGDPPIALRHDSKGRKILAMKVEIRKLDYHTYPTAFR KYYRKGDPPIALRHDSKGRKILAMKVEIRKLDYHTYPTAFFR KYYRKGDPPIALRHDSKGRKILAMKVEIRKLDYHTYPTAFFR KYYRKGDPPIALRHDSKGRKILAMKVEIRKLDYHTYPTAFFR KYYRKGDPPIALRHDSKGRKILAMKVEIRKLDYHTYPTAFFR KYYRKGDPPIALRHDSKGRKILAMKVEIRKLDYHTYPTAFFR KYYRKGDPPIALRHDSKGRKILAMKVEIRKLDYHTYPTAFFR KYYRKGDPPIALRHDSKGRKILAMKVEIRKLDYHTYPTAFFR KYYRKGDPPIALRHDSKGRKILAMKVEIRKLDYHTYPTAFR KYYRKGDPPIALRHDSKGRKILAMKVEIRKLDYHTYPTAFR KYYRKGDPPIALRHDSKGRKILAMKSVAGGRAPTINKTVUD TYRSCLIA  6331 3 495 QGGRVRTRGERACASATPLEGCVDLSYPRHAALLKVAQMVTL LIAPICVRSSLWTNSAYSYFEVVTICDLIMILAFYLVHLFPFY KVLTCISRPLSKLIHLLIGTILLLIASIVAASKSYNQGGIVAGA IVGPMATFICHASSIMISTKISCVYQGTBAFTHALKVUD TYRSCLIA  6332 1 878 JYTESNEPDLOSSPEPLARRTYSINGYARQFIISHTICKGPPREP VIGYALGPHLSNODYBMYTHTVAATQRSGSSGSPPECRODTG KLETMATHSOLVETTGGELGDGGTASGERTPSLHITSCROPREP VIGYALGPHLSNODYBMYTHTVAATQRGRNDFPDHALLFYGDBLD BERPGGROARSPTDDALLFYGGRARGA	l			
6328 1030 276 HASAEVITAAARGIGAMEBERHITDHKIRAENGTGSSPRGYGCSL RHFACEQILLSRPGGSAFILGGUTSLLAGVIGPABVKOKEL FN KATLEVILEPKIGLEPVARKERRELIENTCEAVVIGTHERTSI TVVLQVVSDAGSILACCLAVAACMALVDAGVPRAFALGCVACALD SOCTULUDPTSKORKRARAVUTFALDSVERKLIMSTKGLYSDT ELQOCLAAAQAASGHVPFYFRSLQRYSKS  6329 3 2016 SEEVAAGGGTRSARAEGGGEVVTVSATGAAMGLANGAGGTSATT SNPLSRKIMKLIETRIDNNKENLERLIAGSTFFVENSLRTRRIL RGDIERKSLAINEFYSIFKBVKEELESISEDVQAMSKCCQDMT SRLQAAKSGTQDLIVKTILOSSGOKLRAQVADAFISKGULT SDEMSLLEGTERGPITEDFFKALGRVKQHINDVKVLLETNQQTA MRALQDRPVLYKKTILDEFGTARRSTVVGSTOLAURGVCQDMT GLEMEQMALLQPTAYERLYRWAQSECRTLTQSSCCUSPVLTQA MRALQDRPVLYKKTILDEFGTARRSTVVGFTIDALTRGGFGGTER PIEMISHDPLRYVCDMLAMLHQATASEKERILEALIKHVTTQGVE BNTQBVVGHITEGGVGRFJKVRTGGVTVABFGAVLLYKTSIALKFV YHHTISGIVGNSATALLTIERMILLSKHIFFNSLSLIFASKLMD KVPLPPPDEJGPSALNQTILMLREVLASPOSVLPLARAGADAFV QVISCULDPLLQMCTVSASNIGTADMATFMVNSLYMMKTTLALF EFTDRRIEMLOFQIEAHLUTLINBQASVVLTRVGDFSYLTATAVQ HKPEQGSIAAMPHILDSVTILKARMVGPTSRSVVPLDRAQADFV QVISCULDPLLQMCTVSASNIGTADMATFMVNSLYMMKTTLALF EFTDRRIEMLOFQIEAHLUTLINBQASVVLTRVGDFNIFAKAN KVPLPPPDFDLAGGTSKANAVNLOSVVLGEPAAGAFKRPTXFTAFK KPTERCIDPILABSTVLKAMVANVYDFORTLSAPDMLLTPOLINFI LSATVKEQILVOSSTELVCRAYGEVYAAVNNPINEYKOPPENILHR SPQOVCTILLS  6330 1151 333 FFYYTYYERKTFFRKWVAEKETLSLINKCPDRMFKRTKLLAQOPL PVHQPHSLVSGGFTVKAMMKNSVVGGPPAAGAFKRPTXFTAFK KPTERCIDPILLSGENKILAVVYDRQCHAMILTHYPOLLDINITIFKNDNV NSGDGIDVSQQKRENIGDLIQSTLERAFRYGGBNAPINIKYVVP TYBSCLLN NSGDGIDVSQQKRENIGDLIQSTLERAFRYGGBNAPINIKYVVP TYBSCLLN OGGGRVRTTGRRACAGATPLBGCVDLSYPRTHAALLKVAQMVTI. LLAPICVRSSLMTMYSAYSYFSVVTICOLIMILAFYLVHLERFY RVITCISMPLSELLHYLIGTILLLLAIVAASKSYNQSGLVAGA 1POFMATPLCMSSIMISTKISCVTQTSDAAV 1POFMATPLCMSSIMISTKISCVTQTSDAAV 1POFMATPLCMSSIMISTKISCVTQTSDAAV 1POFMATPLCMSSIMISTKISCVTQTSDAAV 1POFMATPLCMSSIMISTKISCVTQTSDAAV 1POFMATPLCMSSIMISTKISCVTQTSDAAV 1POFMATPLOCATORDHARGETGLAGRWHLPY SSGLITAVLPCLAYDDRKKSIKVANVCNGSIMKLVTPEDDELD BLAPGGRQAPFTPDDALPRQGSTARSSISFTSHHIJTSCRPPEPTOTGABG GLAMHGIBEGGHAMPHOGNAMPPVOGNEMPVPMGGPPP VIGYALGPRISADQVFRYVTHTUAATGRSSSSGSSFPFCRODTG GLAMHGIBEGHAMAPAMSHAPHOGQAAMPPVPHIGMPPQMMPP	í		Ĭ	
RHFACEQNILSERPOGSASFICODTSVLAGVYOPABVKYEKSINY KATLEVILRYKIGLPGVAEKSRERLIKITCERVUGTLHPRTSI TVVLQVVSDAGSILACCLMAACMALVDAGVPRRALFCCVACALD SDCTTULDPTSKOBKRARAVLTFALDSVERKLIMSSTKGLYSDT ELQOCLAAAQAASGUPRYFYRSIGLYSTYSES  6329 3 2016 SEEVAAGGGTRSAMABGGGEVVTVSATGAAMGLANGAGCTSATT SNPLSRKHLKILETRIDNDKRULBALKALSTFFVENSLRTRRNL RGDIERKSLAINBEFVS IKRVKEELESISEDVQAMSGCCQDMT SRLOAAKSGTQDLIVKTTKLGSSQKLEIRAQVADAFLSKFQUT SDEMSLIKGTREGP ITSPFPKALGRYKDTFFVENSLRTRRNL GDLEMEQMALLQPTAYERLYRWAQSECRTLTQSSCDVSPVLTQA MRALQDRPVIXKYTLDEFGTARRSTVVRGFIDALTRGGFGSTR PIEMESHPDLEYVCOMLANHIQACTASELERALIKHVTTQGVE BNTOEVVGHITEGYCRPLKVRIEQVIVARPGAVLLYKISHLLKF YHHTISGIYGMSATALLTTIERMHLSFKFNISLIKASKLMD KVELPPPDLGPSSALMQTIMLREVLASHDSSVVPLDARQADFV QVISCULDPLLQMCTVSASNLGTADMATTFWINSLIKMSKIMD KVELPPPDLGPSSALMQTIMLREVLASHDSSVVPLDARQADFV QVISCULDPLLQMCTVSASNLGTADMATTFWINSLIKMSKIMD KVELPPPDLGPSSALMQTIMLREVLASHDSSVVPLDARQADFV QVISCULDPLLQMCTVSASNLGTADMATTFWINSLIMMSKTHAL EFTDRIERMLOFGIRAHLUTILINBLASTVINTSGLIYTYNTVQQ HKPEQGSLAMMPNLDSVTLKAMMVQFDRYLKRGKYNTRUGLSYTYNTVQ HKPEQGSLAMMPNLDSVTLKAMMVQFDRYNERKTHLAQQFL LSATVKEQIVKQSTELVCRAYGEVYAAVMNPINEYKDPSNIPKRTAFR KYYERGDPPIALBEBSKGRKTAMKVBIEKLDYHHYLPIP.FPGLC BMTFPYEPFRAGHHMLSHGSKKILDVLDQLIPINTSKMMN NSGDGIDYSQQKRENIGDLIQSTLEAFFRYGGENAFINIKYVV TYSSCLILM  6331 3 495 QQQCVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLMTNYSAYSYFSVVTICOLIMILAFYLVHLEPREY RVLTCTSBYELSHLYLIGTLILLISAUSKSKNYGSLVAGA IYGFMATHLCMASIMLSYKISCVTQSTDAAV  VTESNKPDLVSFIPLLRERIYSINQYARQFIISWILVLESVEDI NLLDYLPBELLGHQILGDINGKEIRKMCEVULGBELERIKKNEN SVKFABMANILVHICQTTDDLIQITAMCMREFI ISWILVLESVEDI NLLDYLPBELLGHQILGDINGKEIRKMCEVULGBELERIKKNEN SVKFABMANILVHICQTTDDLIQITAMCMREFI IGLAGRWILEPY SGGLTAVLPCLATORKSI HERVACVNQSIMKLVTPEDDELD ELAPGGGRAFPTDDALPKGGERATSSHPSLHILTSCRGPREPD VIGWALGERLSNQYKMYTHYTHAATQRSGSSGSFPPECROTTS KLSTMATHSGLVKTGTGTLERPQGAVSSHI  6333 3 1467 TRTPSEARGGGSPQSCVSAAHSDWTAGKEVUSLELBPREAGGEP	<u></u>	<u> </u>		
KATLEVILRPKIGLPOVARKSRRILINNTCRAVULGTHIPPTST TVVUQVVSDAGSILACCIANACMALVDAGVPRAIPCEVACALD SOGTUTUDPTSKORKRARAVITPALOSVERILIMSSTKGLYSDT ELQOCLAAAQAASQHVPRYTRSIQRTYSKS 6329 3 2016 SERVAAGGTISAMARSIGUVTVSATQAANGIANGAGGTSATT SNPLSRKHIKILETRLDNNKRHLRALKALSTPFVRNSLRTRRIL RGDIERKSLAINERVS IPKEVKRELES ISEDVQAMSNCOQDMT SRLQAAKKQTQDLIVRITTIGJSSSKULIKAQVADAPISKRQIT SDEMSLLRGTREGP ITEDFYKALGRUXQIHNDVKALETINQQTA GLEIMEGMALLQEPAVERILYRRAGSECKTITQESCOVSPVILTOA MRALQDRPVILKYTIDDEGTAARSTUVRGP IDALTRGGPGGTPR PIEMHSHDPLRYVGDMLANLHQATASEKEULBALLKHVTTQGVE BNIQEVVGHITEGVCRPLKVRIGQUTVARPGAVLLYKISMLLKP YHHTISGIVGNSATALLTIERMHLSKKIFFNSISHASKLMD KVSLPPPDLGGSSLANGTIMLRRULASRSVVPLDARGADFV QVISCULDPLIQMCTVSASNLGTAMMATFWNSLYMMKTTLALF EFTDRRLEMLQFQIEAHLDITLINBQASYVLTRRGGSYTPTAVA KVSLPPDLGGSSLANGVBAVAVMPINEXKDPENILHR SPQOVQTILLS 6330 1151 333 FFYYTTYERKFTSKMVARKRSTUSINKCPDKWPKKTKLLAQOPL LSATVKEQIVKQSTELVCRAYGEVYAAVMPINEXKDPENILHR KPIERGDP IALBRIDSKGRKIMKVVRGPPAAGAFKERPTKPTAFR KPYERGDP IALBRIDSKGRKIMKVVRGPPAAGAFKERPTKPTAFR KPYERGDP IALBRIDSKGRKIMKVRUSITERKLDTHHTLPFFDGLC EMTFPYEPPARQGHMMLSHGGNKILEVLPQLII IPIKMALMLIKN NSGGIDVSQQKRENIGDLIQETLERAFRYGGBNAPINIKYVVP TYBSCLIN 6331 3 495 QGGQKVRTRGERACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLMTNYSAYSYFSVVTICDLIMILAPILVHLFRFY RVILTCISPBLESHHIVLIGTLILLIALISVASKSYNQSGLVAGA 1FGFMATPLCMASIMLSYKISCVTQSTDAAV 7TSSCLIN NLIDYLPBLESHHIVLIGTLILLIATAVASKSYNQSGLVAGA 1FGFMATPLCMASIMLSYKISCVTQSTDAAV 6332 1 878 VTESNEPDLVSPJELGRERIYSHNQYARQPIISMILVLESVPDI NLIDYLPBLESHHIVLIGTLILLIATAGSSGNTEMLIVLESVPDI NLIDYLPBLESHHVILGTLILLIATAGSSGNTEMLIVLESVPDI NLIDYLPBLESHHVILGTHARGNKREFIGLAGRVHLPY SSGLLTAVLPCLAYDDRKKSIKVANVCNGSIMKLVTPEDDELD BLAPGGRQABFTPDDALPRQGSTARSSLSPFTCRQDTG KLSTMATHSQLVKTGTGLERPGAVASSSI 6333 3 1467 TRTPSEARAGGSSPQSCVSAAHSDWTAGKRVSLLAPLIPPREAG GLMMGHEGGHANDAVSHYDMGCARAMPPDMMPPMGGPP	6328	1030	276	
6329  3 2016 SERVANGGOTRANACHALVDRASVERKLINSSTKGLYSDT ELQCLARAQASGBVFRYRRSLQRRYSKS 6329 3 2016 SERVANGGOTRSANAEGGBVFRYRSSLQRRYSKS 6329 3 2016 SERVANGGOTRSANAEGGBVFRYRSSLQRRYSKS 6329 8 SERVANGGOTRSANAEGGBVFRYRSSLQRRYSKS 8 SERVANGGOTRSANAEGGBVFRYRSSLQRRYSKS 8 SERVANGGOTRSANAEGGBVFRYRSTLANKAGAGGTSATT SRLGSKLIKLINETLENDKERLLRALKALSTFFVENSLATRRILL RGDIERKSLAINERFVSIFKEVKEELESISEDVQAMSINCOQDWT SRLQARKGYTODLIVKTTKLQGSCGKLIKJQADAPLSKFQLT SREWALGARKGYTODLIVKTTKLQGSCGKLIKJQADAPLSKFQLT SREWALGARKGYTODLIVKTTKLQGSCGRACHQADAPLSKFQLT SREWALGARGAGGTSATT GESIMBQMALLQETAYRRLYRANGSCCRILTQSSCOUSPULTOQA MRALQDRPVLYKYTLDEFGTARRSTVURGFIDALTGAGGFGTFR FRIGHT SPREWALGATAGSCTLITTGSCOUSPULTOQS MRALQDRPVLYKYTLDEFGTARRSTVURGFTDALTKGGPGGTFR FRIGHT STORT STATE	I		1	
SDOTT.ULDPTSKQEKRARAVLTPALDSVERKLIMSSTKGLYSDT ELQQCLAAAQAASQHVPRFYRESLQRRYSKS  SEVBAAGGGTESBAAEGGGEVTVSATGAARKIANGAGGTSATT SNPLSRKLHKILETRLDNDKERLBALKALSTYFVENSLETRENL RGDIERKSLAINEBFVS IFKEVKERLESISEDVQAMSNCOODMT SRQAAKKQTQDLIVKTTKLQSESQKLBIRAQVAADPLSKFQLT SDEMSLLRGTREGP ITEDFYKALGRVKQIHBUVKVLLETTQQTA GEIMROMALLQETAKRLYRHAQSSCKTLTQSSCOVEPVLTQAY MRALQDRPVLYKYTLDEFGTARRSTVURGFIDALTREGGFGFTPR PIEMHSHDPLRYVCDMLAMLHQATASEKEHLEALLKHVTTQSVE BYTOPVUSHTITEGGVEGTERVRIGVQUTVARPGAVLLYKISMLLKR YHHTISGIVGNSATALLTTIERHHLLSKKIFFNSLSHASKIMD KVELPPPDLGPSSALNQTLMLREVLASHDSSVVPLDARQADFV QVISCVLDEPLLQMCTVSASNLGTAMATTMVNSLYMMKTTIALF EFTDRRIBMLDFQIRAHLDTLINEQASVLTTRUGLSYTYMTVQQ HKEPQGSLAMMPHLDSVTLKAMVYDFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTELVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTTLLS SPQVQTTLLS FFYYTFYBRKFFSRKMVABKETLSLNKCPDKMPKRTKILAQOFL PVHQPHSLVSSGFTVKAMMKNSVVRGPPAAGAFKRRPTKPTAFR KFYERGDFPIALBHDSKGNKLAWKVEIBKLDYHPYLPFDGLC EMTFPYEFPARGGHDMLBHGGKKLLPVLPQLIIIPIKRALNLKN RQVICTTLKULQHLVVSABMUGKALLPVLPQLIIPIKRALNLKN NSGGIDVSQQXRRENIGDLIQETLRAFERYGGENAFINIKYVVP TYBSCLIN  6331 3 495 QGGRVRTTEGRRACASAFPLEGCVDLSYPRTHAALLKVAOMVTL LAFFICKRSLMTNSYASYSFEVYTICDLIMILAPYLVHLFRFY RVLTCISWPLSELHYLIGTLLLIAISIVAASKSYNQSGLVAGA IPOFMATFICMSLMTSATSYSTYSTYTICDLIMILAPYLVHLFRFY RVLTCISWPLSELHYLIGTLLLIAISIVAASKSYNQSGLVAGA IPOFMATFICMSLMTSAYSYSTYTYTICDLIMILAPYLVHLFRFY SGGLTAVLPCLANDDRKSIERSWANVCNQSIMKLVTEEDDELD BLRPGQRQABPYPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGFHLINQDYFMYVTHTIVAATORSGSSSPFFCRQDTG KLTMMATHSQLIVETGTGLRPRAVSSSH  6333 3 1467 TRTFSEREAGGGEPGSCVSAAHSDWTAGRVSLLAPLIPPRSAG GLMMGHEGHHYAPHCMHEPMGCRAMPPVFROMMPPPHGAGEP	1	(	1	
6329 3 2016 SEVAAGGTRSAMAEGGEVTVSATGAMGIANGAGGTSATT RGDIERKSLAINERVSIPKEVERLESISEBUQAMSNCCODMT SEVAAGGTRSAMAEGGEVITVSATGAMGIANGAGGTSATT RGDIERKSLAINERVSIPKEVERLESISEBUQAMSNCCODMT SEVAAGRTQDELIVETTIKLGSESDUQAMSNCCODMT SEVAAGRTQDELIVETTIKLGSESDUQAMSNCCODMT SEVAAGRTQDELIVETTIKLGSESDUQAMSNCCODMT SEVAAGRTQDELIVETTIKTIKGSESDUQAMSNCCODMT SEVAAGRTQDELIVETTIKTIKGASSOKLEERAQVADAPISEKPULTIQA MEALODPPULKYRIDDEPGTARRSTVYRGFIDALITRGPGGTETE PIEMISHDPLRYVGDMLAMILHQATASEKEHLEALLKHVTTQGVE ENIQEVVGHITBGVCRPLKVRIEQVIVASPEGALLIKHVTTQGVE ENIQEVVGHITBGVCRPLKVRIEQVIVASPEGALLIKHVTTQGVE ENIQEVGHITBGVCRPLKVRIEQVIASPEGALLIKHVTTQGVE HYBELGESSLAIMPILLERVLASSHOSVVFLDARGADEV QVISCULDPLLQMCTVSASNLGTAMTMVMSISVMRITTIALE EPTDREBMLQFQIEAHLDYLINERQASVVFLDARGADEV QVISCULDPLLQMCTVSASNLGTAMTMVMSISVMRITTIALE EPTDREBMLQFQIEAHLDYLINERQASVVFLDARGADEV HKEGQSIAMMPILDSVTLKAMVQFDRYLSAPDINLIPQLIPL EPTYPTYERQDIVKSGFITVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KPYERGDFFIALBHDSKGNKLMKVRIBELDYHHYLDELFPGLC EMTPPYEPPARGGHDMLEHGGGKLUPUPQLII PJEKNALMLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQLLPVLAITFKNMOV NSGDGIDYSQQGRRNIGDLIQBTLRAFERYGGBNAFINIKYVVP TYSSCLIAN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQLLPVLAITFKNMOV NSGDGIDYSQQGRRNIGDLIQBTLRAFERYGGBNAFINIKYVVP TYSSCLIAN 13 495 QQGGRVRTEGRACASATPLEGCUDLSYPRTHAALLKVAGMVTL LIAPICVRSLENTNYSAYSYFEVVTICDLIMILAPYLVHLFFPY RVLTCISMPLSELHYLIGTLLLLISIVAASKSYNQSGLVAGA IVGFMATFLCMASIMLSYKISCUTQSTDAM VTESNKFDLVSFILJHERTYSNOVQARQFTISMTLVLESVPDI NLLDYLPBELIDGLPQILGDNGKEIRKMCEVVLOBFLKEIKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMREFTQLAGRVMLPY SGGLTAVLPCLATNDARKSIKKSMOVARQFTISMTLVTEEDDEL BLRPQQRQABPTPDDALPKQEGTASGEWTPSLHITSCRGPREPP VIGVALGPHLSNQDYFMYVTHTIVAATQRSSGSEPPFCRQDTG KLSTMATHSQLIVETGTGLERPRQAYSSH  6333 3 1467 TRTPSEAEAGGESPQSCVSAAHSDWTAGREVSLLAPLIPPRAGG GPMFFFSFRAGGESPQSCVSAAHSDWTAGREVSLLAPLIPPRAGG QPMFFFSFRAGGESPQSCVSAAHSDWTAGREVSLLAPLIPPRAGG QPMFFFSFRAGGESPQSCVSAAHSDWTAGREVSLLAPLIPPRAGG	ŀ	1		
6339 3 2016 SSEVARGGGTRSAMABGGGEVYTVSATGANAGLINNGAGGTSATT SMPLSRKHKLIETELDDKINLEALKALSTFFVENSLRTRRNL RGDIERKSLAIMERVSIFREVKEELESISEDVQAMSINCOQDMT SRLQAARBGTQDLIVKTTKLQSESQKLBIRAQVADAPISRFQDT SDEMSLLRGTREGPITEDFFKALGRYKQIHDVKVLLRTNQQTA GLEIMEQMALLQETAYBRLYRMAQSECRTHTQSSCOVSPUITQA MRALQDRPVIJKYTLDEFGTARRSTVURGIDALTRGGEGGTER PIEMHSHDELRYVGDMLAMILGQATASEREHLBALLKHVTQGVE ENIQEVVGHITESVCRPLKVRIEQVIVABPGAVLLYKISNLKF YHHTISGIVGNSATALLTTIERMHLISKKIFNSLSHHASKLMD KVELPPPDLGPSSAINQTTMLRUJASHDSSVVDLDARQADPV QVLGCVLDPLLQMCTVSASNLGTADMATFMVNSLYMMKTIALF EFFTDRRIKMLQFOLBAHLDTLINEQASYVLTRVGLSYIYNTVQQ HKPEQCSLANMINLDSVTIKAAMVQFDRYLSAPDNLLIPQLNIL LSATVKEQIVKQSTELVCRAYGEVYAAVMNFINEYKDPENILHR SPQQVOTLLS  6330 1151 333 FFYYTTYBRKTFSRKMVAEKETLSINKCPDRMPKRTKLLAQQPL PVHQPHSLUSEGFTVKAMKNSVVRGPPAAGAFKEPTKVTAFR KPYERGDFPIALBHDSGNKILAWLIRKLDYHYLPLIFPGGLC EMTFPYEFFARGIHDMLBHGGNKILPVLPQLIIIPKNALNLRN RQVICVTLKVLQHLVVSABMVGKALVPYYRQILPVLINIFKNMVN NSGGGIDYSQQKRENIGDLIQBTLBAFERYGGENAPINIKYVVP TYESCLIN  6331 3 495 QGGGRVRTRGRRACASATPLEGCVDLSYPTHAALLKVAQMVTL LIAPICVRSSLMTNVSATSYFEVVTICDLIMILAFYLVHLFRFY RVILTCISWPLSELHYLIGTLLLLASIVAASKSYNQSGLVAGA IPGFMATFLCMASIMLSYKISCVTQSTDAAV  6332 1 878 VTESNKFDLVSF IPLLBRERIEVENNOYARQFTISWILVLESVPDI NLLDYLPBILDGLFQILGDINGKEIRKMCGVVLGBFLRBIKNPS SVKFARMANILVHCQTTDDLIQITAMCMRREFIQLAGRVULPY SSGILTAVLFCLAYDDRKKSI KEWADVVLNGSLMKLVTPEDDELD BLRPGGRQAAPTPDDALFKQSGSSGSPPFCRQDTG KLSTMATHSQLVETGTGLEPRQAVSSSH 6333 3 1467 TRTPSERBAGGSEPQSCVSAAHISDWTAGKPVSLLAPLIPPRAGG GLAMGHECHNIYAPMCMHUMGGGSRKRSSLSPTMRPGGARG				SDGTLVLDPTSKQEKKARAVLTFALDSVERKLLMSSTKGLYSDT
SNPLSRKLHKILETRLDNOKEMLEALKALSTPFVENSLERTRRN. RGDIRKSLAIMERVSIFKBVKEELESISEDVQAMSNCCQDMT SRIQARAKGTQDIJVKTTKLQSSSQKLEIRAQVADAPLSKFQLT SDEMSLLRGTREGP ITEDFFKALGRVKQIIMDVKVLLRTMQQTA GLEIMEQMALLQETAYERLYRWAQSECRTLTQESCDVSPVIJOA MRALQDRPVIYKYTLDEFGTARRSTVVRGFIDALTRGGEGGTER PIEMHSHDPLRYVGDMLAMLHQATASEKEHLEALLKHVTTQGVE BNIQBVVGHITEGVCRPLKVRIGEVVABFGAVLLYKISALLKF YHHTISGIVGNSATALLTIERMHLLSRKIFFNSLSHASKLMD KVELPPPDLGPSSAINQTIMLIRBVLASHDSSVVPLDARQADFV QVLSCVLDPILQMCTVSASNLGTADMATFMVNSLYMMKTFLALF EFTDRELEMLQRQIBAHLDTLINBQASTVLTRVGLSYIYMTVQQ HKPEQCSLAMMPNLDSVTIKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTELVCRAYGEVYAAVMPINEKYDFBNILHR SPQQVQTTLLS  FYYTTYTHRKTFSRKWARKETLSINKCPDMFKRTKLLAQQFL PVHQPHSLVSRGFTVKAMMKNSVVRGPPBACAFKERFTKFTAFR KYTERGDFPIALEHDSKGNKLMKVVRGPPBACAFKERFTKFTAFR KYTERGDFPIALEHDSKGNKLMAKVEIEKLDYHHYLDFLFFDGLC EMTFPYEFFARGGIHDMLSHGGNKLLVUPQLIIPIKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGBNAPINIKYVVP TYBSCLIN  6331 3 495 QQGRVTTRGRRACASATPLEGCVDLSYPRTHAALLKVACMVTL LIAPICVRSSLETHYLIGTLILLIASIVARSKSYNGSGLVAGA 1YGFMATFLCMASIHLSYKISCVTQSTDAAV  6332 1 878 VTESNKFDLVSFIPLLRERTYSNNQYARQFIISWILVLESVPDI NLLDYLPBILDGLFQILGDNGKEIRKMCEVVLOGFIKEIKKNES SVKFAEMANILVIHCQTTDDLQLITAMACMREFFICLAGTVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQARPTPDDALPRQGGTASGEMTPSLHHTJSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPFFCRQDTG KLSTMATHSQLVKTGTGGLEPRQAVSSSH 6333 3 1467 TRTFSERERGGBSPGSCVSAAHSDWTAGKVYSLLAPLIPPRAGG GLAMGHECHHYAPMCMHUMGGGSRRRSSLSPTMRPGTGAERG	1	1		ELOOCLAAAQAASQHVFRFYRBSLQRRYSKS
SNPLSRKLHKILETRLDNOKEMLEALKALSTPFVENSLERTRRN. RGDIRKSLAIMERVSIFKBVKEELESISEDVQAMSNCCQDMT SRIQARAKGTQDIJVKTTKLQSSSQKLEIRAQVADAPLSKFQLT SDEMSLLRGTREGP ITEDFFKALGRVKQIIMDVKVLLRTMQQTA GLEIMEQMALLQETAYERLYRWAQSECRTLTQESCDVSPVIJOA MRALQDRPVIYKYTLDEFGTARRSTVVRGFIDALTRGGEGGTER PIEMHSHDPLRYVGDMLAMLHQATASEKEHLEALLKHVTTQGVE BNIQBVVGHITEGVCRPLKVRIGEVVABFGAVLLYKISALLKF YHHTISGIVGNSATALLTIERMHLLSRKIFFNSLSHASKLMD KVELPPPDLGPSSAINQTIMLIRBVLASHDSSVVPLDARQADFV QVLSCVLDPILQMCTVSASNLGTADMATFMVNSLYMMKTFLALF EFTDRELEMLQRQIBAHLDTLINBQASTVLTRVGLSYIYMTVQQ HKPEQCSLAMMPNLDSVTIKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTELVCRAYGEVYAAVMPINEKYDFBNILHR SPQQVQTTLLS  FYYTTYTHRKTFSRKWARKETLSINKCPDMFKRTKLLAQQFL PVHQPHSLVSRGFTVKAMMKNSVVRGPPBACAFKERFTKFTAFR KYTERGDFPIALEHDSKGNKLMKVVRGPPBACAFKERFTKFTAFR KYTERGDFPIALEHDSKGNKLMAKVEIEKLDYHHYLDFLFFDGLC EMTFPYEFFARGGIHDMLSHGGNKLLVUPQLIIPIKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGBNAPINIKYVVP TYBSCLIN  6331 3 495 QQGRVTTRGRRACASATPLEGCVDLSYPRTHAALLKVACMVTL LIAPICVRSSLETHYLIGTLILLIASIVARSKSYNGSGLVAGA 1YGFMATFLCMASIHLSYKISCVTQSTDAAV  6332 1 878 VTESNKFDLVSFIPLLRERTYSNNQYARQFIISWILVLESVPDI NLLDYLPBILDGLFQILGDNGKEIRKMCEVVLOGFIKEIKKNES SVKFAEMANILVIHCQTTDDLQLITAMACMREFFICLAGTVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQARPTPDDALPRQGGTASGEMTPSLHHTJSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPFFCRQDTG KLSTMATHSQLVKTGTGGLEPRQAVSSSH 6333 3 1467 TRTFSERERGGBSPGSCVSAAHSDWTAGKVYSLLAPLIPPRAGG GLAMGHECHHYAPMCMHUMGGGSRRRSSLSPTMRPGTGAERG	6120	1	2016	
RGDIERKSLAINERFYS IFRBYKRELESISEDVQANSNCCQDMT SRKQAAKRQTQDLIVKTTKLQSESQKLBIRAQVADAPLSKPQLT SREMSLLRGTREGPITEDFFKALGRVKQIBNDVKVLLRTNQQTA GLEIMEQMALLQETAYERLYRHAQSECRTLTQESCDVSPVLTQA MEALQDRPVLYKYTLDEFGTARRSTVVRGFIDALTRGGPGGTFR PIEMHSHDPLRYVGDMLANLLGATASEKEBLERLLKHVYTQGVB ENTQEVVGHITEGVCRPLKVRIRQVTVABEGAVLLYKISNLLKF YHHTISGIVGNSATALLTIERMHLLSKRIFRNSLSLHASKLMD KVBLPPPDLGPSSALNQTIMLLREVLASHDSSVVPLDARQADFV QVLSCVLLDPLLQMCTVSASNLGTADMATTMVNSLYMMKTTLALF EFTDRRIEMLQFQIRAHDULINBQASYVLTRYGLSYLTMTVQQ HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKRQIVKQSTBLVCRAYGEVYAAVVNPLNEYKDPENILHR SPQQVQTLLS  6330  1151  333  FFYYTFYENKTFSRKMVARKETLSLNKCPDKMPKRTKLLAQQFL PVHQPHISLVSEGFTVLAMMKNSVVRGPPAAGAFKREPTKPTAFR KYYERGEDFPLALEHDSKGNKINMKVSIRKLDYHHYLPLFPDGLC EMTFPYEFPARQGIHMMLSHIGGNKILDVLPQLLIPIKNALNLKN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENICDLIGETLEAFERYGGENAFINIKYVVP TYBSCLIN  6331  3 495  QGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LLAFICVRSSLMTNYSAYSYFKVVTICDLIMILAFYLVHLPRFY RVLTCTSWPLSEILHTV.IGTLLLLASIVASKSYNQSGLVAGA 1PGFMATFLCMASIWLSYKISCVTQSTDAAV  6332  1 878  VTESNKEDLVSFTPLLRERTYSNNQVARQFIISWILVLESVEDI NLLDYLBEILDGLPQILGDNGKSIRKNCEVVLOBFIKEIKKNPS SVKPAEMANILVIHCQTTDDLIQLTAMCMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIRSVANVCNQSIMKLVTPEDDELD BLRPGQRAPFTPDALPKGGGTASGEWTPSLHITSCRGPREPD VIGVALGPHLSNQDYPMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVXTGTGLEBPQAVSSSH  6333  3 1467  TRTTSERBRAGGESPGSCVSAAHSDWTAGRVSLILAPLIPPRAGG GLMMGHCMHYAPMCGSGRRRSSLSPTMRPQOTGAERG GLMMGHCMHYAPMCGSGRRRSSLSPTMRPQOMPPMCGFP	0323	,	2020	
SRLQAAKEQTQDLIVKTTKLQSESQKLETRAQVADAPLSKPQLT SDEMSLLRGTRESPITEDFFKALGRVKQIENDVKVLLRTNQGTA GLBIMRQMALLQETAYERLYRNAQSECRTLTQRSCDVSPVLTQA MRALQDRPVLYKYTLDEFGTARRSTVVRGFIDALTRGGFGGTFR PIEMHSHDPLRYVGDMLAWLHQATASEKEHLEALLKHVTTQGVE BNTQGVVGHITEGVCRPLKVRIGVUVABPGAVLLYKISNLLKF YHHTISGIVGNSATALLTITERMHLISKIFFNSLSLHASKLMD KVELPPPDLGPSSALNQTLMLLEKVLASHDSSVVPLDARQADFV QVLSCVLDPLLQMCTVSASNLGTADMATTMVNSLYMMKTTLALF BFTDRRLEMLQFDLEAMLUTLINBQASVVLTRVGLSYIVNTVQQ HKPPQGSLANMPNLDSVTLKAAMVQFDYNLSAPDNLLIPQLNFL LSATVKEQIVKQSTELVCRAYGEVYAAVMNPLNEYKDPENILHR SPQQVQTLLS  FFYYTTFNKTFSRKWARRETLSLNKCPDKMPKRTKLLAQQPL PVNQPHSLVSBGFTVKAMMKSVVRGPPARGAFKREPTKPTAFR KPYERGDFPIALBHDSKGNKIAWKVSIKKLDVHDPLIPLKNALNLRN RQVICVTLKVLQHLVVSASHWAVKSLLVPYVRQLLPVLNLIFKNMNV NSGDGIDYSQQKRRNIGDLIQETLEAFERYGGENAFINIKYVVP TYBSCLLN  6331  3 495 QGGRVRTRGRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVASKSYNQSGLVAGA 1PGFMATPLCMASINLSYKISCVTQSTDAAV  6332 1 878 VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQLLGDNGKSIRKMCZVVLGEFKKEIKKNPS SVKRZMANILVLHCQTTDDLIQLTAMCMMREFIOLAGRWILPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQARPTPDDALPRGGGTSSGGTFSSLHITSCRGPREPI VIGVALGPHLSNQVYMYYTHTVAATQRSGSSGSPPFCRQDYG KLSTMATHSQLVXTGTGLEPRQAVSSSH  6333 3 1467 TRYPSERBAGGGEGPGSVSAAHSDWTAGKVSILLAPLIPPRSAG GIAMMSHCMHYABWGGRANMPPVPRIGMPQMMPPNGGPP		i	į	
SDEMSLLRGTREGPITEDFFKALGRVKQIENDVKVLLRTNQQTA GLEIMEGMALLQETAYERLYRWAQSECRTLTQESCDVSPVLTQA MRALQDRPVLYKYTLDEFGTARRSTVVRGFIDALTRGGPGGTFR PIEMHSHDPLRYVGDMLAWLHQATASEKEHLEALLKHVTTQGVE ENTQEVVGHITEGVCRPLKVRIRQVTVABFGAVLLYKISNLLKF YHHTISGIVGNSATALLTTERMHLLSRKIFNSLSLHASKLMD KVELPPPDLGPSSALNQTIMLLREVLASHDSSVVPLDARQADFV QVLSCVLDPLLQMCTVSASNLGTDMARTMVNSLYMMKTTLALF EFTDRRIEMLQFQIRADLTHALBROASVVLTRVGLSYINTVQQ HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKRQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS  6330 1151 333 FFYYTTYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSBGTVKAMMKNSVVRGPFBAGAFKRRPTKPTAFR KYYERGDFPIALEHDSKGNKIAWKVBIEKLDYHHYLDFLFPDGLC EMTFPYEFFARQGIHMMLEHGGNKILPVLPQLIIPTKNANNV NSGDGIDYSQQKRENIGDLIQETLBAFERYGGENAPINIKYVVP TYBSCILN  6331 3 495 QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSAYSYFEVVTICDLHILLAFVLVHLFRFY RVITCISMPLSBLHYNIGTLLLLLASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCVTQSTDAAV  1 878 VTESNKFDLWSFIPLLRERIYSSNQVARQFIISWILVLESVPDI SVKKFAEMANILVHCQTTDDLIQLTAMCMRREIQLAGRWMLFY SGGLTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD ELRPGQRQARPTDDDLIPQLIGITAMCMRREIQLAGRWMLFY SGGLTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD ELRPGQRAFTDDDLIPKQGSTASGEWTPSLHITSCRGPREPD VIGWALGPHLSNQDYFMYVHTIVAATORSGSSGSPFFCQDTG KLSTMATHSQLVKTGTGLEPRQAVSSH  6333 3 1467 TRTTSERBAGGGESPGCVSAAHSDWTAGKFVSLLAPLIPPERSAG GLMMGHCMHYAPWGMCRAMMPPVPRIGMPPQMMPPMGGPP			i	
GLEIMEQMALLQETAYERLYRMAGSECRTLTQESCDVSPULTQA MRALQDRPVLYKYTLDEFGTARRSTVVRGFIDALTRGFGGGTFR PIEMHSHDEJRYVQDMLAMJHQATASEKEHLEALLKHVYTQGVE ENIQBVVGHITEGVCRPLKVRIEQVIVAEPGAVLLYKISNLLKF YHHTISGIVGNSATALLTTIERHILSKKIFFNSLSLHASKLMD KVELPPPDLGGFSALNOTIAMLREVLASHDSSVVELDARQADFV QVLSCVLDPLLQMCTVSASNLGTADMATFMVNSLVMMKTTLALF EFTDRRLEMLQFQIERAHLDTLINEGASYLTRVGLSYIYNTVQQ HKPEQGSLAMMPNLDSVTLKAMVQFDRYLSAPDMLLIPQLWFI LSATVKEQIVKQSTELVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVOTLLS  6330 1151 333 FFYYTFYSENKFFSRKMVAEKETLSINKCPDKMPKRTKLLAQOFL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KYYERGDFPLALEHDSKGNKLMKVEIKKLDYHHYLPLFFDGLC EMTFPYNEFFARQGHIMDLEGONKLIPUPQLIIFIKNINLNLKN NSGDGIDYSQQKRENIGDLIQETLEAFERYGGBNAFINIKYVVP TYESCILN  6331 3 495 QGGGRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LLAFICVRSSLMTNYSAYSYFEVVTICDLIMILAFYLVHLFRPY RVLTCISMPLSELHHYLIGTLLLLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIMLSYKISCVTQSTDAAV  6332 1 878 VTESNKFDLVSFIPLARERIYSNNQYARQFIISMILVLESVEDI NLLDYLBEILDGLFQILGDNGKEIRKCEVVLGEFLKEIKKNPS SVKKREMANILVHICQTTDDLIQITAMCMMREFIQLAGRWMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSIMKLVTPEDDELD ELMPGGRQABFTPDDALPKGSGTASGENTPSLHLTSCRGPREPD VIGMALGPHLSNQVYFMYVTHTIVAATORSGSSGSPFFCRODTG KLSTMATHSQLVKTGTGLEPRQAVSSSH  6333 3 1467 TRTFSERAGGGSSPGSCVSAAHISDMTAGKPVSLLAFLIPPERSAG GPLMTSHRMTAPMCMIPMGGRANMPPVPHGMMPPMRGGPP	ì	ļ		
MRALQDRPULYKYTLDEFGTARRSTUVRGFIDALTRGGFGTFR PIEMHSHDPLRYUGHLAMLHQATASEKEHLEALIKHVTTQGVE ENIQEVVGHITTEGVCRPLKVRIEQVIVAEPGAVLLYKISHLKKP YHHTISGIVGNSATALLTTIEMHLLSKKIPFNSLSLHASKLMD KVELPPPDLGGFSGALNQTIMLREVLASHDSSVVELDARQADBV QVLSCVLDPLLQMCTVSASNLGTADMATTMVNSLYMMKTILAIF EFTDREBMLQFQIRANLDTLINEQASYVLTRVGLSYIYNTVQQ HKPEQGSLAMMPRIDSVTLKAAMVQFDRYLSAPDDNLLIPQLWFL LSATVKEQIVKQSTELVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTILS  6330 1151 333 FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSSGFTVKAMMKNSVVRGPPAAGAFKERPTKFTAFR KFYERGOFP JALBEIDSKGNKTAMKVEIKKLDYHHVLPLFFDGLC ENTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN NSGGGIDYSQQKRENIGDLIQETLBAFERYGGENAPINIKYVVP TYESCLLN  6331 3 495 QQGQRVETRGRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSLEMTNYSAYSYFEVTICDLIMILAPYLVHLFFFY RVITCTSWPLSELHTYLGTLILLIASTVARSKSNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV  1 878 VTESNKFDLVSFIPLLRERIYSNNQYARQFIISMILVESVPDI NLLDYLPEILDGLPQLIGDINGKEIRKMCEVULGEFIKEIKKNPS SVKFAEMANILVHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY SSGLTAVLPCLAVDDRKKSIKEVANVCNQSLMKLVTPEDDELD ELRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGWALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH 6333 3 1467 TRTFSEREAGGGSFOSCVSAAHSDWTAGKPVSLLAPLIPPRSAG GLMMGHEGMIYAPMCMIPMGGRANMPDPHCMMPPMGGPP	l	1	ł	
PIEMHSHDPLRYVGDMLAWLHQATASEKEHLEALLKHVTTQGVB ENTOGVVGHITEGVCRPIKVRI IRQVIVABEGAVLLYKISHLLKF YHHTISGIVGNSATALLTIERMHLIJSKKIFFNSISLIASKKMD KVELPPPDLGPSSALNQTLMLLTERMHLIJSKKIFFNSISLIASKKMD KVELPPPDLGPSSALNQTLMLREVLASHDSSVVPLDARQADFV QVILSCVILDPLLQMCIVSASNIGTADMATFMYNSISYMMITTLALF EFTDRRLBMLQFQIRAHLDILINBQASYVITRVGLSYIYNTVQQ HKPEQCSLAMMPNLDSVTLKAAMVQPDRYLSAPDNILLTPQLMFL LSATVKEQIVKQSTKLVCRAYGEVYAAVMPINEYKDPENILHR SPQQVQTLLS  6330  1151  333 FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSRGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KPYERGDFPIALRHDSKGMKIAWKVBIBKLDYHHYLPIFFDGLC EMTFPYEFFARQGIHDMLEHGGNKLLPVLPQLIIPIKNALNLKN NSGDGIDYSQQKRENIGDLIQETLEAFERYGGBNAPINIKYVVP TYBSCILN NSGDGIDYSQQKRENIGDLIQETLEAFERYGGBNAPINIKYVVP TYBSCILN NSGDGIVSQQKRENIGDLIQETLAFERYGGBNAPINIKYVVP TYBSCILN NSGDGIVSQQKRENIGDLIQETLAFERYGGBNAPINIKYVVP TYBSCILN NSGDGIVSQQKRENIGDLIQETLAFERYGGBNAPINIKYVVP TYBSCILN NSGDGIVSQQKRENIGDLIQETLAFERYGGBNAPINIKYVVP TYBSCILN NSGDGIVSQQKRENIGDLIQETLAFERYGGBNAPINIKYVVP TYBSCILN NSGDGIVSQQKRENIGDLIQETLAFERYGGBNAPINIKYVVP TYBSCILN NSGDGIVSQQKRENIGDLIQETLAFERYGGBNAPINIKYVVP TYBSCILN NSGDGIVSQQKRENIGDLIQETLAFERYGGBNAPINIKYVVP TYBSCILN NSGDGIVSQQKRENIGDLIQETLAFERYGGBNAPINIKYVVP TYBSCILN NSGDGIVSQQKRENIGDLIQETLAFERYGGBNAPINIKYVVP TYBSCILN NSGDGIVSQQKRENIGDLIQETLAFERYGGBNAPINIKYVVP TYBSCILN NSGDGIVSQQKRENIGDLIQETLAFERYGGBNAPINIKYVVP TYBSCILN NSGDGIVSQQKRENIGDLIQETLAFERYGGBNAPINIKYVPP RVITCISWPLSELHYLIGTLILLIASIVAASKSYNQSGLVAGA IVGFMATFICMASIMISYKISCUTQSTDAAV  SVITCISWPLSELHYLIGTLILLIASIVAASKSYNQSGLVAGA IVGFMATFICMASIMISYKISCUTQSTDAAV  SVKFAEMANILVIHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKSIKKKEVVLOGSFLKBIKKMPS SVKFAEMANILVIHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKSIKKVEVVLOGSFLKBIKKMPS SVKFAEMANILVIHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY UCGVALCFHANAPMCHTAMCMTATATATATATATATATATATATATATATATATAT	i -			
ENIQBVVGHITEGVCRPLKVITEGVTVAERCAVLLYKISHLIKF YHHTISGIVGNSATALLTTIERMHLLSKKIFPNSLSLHASKLMD KVBLPPPDLGESSALNQTIMLLRBVLASHDSSVVFLDARQADFV QVLSCVLDPLLQMCTVSASNLGTADMATFMVNSLYMMKTTLALF EFTDRRIEMLQFQTEAHLDTLINBQASYVLTRVGLSYTYNTVQL HKPPQGSLANMPNLDSVTLKAMVQFDRYLSAPDNLLTPQLNFL LSATVREQIVKQSTELVCRAYGCVYAAVNNPINETKYDENILHR SPQQVQTLLS  6330  1151  333 FFYYTFYENKTFSRKMVAKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALBHDSKGNKIAWKVEIBKLDYHHYLPLFFPDGLC EMTFPYEFFARQGIHDMLSHGGNKILPVLPQLITPIKNALNLEN RQVICVTLKVLQHLUVSABMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCILN  6331  3 495 QGGQVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLMTNYSATSYFEVVTICDLIMILAFYLVHILFRFY RVLTCISWPLSELHYLIGTLLLLIASIVAASKSYNQSGLVAGA IPGGMATFLCMASIMLSYKISCUTQSTDAAV  6332 1 878 VTESKPDLVSTPILLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLPQILGDNGKSIRKMCEVVLOEFLKBIKKNPS SVKPAEMANILVHCQTTDDLIQLTAMCMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKKVANVCNGSIMKLVTPEDDELD ELRPGQRQAEPTPDDALPKGGTASGEWTPSLHITSCRGPREPD VIGWALGPHLSNQDYFMYVTHTIVAATQRSGSSSSSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSH  6333 3 1467 TRTPSEAEAGGGESPQSCVSAAHSDWTAGKFVSLLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRSSLSPTMRPGTGAERG GLMMGHEGMHVAPMGMLPMGQRANMPPVPRIGMTQMMPPMGGPP	1	ł	l .	
YHHTISGIVGNSATALLTTIERMHLLSKKIFFNSLSLHASKUMD KVELPPPDLGESSALNQTIMLREVLASHDSVVPLDARQADFV QVLSCVLDPLLQMCTVSASNLGTAMATFMVNSLDARQADFV QVLSCVLDPLLQMCTVSASNLGTAMATFMVNSLYMKTTLALF BFTDRREMLQFQIEAHLDTLINEQASYVLTRVGLSYIYNTVQQ HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLMFL LSATVKEQIVKQSTELVCRAYGEVYAAVMPINEYKDPENILHR SPQQVOTLLS  6330 1151 333 FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQFL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFP JALBHDSKGNKILDVLFPQLIIPJKNALNLEN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGGGIDYSQQKRENIGDLIQETLEAFERYGGENAPINIKYVVP TYESCLIN 6331 3 495 QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLNTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLICISMPLSELLHYLIGTLILLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCVTQSTDAAV 1 B878 VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVEDI NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMRREFIQLAGRVMLPY SSGLITAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQAPPTPDDLPKQEGTASGEWTPSLHITTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVETGIGLPRQAVSSSH 6333 3 1467 TRTPSEAEAGGESPQSCVSAAHSDMTAGKFVSLLAPLIPPRSAG GLMMGHPGMHYAPMGHPMGQRANMPPVPHGMPQMMPPMGGPP	Į.	1		
KVELPPPDLGPSSALNQTLMLREVLASHDSSVVPLDARQADFV QVISCVILDPILQMCTVSASNIGTADMATFMYNSLYMMKTTLALF EFTDRRLEMLQFQIEAHALDTLINBQASYVLTRVGLSYIYNTVQQ HRPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNILLPQLMFL LSATVKEQIVKQSTELVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTTLLS  6330  1151  333  FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQFL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKRRPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEPFARQGIHDMLEHGGNKILPVLPQLII IPTKNALMLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMVV NSGDGIDYSQQKRRNIGDLIQETLEAFERYGGENAFINIKYVVP TYESCILN  6331  3  495  QQGRVRTTGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSASYSFEVVTICDLINILAFTLVHLERFY RVLTCISWPLSELLHYLIGTLLLLISIVAASKSYNQSGLVAGA 1FOFMATFLCMASIWLSYKISCUTQSTDAAV  1FOFMATFLCMASIWLSYKISCUTQSTDAAV  SVKFAEMANILVHCQTTDDLIQLITAMCMMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTYEDDELD BLAPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPFFCRQDTG KLSTMATHSQLVXTGTGLEPRQAVSSSH  6333  3  1467  TRYPSEAEAGGESPQSCVSAAHSDWTAGKPVSILAPLIPPRSAG GLMMGHPGMHYARMGMIPMGQRANMPPVPHGMMPQMMPPMGGPP	1	ł .	i	
QVISCVLDPLLQMCTVSASNLGTADMATFMVNSLYMMKTTLALF BFTDRRIBMLQFQIRAHLIDTLINBQASYVLTRVGLSY1YNTVQQ HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTILLS  6330 1151 333 FFYYTFYRNKTFSRKMVARKETLSINKCPDRMPKRTKLLAQQFL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAGAFKERPTKPTAFR KYYERGDFPIALRHDSKGNKIAWKVBIRKLDYHHYUPLFFPGLC EMTFPYEPFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHIJVVSAEMVGKALVPYYRQILPVLNIFKNINV NSGDGIDYSQQKRENIGDLIQETLBAFERYGGBNAFINIKYVVP TYSSCILM  6331 3 495 QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLMYNYSAYSYFEVUTICDLIMILAFYIVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCUTQSTDAAV  6332 1 878 VTESNKFDLVSFIPLLEERIYSNNQVARQFIISWILVLESVPDI NLLDYLPBILDGLFQILGDNGKBIRKMCEVVLGEFLKBIKKNPS SVKFAEMANILVHCQTTDDLQLITAMCMMRBFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLAPPGQRQAPFPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVXTGTGLEPRQAVSSSH  6333 3 1467 TRYPSEABAGGESPQSCVSAAHSDWTAGKFVSILLAPLIPPRSAG GPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGABRG GLMMGHPGMHYARMGMIPMGCSGSGRRRSSLSPTMRPGTGABRG GLMMGHPGMHYARMGMIPMGCSANMPPVPHGMMPDMMPPMGGPP	1	1	I .	YHHTISGIVGNSATALLTTIERMHLLSKKIFFNSLSLHASKLMD
6330 1151 333 FFYTPYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQOPL  ENTERGEN PLANTEN CHANGE OF THE REPORT OF	1		ļ	KVELPPPDLGPSSALNQTLMLLREVLASHDSSVVPLDARQADFV
HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENIIHR SPQQVQTTLS  333 FFYYTFYENKTFSRKMVAEKETLSINKCPDKMPKRTKLLAQQPL PVHQPHSLVSBGFTVKAMMKNSVVKGPPAAGAFKERPTKPTAFR KYTERGDFPIALBHDSKGNKIAWKVBIBKLDYHHYLPLFFDGLC EMTFPYBFPARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLUVSAEMVGKALVPYYRQILPVLNIFKMMVV NSGDGIDYSQQKRENIGDLIQBTLEAFERYGGENAPINIKYVVP TYESCLIN  6331 3 495 QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFFFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCVTQSTDAAV  6332 1 878 VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPBILDGLFQILGDNGKEIRKMCEVVLGEFLKBIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMMRBFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQABPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGYALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKETGTGLBPRQAVSSH  6333 3 1467 TRTPSEARAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG GUMMGHPGMHYAPMCMCSGSGRRSSLSPTMRPGTGABRG	(			QVLSCVLDPLLQMCTVSASNLGTADMATFMVNSLYMMKTTLALF
LSATVKEQIVKQSTELVCRAYGEVYAAVMNPINEYKDPENIIHR SPQQVOTILS  6330 1151 333 FFYYTFYENKTFSRKWVARKETLSLNKCPDKMPKRTKLLAQOPL PVHQPHSLVSBGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALBHDSKGNKTAWKVEIKKLDYHHYLPLFFDGLC EMTFPYEFPARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLEN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGBNAFINIKYVVP TYESCLIN  6331 3 495 QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCUTQSTDAAV  6332 1 878 VTESNKFDLVSFIPLLRERIYSNDQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKBIRKMCEVVLGEFLKBIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTTTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH QPLTFSPSGRQPLRSDLVGMCSGSGRRSSLSFTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	l	i	Ì	BFTDRRLEMLQFQIRAHLDTLINEQASYVLTRVGLSYIYNTVQQ
LSATVKEQIVKQSTELVCRAYGEVYAAVMNPINEYKDPENIIHR SPQQVOTILS  6330 1151 333 FFYYTFYENKTFSRKWVARKETLSLNKCPDKMPKRTKLLAQOPL PVHQPHSLVSBGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALBHDSKGNKTAWKVEIKKLDYHHYLPLFFDGLC EMTFPYEFPARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLEN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGBNAFINIKYVVP TYESCLIN  6331 3 495 QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCUTQSTDAAV  6332 1 878 VTESNKFDLVSFIPLLRERIYSNDQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKBIRKMCEVVLGEFLKBIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTTTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH QPLTFSPSGRQPLRSDLVGMCSGSGRRSSLSFTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	1		1	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL
SPQQVQTILS  SPQQVQTILS  SPQQVQTILS  SPQQVQTILS  SPYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSRGFTVKAMKKNSVVRGPPAAGAFKERPTKPTAFR KPYERGDFPIALBIDSKGNKIAWKVEIBKLDYHHYLPLFFDGLC EMTTPYEFFARQIHDMLEHGGNKILPVLPQLIIPIKNALMLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCILM  495 QQGQVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFFRY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCVTQSTDAAV  6332 1 878 VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLBILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTTGTGLEPRQAVSSSH GPLTFSPSGRGSPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRSSLSFTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP		1	1	
6330 1151 333 FFYYFYENKTFSRKWAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSBGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALBHDSKGNKTAWKVEIKKLDYHHYLPLFFDGLC EMTFPYEFPARQGIHDMLEHGGNKILPVLPQLITPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLIN 6331 3 495 QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCVTQSTDAAV  VTESNKFDLVSPIPLLRERIYSNNQYARQPIISWILVLESVPDI NLLDYLPEILDGLPQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQARPTPDDALPKQEGTASGEWTPSLHHTSCRGPREPD VIGVALGPHLSNQDYPMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH 6333 3 1467 TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP			ì	1 7 7
PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KPYERGDFPIALBHDSKGNKIAWKVEIEKILDYHHYLPIFFDGLC EMTTPYEFFARQGIHDMLEHGSNKILEVLPQLIIPIKNALNIRN RQVICVTLKVLQHLUVSAEMUGKALVPYYRQILPULNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCILM  6331 3 495 QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLILLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCVTQSTDAAV  6332 1 878 VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLOEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGYALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH  6333 3 1467 TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG GPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSFTMRPGTGABRG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	(774	1151	322	
KPYERGDFPIALBHDSKGNKTAWKVEIEKLDYHPYLPFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLITPIKNALNIRN RQVICVTLKVLQHLVVSAEMYGKALVPYYRQILPVLNIFKNMNV NSGDGLDYSQQKRENIGDLIQETLEAFERYGGENAPINIKYVVP TYESCLIN  6331 3 495 QQGGRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLILLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCVTQSTDAAV  6332 1 878 VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGBFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSIMKLVTPEDDELD BLRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGYALGPHLSNQDYFMYVTTTIVAATQRSGSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH QPLTFSPSGRGPLRSDLVGMCSGSGRRSSLSFTMRPGTGABRG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	6330	1 1121	333	
EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNIRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQIIPVINIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCILN 6331 3 495 QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCUTQSTDAAV 6332 1 878 VTESNKFDLVSFIPLLRERIYSNQYARQFIISWILVLESVPDI NLLDYLPEILDGLPQILGDNGKBIRKMCEVVLGEFLKBIKKNPS SVKRAEMANILVIHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGYALGPHLSNQDYFMYVTTTIVAATQRSGSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH QPLTFSPSGRGPLRSDLVGMCSGSGRRSSLSFTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVHGMMPQMMPPMGGPP	1	ŀ	]	
RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGGGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLIAN  3 495 QQGVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLMTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVITCISWPLSELLHYLIGTLLLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCUTQSTDAAV  6332 1 878 VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPBILDGLPQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTTGTGLERRQAVSSSH QPLTFSPSGRQPLRSDLVGMCSGSGRRSSLSFTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	Į.	1		
NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAPINIKYVVP TYESCLIN  3 495 QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLILLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCUTQSTDAAV  6332 1 878 VTESNKPDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPBILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLAPGQRQARPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH  6333 3 1467 TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG GPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	1	1	į	
TYESCLIN  495 QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LLAPICVRSSLWTNYSAYSYFSVUTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCVTQSTDAAV  6332 1 878 VTESNKPDLVSPIPLLRERIYSNNQYARQPISWILVLESVPDI NLLDYLPEILDGLPQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKPAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQARPTPDDALPKQEGTASGEWTPSLHHTSCRGPREPD VIGVALGPHLSNQDYPMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH  6333 3 1467 TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG GPLTFSPSGRQPLRSLLVGMCSGSGRRSSLSFTMRPGTGABRG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	1			
6331 3 495 QQQQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LLAFICVRSSLWTNYSAYSYFRVOTICDLIMILAFYLVHLPRFY RVLTCISWPLSELLHYLIGTLILLIASTVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCVTQSTDAAV  6332 1 878 VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQTLGDNGKEIRKMCEVVLOEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGYALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH 6333 3 1467 TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRSSLSFTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	1	1	ì	
LIAPICVRSSLWTNYSAYSYFEVUTICDLIMILAFYLVHLFRFY RVITCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIMLSYKISCUTQSTDAAV  6332 1 878 .VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGBFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLITAMCMMRBFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSIMKLVTPEDDELD BLRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGYALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH CHAGT TRTPSEAEAGGBSPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRSSLSFTMRPGTGABRG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP		I	1	
LIAPICVRSSLWTNYSAYSYFEVUTICDLIMILAFYLVHLFRFY RVITCISWPLSELLHYLIGTLILLIASTVAASKSYNQSGLVAGA IPGFMATFLCMASIMLSYKISCUTQSTDAAV  6332  1 878 VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLOBFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLITAMCMMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGYALGPHLSNQDYFMYVTHTIVAATQRSGSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH CHMGHPGMHYAPMGRANMPPVPHGMMPQMMPPMGGPP	6331	3	495	
RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCUTQSTDAAV  6332  1 878 VTESNKPDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLPQILGDNGKBIRKMCEVVLGEFLKBIKKNPS SVKRAEMANILVIHCQTTDDLIQLTAMCMMRBFIQLAGRYMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH CHACT TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSFTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP		Ī	ł	LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY
1 878 VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSIMKLVTPEDDELD BLRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH 6333 3 1467 TRTPSEÄBAGGESPQSCVSAAHSDWTACKPVSLLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP			1 .	
6332 1 878 VTESNKPDLVSFIPLLRERIYSNNQYARQPIISWILVLESVPDI NLLDYLPBILDGLPQILGDNGKBIRKMCBVVLGBFLKBIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMMRBFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKBVANVCNQSLMKLVTPEDDELD BLRPGQRQABPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLBPRQAVSSSH 6333 3 1467 TRTPSEÄBAGGBSPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGABRG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP		}		VVV
NLLDYLPBILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLAPGQRQARPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH  6333 3 1467 TRTPSEARAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	6335	<del> </del>	070	
SVKPAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQARPTPDDALPKQEGTASGEWTPSLHITSCRGPREPD VIGVALGPHLSNQDYPMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH  6333 3 1467 TRTPSEABAGGBSPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSFTMRPGTGABRG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	6.532	1 1	8/8	
SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH 6333 3 1467 TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSFTMRPGTGABRG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	1		i	
BLRPGQRQARPTPDDALPKQEGTASGEWTPSLHLITSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH 6333 3 1467 TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	1	I		
VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH  6333 3 1467 TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	1	1		
KLSTMATHSQLVKTGTGLEPRQAVSSSH  6333 3 1467 TRTPSEABAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	1	1	1	
6333 3 1467 TRTPSEARAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	J	1		VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG
6333 3 1467 TRTPSEARAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	1	1	Į.	KLSTMATHSQLVKTGTGLEPRQAVSSSH
QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	6222	1 7	1467	
GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP	0333	}	1 40'	
	1	1		
MGQMPGMMSSVMPOMMMSHMSQMSMQVALEEGVMSMDVARALIAS	1	I	İ	
	L	<u> </u>	<u> </u>	MPANARAMAP ANARAMMANTAPANARAMARANA AND AND AND AND AND AND AND AND AND

CPA	Predicted	Drodi atad and	I mine and govern
SEQ	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
]	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	_	\-possible nucleotide insertion)
			GAKSMWTEHKSPDGRTYYYNTETKQSTWEKPDDLKTPAEQLLSK
		ļ	CPWKEYKSDSGKPYYYNSQTKBSRWAKPKELEDLEGYQNTIVAG
			SLITKSNLHAMIKAEBSSKOEECTTTSTAPVPTTBIPTTMSTMA
ļ	ŀ	:	AABAAAAVVAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
1			EVTSIVATVVDNENTVTISTEEQAQLTSTPAIQDQSVEVSSNTG
		ĺ	RETSKQETVADFTPKKEERESQPAKKTYTWNTKEEAKQAFKELL
,		ĺ	KEKRVPSNASWEQAMKMI INDPRYSALAKLSEKKQAPNAYKVQT
6334	17		EKK
6334	. 17	644	GGNPSGRAAGPAAAMPSSPLRVAVVCSSNQNRSMEAHN1LSKR
		1	GPSVRSFGIGTHVKLPGPAPDKPNVVDFKTTYDQMYNDLLRKDK KLYTQNGILHMLDRNKRIKPRPKRFQNCKDLFDLILTCKBRVYD
	1		CAARDINZERGELCÖBAHAANADIÖDNHEBYTIGYLIGEFCOC
			IQHTEDMENBIDELLQBFEEKSGRTFLHTVCFY
6335	82	529	AARARPOVLCCRELGAALGDQSRVEMSYIPGQPVTAVVQRVBIH
			KLRQGENLILGFSIGGGIDQDPSQNPFSEDKTDKGIYVTRVSEG
			GPARIAGLQIGDKIMQVNGWDMTMVTHDQARKRLTKRSEEVVRL
		<b>[</b>	LVTRQSLQKAVQQSMLS
6336	1003	438	HEPASKGRAEVGNMRLSVAAAISHGRVFRRMGLGPESRIHLLRN
			LLTGLVRHERIEAPWARVDEMRGYAEKLIDYGKLGDTNERAMRM
·			ADFWLTEKDLIPKLFQVLAPRYKDQTGGYTRMLQIPNRSLDRAK
			MAVIEYKONCLPPLPLPRRDSHLTLLNQLLQGLRQDLRQSQEAS
			NHSSHTAQTPGI
6337	76	524	EGIOMLSVQPDTKPKGCAGCNRKIKDRYLLKALDKYWHEDCLKC
			ACCDCRLGEVGSTLYTKANLILCRRDYLRLFGVTGNCAACSKLI
			PAFKMVMRÄKDNVYHLDCFACQLCNQRFCVGDKFFLKNNMILCQ TDYBEGLMKEGYAPOVR
6338	66	1349	APNSESGTQGPLPTPANLFWTRRANPDPTTSMSATDRMGPKAVP
			GLRLALLLLGLGTPKSGVQGQEGLDFPBYDGVDRVINVNAKNY
			KNVFKKYEVLALLYHEPPEDDKASORQPEMEBLILELAAQVLED
			KGVGFGLVDSEKDAAVAKKLGLTEVDSMYVFKGDEVIEYDGEFS
			ADTIVEFILDVLEDPVELIEGERELQAFENIEDEIKLIGYFKSK
			DSEHYKAFEDAABEFHPYIPFFATFDSKGAKKLTLKLNBIDFYE
			AFMEEPVTIPDKPNSEEBIVNFVBEHRRSTLRKLKPESMYETWE
			DDMDGIHIVAFAERADPDGFBFLETLKAVAQDNTENPDLSIIWI
			DPDDFPLLVPYWEKTPDIDLSAPQIGVVNVTDADRLWMEMDDER
6339	245	1077	DLPSARRLEDWLEDVLEGEINTEDDDDDDDD
0337	470	1813	NRCDRGGGGOARQAGOGCRTQGAGPGFGFGFSFFSQGAMKAFH
			TFCVVLLVFGSVSRAKFDDFEDERDIVEYDDNDFAEFEDVMEDS VTESPQRVIITEDDEDETTVELEGODENQEGDFRDADTQEGDTE
			SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLONSWESYY
	ł		LEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNTHRELLESNFTL
	ł		VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCBGMLIQLRFL
			KRQDLLNVLARMMRPVSDQVQIKVTMNDRDMDTYVFAVGTRKAL
			VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM
	ļ		DTKMVHFLTHYADKIRSVHFSDQFSGPKIMQEEGQPLKLPDTKR
			TLLLTFNVPGSGNTYPKDMRALLPLMNMVIYSIDKAKKFRLNRE
			GKQKADKNRARVEENFLKLTHVQRQEAAQSRREEKKRARKERIM
			NEEDPEKQRRLEEAALRREQKKLEKKQMKMKQIKVKAM
6340	2	583	EACAHTLSCPAFARLGRARRRPWMSHRTSSTFRAERSFHSSSS
			SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSBPLAF
	İ		PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA
			BKLAADGTVMNNFAHKCQLPEDVDPTSVTSALREDGSLTIRARR
		-	HPHTEHVQQTPRTEIKI
6341	2	645	KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ
ŀ			PALPKARAVAPKPSSRGRYVVAKIDDLVNWARRSSLWPMTFGLA
			CCAVEMMHMAAPRYDMDRFGVVFRASPRQSDVMIVAGTLTNKMA

	~		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I-Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1	1		PALRKVYDQMPEPRYVVSMGSCANGGGYYHYSYSVVRGCDRIVP
L			VDIYIPGCPPTAEALLYGILQLQRKIKRERRLQIWYRR
6342	2	1191	DPRVRAMLATLARVAALRKTCLFSGRGGGRGLWTGRPQSDMNNI
l .	ł		KPLEGVKILDLTRVLAGPFATMNLGDLGAKVIKVERPGAGDDTR
1	1		TWGPPFVGTESTYYLSVNRNKKSIAVNIKDPKGVKIIKKLAAVC
j			DVFVENYVPGKLSANGLGYEDIDBIAPHIIYCSITGYGQTGPIS
ì	l		QRAGYDAVASAVSGLMHITGPEVACLSHIAANYLIGQKEAKRWG
<b>!</b>			TAHGSIVPYQAFKTKDGYIVVGAGNNQQFATVCKILDLPELIDN
Ì			SKYKTNHLRVHNRKELIKILSERFEEELTSKWLYLFEGSGVPYG
ļ			PINNMKNVFAEPQVLHNGLVMEMEHPTVGKISVPGPAVRYSKFK
			MSEARPFPLLGQHTTHILKEVLRYDDRAIGELLSAGVVDQHETH
6343	2	936	GTAMVSDEDELNLLVIVVDANPIWWGKQALKESQFTLSKCIDAV
	,		MVLGNSHLFMNRSNKLAVIASHIQBSRFLYPGKNGRLGDFFGDP
Į.			GNPPEFNPSGSKDGKYELLTSANEVIVEEIKDLMTKSDIKGQHT
ł			BTLLAGSLAKALCYIHRMNKEVKDNQEMKSRILVIKAAEDSALQ
1	ļ		YMNFMNVIFAAQKQNILIDACVLDSDSGLLQQACDITGGLYLKV
Į.	i		POMPSILQYLLWVFLPDQDQRSQLILPPPVHVDYRAACFCHRNL
i			IBIGYVCSVCLSIFCNFSPICTTCBTAFKISLPPVLKAKKKKLK
6344	2500		VSA
6344	2508	147	TMPTATLGNLRGYGMASPGLAAPSLTPPQLATPNLQQPPPQATR
		·	QSLLGPPPVGVPMNPSQFNLSGRNPQKQARTSSSTTPNRKDSSS
l .			QTMPVEDKSDPPEGSEEAAEPRMDTPEDQDLPPCPEDIAKEKRT
l			PAPEPEPCEASELPAKRLRSSEEPTEKEPPGQLQVKAQPQARMT
	1		VPKQTQTPDLLPEALKAQVLPRFQPRVLQVQAQVQSQTQPRIPS
1	,		TDTQVQPKLQKQAQTQTSPEHLVLQQKQVQPQLQQEAEPQKQVQ
			PQVQPQAHSQGPRQVQLQQEAEPLKQVQPQVQPQAHSQPPRQVQ
ł i			LQLQKQVQTQTYPQVHTQAQPSVQPQEHPPAQVSVQPPRQTHEQ PHTQPQVSLLAPEQTPVVVHVCGLEMPPDAVBAGGGMEKTLPEP
1	,		VGTQVSMERIQNESACGLDVGBCENRAREMPGVWGAGGSLKVTI
1 1			LQSSDSRAFSTVPLTPVPRPSDSVSSTPAATSTPSKQALQFFCY
1			ICKASCSSQQEPQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR
1			DVLETEDEEPPPRRWCNTCQLYYMGDLIQHRRTQDHKIAKOSLR
j l			PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKKLKSLEKEIAGODE
			DHFITVDAVGCFEGDEBEBEDDEDBEBIEVEBBLCKQVRSRDIS
			REEWKGSETYSPNTAYGVDFLVPVMGYICRICHKFYHSNSGAQL
[			SHCKSLGHFENLQKYKAAKNPSPTTRPVSRRCAINARNALTALF
			TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT
6345	2	3483	PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEDLOEKV
			HBLEKONDTLKNRLISAKOOLOTOGYROTPYNNVOSRINTGRRK
			ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE
ł .			IRNLENVIQSQRGQIKELKHLABILKTQLRRKENBIBLSLLQLR
i i			EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLOEK
		[	QRTLKISHDALMANGDRLNMQLKEQRLKCCSLKKQLHSMKFSER
		Ī	RIRELODRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ
		İ	QLKVQIAQLETALKSDLTDKTBILDRLKTERDQNBKLVQENRBL
'		ļ	QLQYLEQKQQLDRLKKRIKLYNQENDINADELSBALLLIKAQKE
] .		ļ	QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQBLEKTRNM
			LIMQHKINKDYQMKVEAVTRKMENLQQDYKLKVEQYVHLLDIRA
			ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG
]			ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV
			VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTBYE
ļĺ	]		TLAACQLKFHEILEKSGRIPCTASLIGTKGDIPNFGTVEYWFRL
		j	RVPMDQAIRLYRERAKALGYITSNFKGPBHMQSLSQQAPKTAQL
			SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA
			DHDTAIIPSSNDPQFDDHMYFPVPMNMDLDRYLKSESLSFYVFD
	1		DSDTQENIYIGKVNVPLISLAHDRCISGIFRLTDHQKHPAGTIH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
į.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
I	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W-Trentonham V Thereing V V to
ı	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	sequence	sequence	Codon, /=possible nucleotide deletion,
<b>}</b>	sequence		\=possible nucleotide insertion)
	ļ		VILKWKPAYLPPSGSITTEDLGNFIRSEEPEVVQRLPPASSVST
1	ĺ		LVLAPRPKPRQRLTPVDKKVSFVDIMPHQSDVSQEGSVDEVKEN
1		į	TEKMOOGKDDVSLLSEGQLAEQSLASSEDETEITEDLEPEVEED
1	1		MSASDSDDCIIPGPISKNIKQPSEKIRIEIIALSINDSOVTMDD
1	<b>i</b>	•	TIQRLFVECRFYSLPARETPVSLPKPKSGQWVYYNYSNVIYVDK
1	}		ENNKAKRDILKAILQKQEMPNRSLRFTVVSDPPEDBQDLECEDI
1	ļ		GVAHVDLADMFQEGRDLIBQNIDVFDARADGEGIGKLRVTVEAL
			HALQSVYKQYRDDLEA
6346	2921	533	QDRRLLRLELQKTCQPTSTMSGSHTPACGPPSALTPSIWPQEIL
1 -2.5			AKYTQKEESAEQPEPYYDEFGPRVYKEEGDEPGSSLLANSPLME
1	ł		DAPORLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSBKLRSLVLA
Ī			GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
1			QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
i			QGTGMVAACLLLFLEBEDAFWMMSAIIEDLLPASYFSTTLLGVQ
			TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
1			DIKLLERINDEFFYEGSRVEFQETEGMEHEKERELIQSENSASI
1			FNTLSDIPSOMEDAELLLGVAMRLAGSLTDVAVETORRKHLAYL
1			IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGKDDLEAL
			KAKNIKQTELVADLREAILRVARHPQCTDPKNCSVVSRQLPGLL
			PNTALTPPTPLVGLYSLWQBLTPDYSMBSHQRDHENYVACSRSH
			RRRAKALLDFRRHDDDRLGFRKNDIITIVSQKDEHCWVGELNGL
]			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
1			ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDPASVYSRLVL
1 -			CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL
			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC
			ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW
			DVDG
6347	2921	533	<u>,</u>
1 3317		555	QDRRLLRLBLQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
			AKYTOKEBSAEOPEPYYDRFGPRVYKEEGDEPGSSLLANSPLME
			DAPQRIRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
			GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
1 1			QIBKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPBIGYC
{			QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ
			TDQRVLRHLIVQYLPRLDKLLQEHDIBLSLITLHWFLTAFASVV
, !			DIKLLERIWDLPPYEGSRVLFQLTLGMLHLKEEBLIQSENSASI
į į	l		FNTLSDIPSOMEDABILLGVAMRLAGSLTDVAVETQRRKHLAYL
<b>[</b>			IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
j l	ļ		KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL
!	ĺ		PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
} [	•		RRRAKALLDFERHDDDELGFRENDIITIVSQEDEHCWVGELNGL
ļ l			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
j (			ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL
!!			CKTFRLDEDGKVLTPERLLYRAVOSVNVTHDAVHAOMDVKT.R91.
, ,			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC
j l			
[	}		ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW
<del>⊢</del>			DVDG
6348	3	3679	AGAEKCPVTLLACPLAKQQNKYKYEECKDLIKSMLRNRLQFKRR
i l	[		Klaeqlkqaeelrqykvlvhsqereltqlreklregrdasrsin
ľ	1		RHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
, ,	į		DDDEDVQVEVAEKVQKSSSPREMQKABEKEVPEDSLBECAITCS
1	· .		NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
1	i		ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPOLA
l i	Ĭ		EKKQQFRNLKEKCFLTQLACFLANQQNKYKYBECKDLIKFMLRN
	ľ		ERQFKBBKLAEQLKQAEKLRQYKVLVHSQERELTOLREKLREGR
J	1		
	f		DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKBVPEDSLE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, P=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 1 1	\=possible nucleotide insertion)
<u> </u>		<del> </del>	BCAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
	i	[	EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG
ł ·		ĺ	YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
	1		KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
		Į.	CQPYRSAFYVLEQQRVGLAVNMDEIBKYQEVBEDQDPSCPRLSR
		1	ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
		<u> </u>	QYLGLALDVDRIKKDQEBEEDQGPPCPRLSRELLBVVEPEVLQD
		ľ	SLDRCYSTPSSCLEQPDSCQPYGSSFYALBEKHVGFSLDVGEIE
<b>i</b> !	ĺ		KKGKGKKRRGRRSKKKRRRGRKEGEEDONPPCPRLSRBLLDEKG
		ł	PBVLQDSLDRCYSTPSGCLBLTDSCQPYRSAFYILEQORVGLAV
			DMDEIEKYQEVEBDQDPSCPRLSGELLDEKRPEVLQESLDRCYS
[	ļ		TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE
			DQDPSCPRLSRELLDBKEPEVLQDSLGRCYSTPSGYLBLPDLGO
i i			PYSSAVYSLEEQYLGLALDVDRIKKDQEBEKDQGPPCPRLSREL
!			LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSPYALEEKH
1 1			VGFSLDVGBIBKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP
			RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFOHYRSVFY
]			SFEERHISPALYVDNRFFTLTVTSLHLVFQMGVIFPQ
6349	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELOFKEB
			KLAEQLKQABELRQYKVLVHSQERELTQLRBKLREGRDASRSLN
1 1			RIILQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
i		•	DDDEDVQVEVABKVQKSSSPREMQKAEEKEVPEDSLKECAITCS
}			NSHGPCDSNQPHKNIKITFREDEVNSTLVVDRESSHDECQDALN
1 1			ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
1. 1			KKKOOFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN
		:	ERQFKEEKLAEQLKQAEKLRQYKVLVHSQERELTQLREKLREGR
1 [			DASRSLNEHLQALLTPDEPDKSQGQDLQEQLABGCRLAQHLVQK
( )			LSPENDNDDDBDVQVEVAEKVQKSSAPREMPKAEEKEVPBDSLE
i I			ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
1 1			EDAVHIIPENESDDEEEEBKGPVSPRNLQESEEBEVPQESWDEG
i 1	,		YSTLSIPPEMLASYKSYSSTFHSLERQQVCMAVDIGRHRWDQVK
1			KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
			COPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
			ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
		İ	QYLGLALDVDRIKKDQBBBBDQGPPCPRLSRELLEVVEPBVLQD
	İ		SLDRCYSTPSSCLEQPDSCQPYGSSFYALREKHVGFSLDVGEIE
			KKGKGKKRRGRRSKKERRRGRKEGEEDONPPCPRLSRELLDEKG
			PEVLQDSLDRCYSTPSGCLBLTDSCQPYRSAFYILEQQRVGLAV
ļ <sup>.</sup>			DMDBIRKYQBVERDQDPSCPRLSGBLLDBKBPEVLQBSLDRCYS
	İ		TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVER
			DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
]		i	PYSSAVYSLEEQYLGLALDVDRIKKDQEBEEDQGPPCPRLSREL
Ì			LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH
	ł		VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP
			RLNSMLMEVERPEVLQDSLDICYSTPSMYFELPDSPQHYRSVFY
6350		2670	SFEERHISPALYVDNRFFTLTVTSLHLVFQMGVIFPQ
6330	3	3679	AGAEKCFVTLLACFLAKQONKYKYEECKDLIKSMLRNBLQFKRB
			KLAEQLKQAEELRQYKVLVHSQRRELTQLREKLREGRDASRSLN
			EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
			DDDEDVQVRVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
			NSHGPCDSNQPHKNIKITFBEDEVNSTLVVDRESSHDECQDALN
}			ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
			EKKQQFRNLKEKCFLTQLACFLANQQNKYKYBBCKDLIKFMLRN
	ł	ļ	BRQFKEEKLABQLKQABELRQYKVLVHSQERBLTQLREKLREGR
1	,	İ	DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE

CPO	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
MO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
	sequence		RCAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
	<b>}</b>	}	EDAVHIIPENESDDEEEBBKGPVSPRNLQESEBBEVPQESWDBG
	1		_
			YSTI.SIPPEMLASYKSYSSTFHSLBEQQVCMAVDIGRHRWDQVK
			KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
		1	CQPYRSAPYVLBQQRVGLAVNMDEIEKYQEVEBDQDPSCPRLSR
	{	l .	ELLDRKEPEVIQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
	{		QYLGIALDVDRIKKDQBEBBDQGPPCPRLSRELLEVVEPEVLQD
	1		SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGRIE
	}	l	KKGKGKKRRGRSKKERRRGRKEGEEDONPPCPRLSRELLDEKG
		l	PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV
			DMDETEKYQEVERDQDPSCPRLSGRLLDEKEPEVLQESLDRCYS
'	1	ì	TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVBE
	!	1	DODPSCPRISRELLDEKEPEVLODSLGRCYSTPSGYLELPDLGQ
		1	PYSSAVYSLBEQYLGLALDVDRIKKDQBEEEDQGPPCPRLSREL LEVVEPBVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEBKH
		ł	VGPSLDVGETEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP
			RINSMIMEVERPEVLODSIDICYSTPSMYFELPDSFOHYRSVFY
	Ì		
			SFEREHISFALYVDNRFFTLTVTSLHLVFQMGVIFFQ REARRTTERSOLGRMLVVEVANGRSLVWGARAVQALRERLGVGG
6351	1291	319	REARRIERSQUARMIVVEVANGRSDVWGARAVQALRERIGVGG
			DSRHHSLALTSPKROOEESFOEOSALAABARETRROELLEKITE
		1	
			GQAAKKOKLEQASGASSSQEAGSSQAAKEDETSDGQASGEQKEA GPSSSQAGPSNGVAPLPRSALLVQLATARPRPVKARPLDWRVQS
	ļ	ļ	KDWPHAGRPAHELRYSIYRDLWERGFFLSAAGKFGGDFLVYPGD
	_		PLRFHAHYIAQCWAPBUTIPLQDLVAAGRLGTSVRKTLLLCSPQ
	·	ļ	PDGKVVYTSLQWASLQ
6352	226	923	WSEWLSPCHAAKCKGLSMLRITMKTRAISLAADATEFVQGRSAP
6352	235	323	AMARSLVHDTVFYCLSVYQVKISPTPQLGAASSABGHVGQGAPG
'   .	l .	į	LMCMMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPPEE
	<b>[</b>		PAQAAMEGPOPKNMOPRTRRTKFTLLQVEBLESVFRHTQYPDVP
		[	TRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLANELRADP
			DDCVYIVVD
6353	65	672	RFAGAGATPEARARPPDVQAAEERKEMDLPDSASRVFCGRILSM
4000	) "	} ""	VNTDDVNAI ILAQKNMLDRFEKTNEMLLNFNNLSSARIQQMSER
			FI-HHTRTLVEMKRDLDSIFRRIRTLKGKLARQHPRAPSHIPEAS
	1	}	PLEBEDEDPIPPSTTTTIATSEQSTGSCDTSPDTVSPSLSPGFE
		j	DLSHVQPGSPAINGRSQTDDEEMTGE
6354	965	510	PSLRPMEPTRDCPLFGGAFSAILPMGAIDVSDLRPVPDNQEVFC
0354	200	}	HPVTDQSLIVELLELQAHVRGEAAARYHFEDVGGVQGARAVHVE
			SVQPLSLENLALRGRCQEAWVLSGKQQIAKENQQVAKDVTLHQA
	1	1	LLRLPQYQTDLLLTFNQPP
6355	158	1662	RGSSAAFRGSGLRGAMIRRVLPHGMGRGLLTRRPGTRRGGFSLD
0200	128	1007	WDGKVSBIKKKIKSILPGRSCDLLQDTSHLPPBHSDVVIVGGGV
			IGLSVAYNLKKLESRRGAIRVLVVERDHTYSQASTGLSVGGICQ   OFSLPENIQLSLFSASFLRNINEYLAVVDAPPLDLRFNPSGYLL
			LASEKDAAAMESNVKVQRQEGAKVSLMSPDQLRNKFPWINTEGV
		Ī	ALASYGMEDEGNFDPWCLLOGLRRKVQSLGVLPCQGEVTRFVSS
		1	
			SQRMLTTDDKAVVLKRTHEVHVKMDRSLEYQPVECAIVINAAGA
	ļ		WSAQIAALAGVGEGPPGTLQGTKLPVEPRKRYVYVWHCPQGPGL
			ETPLVADTSGAYFRREGLGSNYLGGRSPTEQEEPDPANLEVDHD
	į		PFQDKVWPHLALRVPAFETLKVQSAWAGYYDYNTFDQNGVVGPH
			PLVVNMYFATGFSGHGLQQAPGIGRAVARMVLKGRFQTIDLSPF
		i	LPTRFYLGRKIQENNII
6356	354	633	TGLTSSCLPLQVMMTKRTKDMGKFSSVTVSTIDEBEBEIEAREV
6356	354	633	

		At the part of the con-	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide ·	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
Į.	sequence		\=possible nucleotide insertion)
6357	2	915	GLLRNMALLVRVLRNOTSISOWVPVCSRLIPVSPTOGOGDRALS
000.		1 3.50	RTSQWPQMSQSQACGGSEQIPGIDIQLNRKYHTTRKLSTTKDSP
i			QPVBBKVGAFTKIIKAMGFTGPLKYSKNKIKIAALRMYTSCVEK
1		Į	TDFBEFFLRCOMPDTFNSWFLITLHVWNCLVRMKQBGRSGKYM
1		į.	CRIIVHFMWRDVOORGRVMGVNPYILKKNMILMTNHFYAAILGY
į.	}	}	DEGILSDDHGLAAALWRTPFNRKCEDPRHLELLVEYVRKQIQYL
1	}		
	2000		DSMNGEDLLLTGEVSWRPLVEKNPQSILKPHSPTYNDEGL
6358	2009	1040	ASDALHSLSAPVLRLSSRSAARPATMTEQAISFAKDFLAGGIAA
i	1		AISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPK
		1	EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKHT
			QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKSGTB
			REFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRAAYFGVY
I	· .	1	DTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPPDTVRRRMM
I	ļ	ļ	MQSGRKGADIMYTGTVDCWRKIPRDEGGKAFFKGAWSNVLRGMG
<u></u>			GAFVLVLYDELKKVI
6359	98	1086	VCRQEBEKMKEDCLPSSHVPISDSKSIQKSELLGLLKTYNCYHE
1	ļ		GKSFQLRHREEEGTLIIEGLLNIAWGLRRPIRLQMQDDREQVHL
	•		PSTSWMPRRPSCPLKEPSPQNGNITAQGPSIQPVHKARSSTDSS
1	•		GPLEBAERAPQLMRTKSDASCMSQRRPKCRAPGBAQRIRRHRFS
1			INGHPYNHKTSVFTPAYGSVTNVRVNSTMTTLQVLTLLLNKPRV
i			EDGPSEFALYIVHESGERTKLKDCBYPLISRILHGPCBKIARIF
		* *	LMEADLGVEVPHEVAQYIKFEMPVLDSFVEKLKEEBEREIIKLT
6360			MKPQALRITMLQRLEQLVEAK
6360	1	345	GTRGAVPSTLERVVLPPRSCRVFWIHSGTTMSKVSFKITLTSDP
			RLPYKVLSVPESTPFTAVLKFAAREFKVPAATSAIITNDGIGIN
6361	615	158	PAQTAGNVFLKHGSELRI I PRDRVGSC
6361	913	128	RPGLGQLQHCALAPQAGNRRCRFHGRLHALTRSTHRGKPMSIMQ FKDTLNTPLPDSSPVAVPLGAPIAVASTLSVEHNDGVETGIWAC
			APGRWRRQITSQBFCHFIQGRCTFTPDDGETLHIQAGDALMLPA
1			NSTGIWDIOBTVRKTYVLIL
6362	350	1576	TTMDGSHSAALKLOOLPPTSSSSAVSEASFSYKENLIGALLAIF
6362	220	12/0	GHLVVSIALNLQKYCHIRLAGSKDPRAYFKTKTWWLGLFLMLLG
l I			BLGVFASYAFAPLSLIVPLSAVSVIASATIGIIFIKEKWKPKDF
		•	LRRYVLSFVGCGLAVVCTYLLVTFAPNSHEKMTGENVTRHLVSW
			PFLLYMLVRIILPCLLLYFYXBKNANNIVVILLLVALLGSMTVV
			TVKAVAGMLVLSIQGNIQLDYPIFYVMFVCMVATAVYQAAPLSQ
			ASOMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF
			ALGCLIAFIGVFLITRNRKKPIPFEPYISMDAMPGMQNMHDKGM
	,		TVQPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG
6363	n <sub>H</sub>	1000	VPYRVLEHTKKE
0363	21	1201	RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGPAG
			DQIPKYCFPNYVGRPKHVRVMAGALEGDIPTGPKAEEHRGLLSI
]			RYPMEHGIVKOWNOMERIWQYVYSKDQLQTFSEKHPVLLTRAPL
1			NPRKNRERAABVFFETFNVPALFISMQAVLSLYATGRTTGVVLD
]			SGDGVTHAVPIYEGPAMPHSIMRIDIAGRDVSRFLRLYLRKEGY
			DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS
			TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR
			RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE
			RLYSTWIGGSILASLDTPKKMWVSKKEYEEDGARSIHRKTF
6364	21	1201	RRTRIGSSPPRRRDSSAMBSYDVIANQPVVIDNGSGVIKAGFAG
[			DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEKHRGLLSI
1			RYPMEHGIVKDWINDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL
[			NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD
			SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY
			DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS
1			TIBIGPSRPRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR
L			

SEQ	Predicted	Predicted end	Daning and assessed assessed as a second
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Clutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	sequence	\=possible nucleotide insertion)
<b>—</b>	bequence		RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE
			RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF
6365	234	1000	
6365	434	1989	KHKSRASCAARAQAFGPSREREVHSRFRSGLRRLGESNSGCCTM
i			ASMGTLAFDEYGRPFLIIKDQDRKSRLMGLEALKSHIMAAKAVA
			NTMRTSLGPNGLDKMMVDKDGDVTVTNDGATILSMMDVDHQIAK
1	,		LMVBLSKSQDDBIGDGTTGVVVLAGALLERAEQLLDRGIHPIRI
1			ADGYEQAARVAIEHLDKISDSVLVDIKDTEPLIQTAKTTLGSKV
			VNSCHROMAEIAVNAVLTVADMERRDVDFELIKVEGKVGGRLED
1			TKLIKGVIVDKDFSHPQMPKKVEDAKIAILTCPFEPPKPKTKHK
1			LDVTSVEDYKALQKYRKEKFEEMIQQIKETGANLAICQWGFDDE
1			ANHLLLONNLPAVRWVGGPEIELIAIATGGRIVPRFSELTAEKL
			GFAGLVQEISFGTTKDKMLVIEQCKNSRAVTIPIRGGNKMIIEE
			AKRSLHDALCVIRNLIRDNRVVYGGGAARISCALAVSQRADKCP
			TLEQYAMRAPADALEVIPMALSENSGMNPIQTMTEVRARQVKEM
		'	NPALGIDCLHKGTNDMKQQHVIETLIGKKQQISLATQMVRMILK IDDIRKPGESEB
6366	200	1898	
6366	257	1838	GNKEGAHSSTFWVLLSIFLGAVAMLCKEQGITVLGLNAVFDILV
i			IGKFNVLEIVQKVLHKDKSLENLGMLRNGGLLFRMTLLTSGGAG
1			MLYVRNRIMGTGPPAFTEVDNPASFADSMLVRAVNYNYYYSLNA
			WLLLCPWWLCFDWSMGCIPLIKSISDWRVIALAALNFCLIGLIC
			OALCSEDGHKRRILTIGLGFLVIPFLPASNLFFRVGFVVAERVL
1			YLPSVGYCVLLTFGFGALSKHTKKKKLIAAVVLGILFINTLRCV
1			LRSGENRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTAAI
			RYYREAVRINPKYVHAMNNIGNILKERNELQEAEELLSLAVQIQ
			PDFAAAWMVLGIVQNSLKRYBAABQSYRTAIKHRRKYPDCYYNL
1			GRLYADLNRHVDALNAWRNATVLKPEHSLAWNNMIILLDNTGNL
			AQAEAVGREALELIPNDHSIMFSLANVLGKSQKYKESEALPLKA
•			IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLLRRKLBLMQKKAV
6367	287	1934	SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTGERWALLDPS
0307	407	1934	QKNLYRDVMQETFKNLTSVGKTWKVQNIEDBYKNPRRNLSLMRE
1 1			KLCESKESHHCGESFNQIADDMLNRKTLPGITPCESSVCGEVGT
1 1			GHSSLNTHIRADIGHKSSRYQEYGENPYRNKECKKAFSYLDSFQ
ì	•		SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF
			CGKAFYFLNLCLIHERIHTGVKPYKCKQCGXAFTRSTTLPVHER
			THTGVNADBCKECGNAFSPPSEIRRHKRSHTGEKPYBCKQCGKV
			PISPSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG
			EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA
1			SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH
			ECKOCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR
			YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC
			GKAFIRASSCREHERTHTINR
636B	1	327	RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFOYDE
""	_	321	l ~ ~ ~
			DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC
6369	1	1745	AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTTHGSPREDTGT
0303	*	1/45	
}			PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQRT
			FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG
			RSFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD
		i	TGHKSSEYQEYGENPYRNKECKKAPSYLDSFQSHDKACTKEKPY
			DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCI.
			IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE
			CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM
			THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA
[			FRCTSDLQRHEKTHTKDKPYGCKQCGKGFRCASQLQIHERTHSG
I			EKPHECKECGKVFKYFSSLRIHERTHTGEKPHECKQCGKAFRYF

1.7	r		- Company (American American Review of Company Company Company Company Company Company Company Company Company - Company Company Company Company Company Company Company Company Company Company Company Company Company Comp	
			and the state of t	terilija sadila ja redsaklik
SEQ ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, K=	
NO:	nucleotide location	location corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,	
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,	l
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,	]
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop	ĺ
	amino acid	sequence	Codon, /=possible nucleotide deletion,	
L	sequence		\=possible nucleotide insertion)	
	1	]	SSLHIHERTHTGDKPYECKVCGKAPTCSSSIRYHERTHTGEKPY	)
	ļ		BCKHCGKAFISNYIRYHERTHTGEKPYQCKQCGKAFIRASSCRE HERTHTINR	
6370	1711	329	FVLSBQRLRTERTWPRSPGLGRGAAAAGARTAGAGLLRLLLGCG	
	1	ĺ	ALVGGLRPVTMTTPANAQNASKTWBLSLYBLHRTPQBAIMDGTB	
			IAVSPRSLHSELMCPICLDMLKNIMITKECLHRFCSDCIVTALR	
1	ł		SGNKBCPTCRKKLVSKRSLRPDPNPDALISKTYPSRBEYRAHQD	
			RVLIRLSRLHNQQALSSSIEEGLRMQAMHRAQRVRRPIPGSDQT	
1	l		TTMSGGEGEPGEGEGDGEDVSSDSAPDSAPGPAPKRPRGGGAGG SSVGTGGGGTGGVGGGAGSEDSGDRGGTLGGGTLGPP8PPGAPS	
1	]	1	PPEPGGEIELVFRPHPLLVEKGEYCOTRYVKTTGNATVDHLSKY	
		Ì	LALRIALERROOORAGEPGGPGGGASDTGGPDGCGGEGGGAGGG	
	1		DGPEEPALPSLEGVSEKQYTIYIAPGGGAFTTLNGSLTLELVNB	İ
			KPWKVSRPLELCYAPTKDPK	İ
6371	3	288	GVANMSTAMNFGTKSPQPRPPDKGSFPLDHLGECKSFKEKFMKC	1
•			LHNNNFENALCRKESKEYLECRMERKLMLQBPLEKLGFGDLTSG KSEAKK	
6372	2141	625	RVSATASEGKABERYKKLEDLLEKSFSLVKMPSLQPVVMCVMKH	ł
			LPKVPEKKLKLVMADKELYRACAVEVRRQINQDNQALFGDEVSP	J
1	1	j	LLKQYILEKESALFSTELSVLHNFFSPSPKTRRQGEVVQRLTRM	
		ł	VGKNVKLYDMVLQFLRTLFLRTRNVHYCTLRABLLMSLHDLDVG	
1		ì	BICTVDPCHKFTWCLDACIRERFVDSKRARBLQGFLDGVKKGQB	
		,	QVLGDLSMILCDPFAINTLALSTVRHLQELVGQETLPRDSPDLL LLLRLLALGQGAWDMIDSQVFKEPKMEVELITRFLPMLMSFLVD	
1 .		1	DALLANGORYMOWIDS OALVESTAND ARTICLE DE LE LE LE LE LE LE LE LE LE LE LE LE LE	
			YVLHITKORNKNALLRLIPGLVETPGDLAFGDIFLHLLTGNLAL	i
		1	LADBPALEDFCSSLFDGFFLTASPRKENVHRHALRLLIHLHPRV	
			APSKLEALQKALEPTGQSGEAVKELYSQLGEKLEQLDHRKPSPA	
	<u> </u>		QAAKTPALELPLPSVPAPAPL	
6373	67	711	PSRAARASPARLPAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK DIKEYVKWMMYWIIFALFTTABTFTDIFLCWFPFYYBLKIAFVA	1.
1	1	1	WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL	ł
			VHPGKRGLNVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD	
1			GAPAPSGPPPPGSGRASGKHGQPKMSRSASESASSSGTA	}
6374	535	2105	HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS	
		1	CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD	
ļ	<b>[</b>		HSCPTHTSCNYTSSTIPLSSTRDHSCPTHTFCNYPRPIIRLSSC	
1	<b>i</b>	1	CPABLQTEGSNGKKEVLSGFQVVLEDTVLPPEGGGQPDDRGTIN DISVLRVTRRGEOADHFTOTPLDPGSQVLVRVDWERRFDHMQOH	{
			SCOHLITAVADHLFKLKTTSNBLGRPRSAIELDTPSMTAEQVAA	
	ļ	1	IBQ9VNBKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR	
1		•	VVNIBGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL	
ļ	<b>{</b>		SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL	
		ł	QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII	
		İ	ANRIGSESTILIFLTVGDBKGGGLFILAGPPASVETIGPRVARVI.	
6375	1	1535	EGKGAGKKGRPQGKATKMSRRMEAQALLQDYISTQSAKE AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT	-
63/3	1	1232	CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK	
			PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAFYLYKLYQHYY	
	ļ		FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY	<b>{</b>
	]		SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFRAWYIHEHVER	
1	1	l	HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP	
1			FVAAIPLLALAGALARNWGENYDRQRAFSRTCAGGLRCLLSDR	l
1		[	RVLLLGTIQALFESVIPIFVFLWTPVLDPHGAPLGIIFSSFMAA	i
1		[	SLIGSSLYRIATSKRYHLOPMHLLSLAVLIVVFSLFMLTFSTSP	1
L	<u> </u>	<u> </u>	GQESPVBSFIAFILIELACGLYFPSMSFLRRKVIPETEQAGVLN	i

SBO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			WFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAV
			VGLFTVVRHDAELRVPSPTKEPYAPRL
6376	380	1437	ISSTDIDHYRFSFLVNSKMPSKESWSGRKTNRAAVHKSKQEGRQ
[	İ	İ	QDLLIAALGMKLGSPKSSVTIWQPLKLFAYSQLTSLVRRATLKE
1	İ		NEQIPKYEKIHNFKVHTFRGPHWCEYCANFMWGLIAQGVKCADC
1			GLNVHKQCSKMVPNDCKPDLKHVKKVYSCDLTTLVKAHTTKRPM
1	!		VVDMCIREIESRGLNSEGLYRVSGFSDLIEDVKMAFDRDGKKAD ISVNMYEDINIITGALKLYFRDLPIPLITYDAYPKPIRSAKIMD
t		·	PDEQLETLHBALKLLPPAHCETLRYLMAHLKRVTLHEKENLMNA
1			ENLGIVFGPTLMRSPELDAMAALNDIRYQRLVVELLIKNEDILF
6377	2311	1.845	SRIRRRSSRRPREPPGPSRRRRRRRPDPRTMPSEKTFKORRTPE
			QRVBDVRLIREQHPTKIPVIIERYKGBKQLPVLDKTKFLVPDHV
			NMSELIKIIRRRLQLNANQAFFLLVNGHSMVSVSTPISEVYESE
		L	KDEDGFLYMVYASQETFGMKLSV
6378	686	191	GAGPWEAFPDGIGRRSRRARLPQYKRPPGRVGGGDSGRRNMAVA
ſ			DLALIPDVDIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYK
			WAEYHADIYDKVSGDMQKQGCDCECLGGGRISHQSQDKKIHVYG
6379	35	378	YSMAYGPAQHAISTEKIKAKYPDYEVTWANDGY
6375	33	370	ERAGSPSPSRAALRRCAPORSQAPRWPDRAACRRSFOGSQGRAY LFNSVVNVGCGPABERVLLTGLHAVADIYCENCKTTLGWKYKHA
			FESSOKYKBGKYIIKLAHMIKDNGWD
6380	1414	462	PAVQQQRGAGPPIGRGSGNMARFALTVVRHGETRFNKEKIIQGQ
			GVDEPLSETGFKQAAAAGIFLNNVKFTHAFSSDLMRTKOTMHGI
ſ	i l		LERSKFCKDMTVKYDSRLRERKYGVVEGKALSELRAMAKAARER
			CPVFTPPGGETLDQVKMRGIDFFEFLCQLILKEADQKEQFSQGS
1			PSNCLETSLAEIFPLGKNHSSKVNSDSGIPGLAASVLVVSHGAY
ı			MRSLPDYFLTDLKCSLPATLSRSELMSVTPNTGMSLFIINPERG
1			REVEPTVQCICMNLQDHLNGLTENSLGLNLPSKSNHFEPLKGVP
6381	1668	218	LALFTSLLC
0301	1000	210	AVVRAQGSRGFSGAGWRPRQAAAMNFSEVFKLSSLLCKFSPDGK YLASCVQYRLVVRDVNTLQILQLYTCLDQIQHIEWSADSLFILC
			AMYKRGLVQVWSLEQPBWHCKIDEGSAGLVASCWSPDGRHILNT
1		_	TBPHLRITVWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER
1			RDCKDYVSIFVCSDWQLLRHFDTDTQDLTGIBWAPNGCVLAVWD
1			TCLEYKILLYSLDGRLLSTYSAYEWSLGIKSVANSPSSQFLAVG
l i			SYDGKVRILNHVTWKMITEFGHPAAINDPKIVVYKRAEKSPOLG
1	1		LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP
1			KIGIGMLAFSPDSYFLATRNDNIPNAVNVWDIQKLRLFAVLEQL
			SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA
6382	2	70/2	VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT
0302	4	1062	PREDEDRILCLIAYPLKGDHGIVDIVDNSDCBPKSKLLRWTTNK
			KIHVLETEKTPKDWVRQHRKREKMKSHKLEEEFEWLKKSEVLYY TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL
]			LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS
}	Ì		AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKRALFQFF
	ļ		HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG
	·		KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM
			IDFAHTTCRLYGEDTVVHRGQDAGYIFGLQSLIDIVTEISEESG
l			В
6383	3159	1061	SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGSKGGHGAASPSEK
			GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP
		ł	AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK
		ļ	PPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGKS
			SSSSASAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS
	· .		GWCVHHYLEEVQQVRRSHQDFSRQREELGQGLQGVEQKVQSLQA
			TFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVLQKLQNBI

		./	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
;	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	· -	\=possible nucleotide insertion)
	204	<u> </u>	LKDLSDGIHVVKDARERDFTSLENTVKERLTELTKSINDNIAIF
	1	1	TEVOKRSOKBINDMKAKVASLEESEGNKODLKALKEAVKEIQTS
			AKSREWDMEALRSTLQTMESDIYTEVRELVSLKQBQQAFKEAAD
	i	[	TERLALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGP
			KEDGGFRHSEAFRALQOKSQGLDSRLQHVEDGVLSMQVASARQT
i	•		ESLESILSKSQEHEQRLAALQGRLEGIGSSEADQDGLASTVRSI.
1			GETOLVLYGDVEBLKRSVGBLPSTVESLQKVQEQVHTLLSQDQA
l			QAARLPPQDFLDRLSSLDNLKASVSQVKADLKMLRTAVDSLVAY
ĺ	Į		SVKTETNENNLESAKGLEDDLENDLDRLFVKVEKIHEKV
6384	738	1904	IWEVPVCLTHLLHLQQANQPLPPPSSSINEEDADEANRAIGEKR
0384	/38	1,703	AAPDSGKKPKTPKTKQQKDPNEPQKPVSAYALFFRDTQAAIKGQ
l		· ·	NPNATFGEVSQIVASMWDSLGEEQKQVYKRKTEAAKKEYLKALA
l .	1		AYRASIJUSKAAAESABAQTIRSVQQTLASTNLTSSLLLMTPLSQ
Į į	Į		HGTVSASPQTLQQSLPRSIAPKPLTMRLPMNQIVTSVTIAANMP
l			SNIGAPLISSMGTTMVGSAPSTQVSPSVQTQQHQMQLQQQQQQQ
1			QQQMQQMQQQQLQQHQMHQQIQQQMQQQHFQHHMQQHLQQQQQH
1	ļ	1	LOGQINQQQLQQQLQQRLQLQQLQHMQHQSQPSPRQHSPVASQI
	i	[	TSPIPAIGSPQPASQOHQSQIQSQTQTQVLSQVSIF
- C30F-	2	1584	PRVRANDVAAGAQAVVSAGMAKSNGENGPRAPAAGRSLSGTRES
6385	4	1364	LAQGPDAATTDELSSLGSDSEANGFAERRIDKFGFIVGSQGAEG
ł	ł	1	ALBEVPLEVLRORBSKWLDMLNNWDKWMAKKHKKIRLRCOKGIP
		1	PSLRGRAWQYLSGGKVKLQQNPGKFDBLDMSPGDPKWLDVIERD
l	İ	1	LHRQFPFHEMFVSRGGHGQQDLFRVLKAYTLYRPEBGYCQAQAP
		1	IAAVLLMHMPAEQAFWCLVQICEKYLPGYYSEKLEAIQLDGEIL
		1	FSLLQKVSPVAHKHLSRQKIDPLLYMTEWFMCAFSRTLPWSSVL
-	Ì		RVWDMFFCEGVKIIFRVGLVLLKHALGSPEKVKACQGQYETIER
1	1	1	LRSLSPKIMQEAFLVQEVVELPVTERQIEREHLIQLRRWQETRG
1		1	BLOCKSPPRLHGAKAILDAEPGPRPALQPSPSIRLPLDAPLPGS
			KAKPKPPKQAQKEQRKQMKGRGQLEKPPAPNQAMVVAAAGDACP
1	ļ ·		POHVPPKDSAPKDSAPQDLAPQVSAHHRSQESLTSQESEDTYL
6386	819	195	TVCGSFYLGIMQRASRLKRELHMLATEPPPGITCWQDKDQMDDL
0300	1		RAQILGGANTPYEKGVFKLEVIIPERYPFEPPQIRFLTPIYHPN
l			IDSAGRICLDVLKLPPKGAWRPSLNIATVLTSIQLLMSEPNPDD
1			PLMADISSEPKYNKPAFLKNARQWTEKHARQKQKADEEEMLDNL
1		i	PEAGDSRVHNSTQKRKASQLVGIBKKFHPDV
6387	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
""	1	1	KOKLAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYLTNQK
ł	1	1	NSNSKNDRRNRKFKKAERLFSKSSVTSAAAVSALAGVQDQLIEK
	1	1	REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
1	1		STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
6388	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELABLVKR
3366		1	KORLAETLANLEROIYAFEGSYLEDTOMYGNIIRGWDRYLTNOK
1	1		NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
1		}	REPGSGTESDTSPDFHNQKNEPSQEDPEDLDGSVQGVKPQKAAS
ì		1	STSSGSHHSSHKKRKNKNRHSPSGMFDYDFBIDLKLNKKPRADY
6389	1074	497	ARPGDRMAGHRLVLVLGDLHTPHRCNSLPAKPKKLLVPGKIQHI
6969	10/4	42,	LCTCNLCTKESYDYLKTLAGDVHIVRGDFDENLNYPEQKVVTVG
1			OFKIGLIHGHQVIPWGDMASLALLQRQFDVDILISGHTHKFEAF
1	ľ	I	EHENKFYINPGSATGAYNALETNIIPSFVLMDIQASTVVTYVYQ
	1	1	LIGDDVKVERIEYKKP
L	<del> </del>		GEERKEGRAPGKAFAPERNPAKMEKEETTRELLLPNWQGSGSHG
	158	535	LTIAQRDDGVFVQEVTQNSPAARTGVVKEGDQIVGATIYFDNLQ
6390		•	DITTENTANTO AT AND A L'AUGESTAUTO I ANDONES CONTANTANTANT
6390		ì	CORVITOTALNEMCHIETUGT.KI.HPKCDRPPPSTGOTWDP
			SGRVTQLLNTMGHHTVGLKLHRKGDRPPPSLGQTWDP
6390	5386	2897	VRWNSKTECYLSIOTOENFPANLNELVNCIVISSLVTTQRKLKA
	5386	2897	SGEVTQLLNIMGHHTVGLKLHRKGDRFFPSLGQTWDP VRWNSKTECYLSIQTQENFPANLNELVNCIVISSLVTTQRKLKA MSLLGSRNQLARAVLNPNPMDFCTKDLLTITSERIIAYLRDFNE DQKKAIETAYAMVKHSPSVAKICLIHGPPGTGKSKTIVGLLYRL

F - 696	1 5 37		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide location	location	Glutamic Acid, P-Phenylalanine, G-Glycine,
j .		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ŀ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
<b> </b>	Bedgerice		LTENQRKGHSDENSNAKIKQNRVLVCAPSNAAVDELMKKIILEF
1			KEKCKOKKNPLGNCGDINLVRLGPBKSINSEVLKFSLDSQVNHR
ı	1		MKKELPSHVQAMHKRKEFLDYQLDELSRQRALCRGGREIQRQEL
1	Į.	ł	DENISKVSKEROELASKIKEVOGRPOKTOSIIILESHIICCTLS
	1	i	TSGGLLLESAFRGQGGVPFSCVIVDEAGQSCEIRTLTPLIHRCN
1	ļ.	į	KLILVGDPKQLPPTVISMKAQEYGYDQSMMARFCRLLEENVKHN
1	1	]	MISRLPILQLTVQYRMHPDICLFPSNYVYNRNLKTNRQTEAIRC
1	Į.	ļ	SSDWPFQPYLVFDVGDGSERRDNDSYINVQEIKLVMEIIKLIKD
İ		1	KRKDV9FRNIGIITHYKAQKTMIQKDLDKBFDRKGPAEVDTVDA
	į	ļ	FQGRQKDCVIVTCVRANSIQGSIGFLASLQRLNVTITRAKYSLF
1	1	}	ILGHLRTLMENQHWNQLIQDAQKRGAIIKTCDKNYRHDAVKILK
j	· ·		LKPVLQRSLTHPPTIAPEGSRPQGGLPSSKLDSGPAKTSVAASL
İ	1		YHTPSDSKEITLTVTSKDPERPPVHDQLQDPRLLKRMGIEVKGG
i	1	1	IFLWDPQPSSPQHPGATPPTGEPGFPVVHQDLSHVQQPAAVVAA
ł	1	1	LSSHKPPVRGEPPAASPEASTCQSKCDDPEEELCHRREARAFSE
1	[		GEQEKCGSETHHTRRNSRNDKRTLEQEDSSSKKRKLL
6392	972	186	GRTGVDLASSMAHRLQIRLLTWDVKDTLLRLRHPLGRAYATKAR
			AHGLEVEPSALEQGFRQAYRAQSHSFPNYGLSHGLTSRQWWLDV
l	Ĭ	i	VLOTFHLAGVQDAQAVAPIAEQLYKDFSHPCTWQVLDGAEDTLR
Į	l		ECRTRGLRLAVISNFDRRLEGILGGLGLREHFDFVLTSEAAGWP
1			KPDPRIPQEALRLAHMEPVVAAHVGDNYLCDYQGPRAVGMHSFL
L			VVGPQALDPVVRDSVPKEHILPSLAHLLPALDCLEGSTPGL
6393	2017	730	TGGSKMAAVATCGSVAASTGSAVATASKSNVTSFORRGPRASVT
[ .			NDSGPRLVSIAGTRPSVRNGQLLVSTGLPALDQLLGGGLAVGTV
}			LLIEEDKYNIYSPLLYKYFLAEGIVNGHTLLVASAKEDPANILQ
1	ł		ELPAPLLDDKCKKEFDEDVYNHKTPESNIKMKIAWRYQLLPKME
			IGPVSSSRFGHYYDASKRMPQELIEASNWHGFFLPEKISSTLKV
1			EPCSLTPGYTKLLQFIQNIIYEEGFDGSNPQKKQRNILRIGIQN
ł			LGSPLWGDDICCAENGGNSHSLTKFLYVLRGLLRTSLSACIITM
Ì	Ì		PTHLIQNKAI IARVTTLSDVVVGLESFIGSERETNPLYKDYHGL
[			IHIRQIPRLNNLICDESDVKDLAFKLKRKLFTIERLHLPPDLSD   TVSRSSKMDLABSAKRLGPGCGMMAGGKKHLDF
6394	1418	511	GAAAGGEGARREPAAMÄTVMÄÄTÄÄERAVLEEEPRWLIHDEVHA
1 3334	1110	J	VLKQLQDILKEASLRFTLPCSGTEGPAKORNFILGSCGTDQVKG
1			VLTLQGDALSQADVNLKMPRNNQLLHFAFREDKQWKLQQIQDAR
1			NHVSQAIYLLTSRDQSYQPKTGAEVLKLMDAVMLQLTRARNRLT
1	İ		TPATLTLPEIAASGLTRMFAPALPSDLLVNVYINLNKLCLTVYQ
			LHALQPNSTKNFRPAGGAVLHSPGAMFEWGSQRLEVSHVHKVEC
]	į į		VIPWLNDALVYFTVSLQLCQQLKDKISVFSSYWSYRPF
6395	13	658	PSGRPTRPLCCAARRGAARHGGSVSGWPAGRTPTETSNPGSSVM
[			ESVTFEDVAVEFIQEWALLDSARRSLCKYRMLDQCRTLASRGTP
1			PCKPSCVSQLGQRAEPKATERGILRATGVAWESQLKPBBLPSMQ
			DLLBEASSRDMQMGPGLFLRMQLVPSIBERETPLTREDRPALQB
			PPWSLGCTGLKAAMQIQRVVIPVPTLGHRNPWVARDSGE
6396	1	1221	ANILSSPSKRGQKGTLIGYSPEGTPLYNFMGDAFQHSSQSIPRF
1			IKESLKQILEESDSRQIFYFLCLNLLFTFVELFYGVLTNSLGLI
1			SDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGF
			INCLFLIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGLIVNL
			IGICAFSHAHSHAHGASQGSCHSSDHSHSHHMHGHSDHGHGHSH
			GSAGGGMNANMRGVFLHVLADTLGBIGVIVSTVLIEQFGWFIAD
			PLCSLFIAILIFLSVVPLIKDACQVLLLRLPPEYEKELHIALEK
}			IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV
İ			TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES
	L		MKYCKDGTYIM
6397	391	122	GAGGVGRFBAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK
	L <b> </b>		KLIAAQTGTRWNKIVLKKWYTIFKDHVSLGDYBIHDGMNLBLYY

WO 01/53312

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l .	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
<b>!</b> "	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	} _	\=possible nucleotide insertion)
	<del> </del>		0
6398	353	1306	HKQMGPLINRCKKILLPTTVPPATMRIWLLGGLLPFLLLLSGLQ
0330			RPTEGSEVAIKIDPDFAPGSFDDQYQGCSKQVMEKLTQGDYFTK
i .	i		DIEAQKNYPRMWQKAHLAWLNQGKVLPQNMTTTHAVAILFYTLN
1	ļ		SNVHSDFTRAMASVARTPQQYKRSFHFKYLHYYLTSAIQLLRKD
l	ł	ł	SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGOFLSTSLLKERA
1		İ	QEFGNQTLFTIFTCLGAPVQYFSLKKEVLIPPYELFKVINMSYH
1	ł		PREDWLQLRSTGNLSTYNCQLLKASSKKCIPDPIAIASLSFLTS
1	}	}	1
			VIIFSKSRV
6399	75	1245	PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKRGVAVSGPTK
	1	1	RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQKKMARCEAEN
]	I	i	EDLLKKLELYKEACEGQHKLECDLQQREEBIABLQKALSDMQVC
1		1	LFQEREHVLRLYSENDRLRIRELEDKKKIQNLLALVGTDAGEVT
ĺ	ļ	J	YFCKEPPHKVTILQKTIQAVGECEQSESSAFKADPKISKRRPSR
i		<b>\</b>	ERKESSEHYQRDIQTLILQVEALQAQLGEQTKLSREQIEGLIED
		·	RRIHLBEIQVQHQRNQNKIKELTKNLHHTQELLYESTKDFLQLR
ĺ	Į	ł	SENONKEKSWMLEKDNLMSKIKOYRVQCKKKEDKIGKVLPVMHE
i _	L		SHHAQSEYIKVMSLCRNEVVYFSGRVEGIPKNLQFVM
6400	2520	1053	KTMKCDEVVYEVQSAILRHNCGYAMKTGKPPHNLMERKDPETWL
1		}	DNISVTFLSLTDLQKNETLDHLISLSGAVQLRHLSNNLETLLKR
1	]		DFLKLLPLBLSFYLLKWLDPQTLLTCCLVSKQWNKVISACTEVW
į.			QTACKNLGWQIDDSVQDALHWKKVYLKAILRMKQLEDHKAFETS
		i	SLIGHSARVYALYYKDGLLCTGSDDLSAKLWDVSTGQCVYGIQT
ì	ł	1	HTCAAVKFDEQKLVTGSFONTVACWEWSSGARTQHFRGHTGAVF
ì	1	}	SVDYNDELDILVSGSADFIVKVWALSAGTCLNTLTGHTEWVTKV
			VLQKCKVKSLLHSPGDYILLSADKYEIKINPIGRBINCKCLKTL
1	1		SVSEDRSICLQPRLHFDGKYIVCSSALGLYQWDFASYDILRVIK
			TPEIANLALLGFGDIFALLFDNRYLYIMDLRTESLISRWPLPEY
		l .	RKSKRGSSFLAGEASWLNGLDGHNDTGLVFATSMPDHSIHLVLW
1	ì	Ì	KEHG
6401	109	766	PGAAMSRPDLRGCCTGPQPALRMLVLPSPCPQPLAFSSVETMEG
	1	1	PPRRTCRSPBPGPSSSIGSPQASSPPRPNHYLLIDTQGVPYTVL
}	1		VDEESQREPGASGAPGQKKCYSCPVCSRVFEYMSYLQRHSITHS
Į.	l	l	EVKPFECDICGKAPKRASHLARHHSIHLAGGGRPHGCPLCPRRF
1		J	RDAGELAQHSRVHSGERPFQCPHCPRRFMEQNTLQKHTRWKHP
6402	1196	279	TTSQCGGIRQSSAIPVASMEPAAICLRNALLLLPKEQQDPKQEN
1 -202	1	1	GAKNSNQLGGNTESSESSETCSSKSHDGDKFIPAPPSSPLRKQE
1	1	ł	LENLKCSILACSAYVALALGDNLMALNHADKLLQQPKLSGSLKF
1	1	1	IGHLYAARALISLDRISDAITHLNPENVTDVSLGISSNEQDQGS
Į.			DKGENBAMESSGKRAPQCYPSSVNSARTVMLFNLGSAYCLRSEY
1	1		DKARKCIHOAASMIHPKEVPPRAILLAVYLELOWSNTOLALQII
]	]	1	KRNOLLPAVKTHSEVRKKPVFOPVHPIQPIOMPAFTTVORK
6400	<del> </del>	1600	
6403	2	1690	RGIHTSVLQCNLQNQMYSHNVVIMNLNALTQVQQRNLITNLQ
i	1		RSVDDTSQAIQRIKNDFQNLQQVFLQAKKUTDWLKBKVQSLQTL
1	l	1	AANNSALAKANNDTLEDMNSQLNSFTGOMENITTISQANEQNLK
1		1	DLQDLHKDARNRTAIKFNQLEERFQLFETDIVNIISNISYTAHH
1		1	LRTLTSNINEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLR
1			MQQDLMRSRLDTEVANLSVIMBEMKLVDSKHGQLIKNFTILQGP
1			PGPRGPRGDRGSQGPPGPTGNKGQKGEKGPPGPPGPAGERGPIG
	ļ		PAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPP
1	1	1	GKEGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGP
ł	1	I	KGPPGPPGPSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY
}	1	1	FSVEKETFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH
1	I		WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC
}	<b>S</b>	}	AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL
6404	1012	222	AAALAMAAPAPGLISVESSSOELGAALAQLVAQRAACCLAGARA

SEQ	Predicted	Predicted end	I Amino
1	1	nucleotide	Amino acid segment containing signal peptide
110	beginning	1	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bequence	\=possible nucleotide insertion)
<u> </u>	Bequence		(-possible nucleotide insertion)
i i	İ	i .	RFALGLSGGSLVSMLARELPAAVAPAGPASLARWTLGFCDERLV
4	ł	ľ	PFDHAESTYGLYRTHLLSRLPIPESQVITINPELPVEEAABDYA
I	1	I .	KKLRQAFQGDSIPVFDLLILGVGPDGHTCSLFPDHPLLQEREKI
	1	1	VAPISDSPKPPPQRVTLTLPVLNAARTVIFVATGBGKAAVLKRI
Į.		İ	LEDQEENPLPAALVQPHTGKLCWFLDEAAARLLTVPFEKHSPL
6405	1	1456	AALPRPTPRAPLGREGTGSDSEMAASMFYGRLVAVATLRNHRPR
1 3.55	1 -	1 -120	
ł		ŀ	TAQRAAAQVI.GSSGLFNNHGLQVQQQQQQRNLSLHBYMSMELLQB
1	!	1	AGVSVPKGYVAKSPDRAYAIAKKIGSKDVVIKAQVLAGGRCKGT
	İ	ļ.	FESGLKGGVKIVFSPBEAKAVSSQMIGKKLFTKQTGEKGRICNQ
	1	<b>!</b>	VLVCERKYPRREYYPAITMERSFQGPVLIGSSHGGVNIEDVAAE
	ľ	ĺ	TPEATIKEPIDIEEGIKKEQALQLAQKMGFPPNIVESAAENMVK
	1	i	LYSLFLKYDATMIBINPMVEDSDGAVLCMDAKINFDSNSAYRQK
}	l	l	KIPDLQDWTQEDERDKDAAKANLNYIGLDGNIGCLVNGAGLAMA
į	ŀ	İ	TMDIIKLHGGTPANFLDVGGGATVHQVTBAFKLITSDKKVLAIL
1	•		VNIFGGIMRCDVIAQGIVMAVKDLEIKIPVVVRLQGTRVDDAKA
I	į.	<u> </u>	
1	l .	i	LIADSGLKILACDDLDRAARMVVKLSEIVTLAKQAHVDVKFQLP
6406	1036	167	HPRQMRGEDTPEAPPYSSGRYDSIKTEVSGCPEDLTVGRAPTAD
i	ļ	1	DDDDDHDDHEDNDKMNDSEGMDPERLKAFNMFVRLFVDENLDRM
1	ļ	ł	VPISKQPKEKIQAIIESCSRQFPEFQERARKRIRTYLKSCRRMK
i	[		KNGMEMTRPTPPHLTSAMAENILAAACESETRKAAKRMRLEIYO
į.		1	SSQDEPIALDXQHSRDSAAITHSTYSLPASSYSQDPVYANGGLN
Į.		i	YSYRGYGALSSNLQPPASLQTGNHSNGESGEARALASRPAPSWV
1		· ·	CRAALGSGMGRGKQRPVMERGCLTA
6407	492	150	
040,	4,52		VGLCLAVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGV
1	1		SWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNAC
	<u></u>		VLTISPVQPEDDADYYCSVGYGFSP
6408	1458	903	RGCITSSQAWRLFGGVTRGFNMRIBKCYFCSGPIYPGHGMMFVR
1			NDCKVFRFCKSKCHKNFKKKRNPRKVRWTKAFRKAAGKELTVDN
1	<u> </u>	1	SFBPEKRRNEPIKYORELWNKTIDAMKRVEBIKOKROAKFIMNR
1 .	<u> </u>		LKKNKELQKVQDIKEVKQNIHLIRAPLAGKGKQLRBKMVQOLOE
l i			DVDMEDAP
6409	150	446	NTALANLLRCFTCDRLCGGCTAPAPPAHQGIVLQPVMPSCDPGP
1 - 202		110	,
1		:	GPACLPTKTFRSYLPRCHRTYSCVHCRAHLAKHDELISKSFQGS
<del></del>			HGRAYLFNSV
6410	85	607	RGGTAGCVACLGCWGQSSSPKAAFPAGSACLPADSCPCLLFQAC
1			AISGLFNCITIHPLNIAAGVWMINNAFILLLCRAPFCCQFIRFA
	i		NTVAEKVDRLRSWQKAVFYCGMAVVPIVISLTLTTLLGNA1AFA
1 !			TGVLYGLSALGKKGDAISYARIQQQRQQADEBKLAETLEGEL
6411	302	772	RLSIMASSLNEDPEGSRITYVKGDLFACPKTDSLAHCISEDCRM
1			GAGIAVLFKKKFGGVQBLLNQQKKSGEVAVLKRDGRYIYYLITK
			KRASHKPTYENLOKSI.BAMKSHCLKNGVTDLSMPRIGCGLDRIO
j :			
- <u>  </u>		1754	WENVSAMIREVFEATDIKITVYTL
6412	61	1709	RPVTSFSPLPGSCGGRLGTRTMLGRSLREVSAALKQCQITPTEL
			CQKCLSLIKKTKFLNAYITVSEEVALKQAEESEKRYKNGQSLGD
j 1			LDGIPIAVKDNFSTSGIETTCASNMLKGYIPPYNATVVQKLLDQ
			GALLMGKTNLDEFAMGSGSTDGVFGPVKNPWSYSKQYREKRKON
			PHSENBDSDWLITGGSSGGSAAAVSAFTCYAALGSDTGGSTRNP
j		•	AAHCGLVGFKPSYGLVSRHGLIPLVNSMDVPGILTRCVDDAAIV
		·	
			LGALAGPDPRDSTTVHEPINKPFMLPSLADVSKLCIGIPKEYLV
] ]			PELSSEVQSLWSKAADLFRSEGAKVIEVSLPHTSYSIVCYHVLC
]			TSEVASNMARFDGLQYGHRCDIDVSTEAMYAATRREGFNDVVRG
1 1			RILSGNFFLLKENYENYFVKAQKVRRLIANDFVNAFNSGVDVLL
į į			TPTTLSEAVPYLEFIKEDNRTRSAQDDIFTQAVNMAGLPAVSIP
<b>i</b> .			VALSNOGLPIGLOFIGRAFCDQQLLTVAKWFEKQVQFPVIQLQE
1 1			LMDDCSAVLENEKLASVSLKQ
, ,			

Predicted	0770	I Some Affician A		I had a second of the second o
No:	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cotresponding				
corresponding to first anino acid residue of anino acid residue of anino acid residue of anino acid sequence anino acid sequence anino acid sequence (Codm. /=possible nucleotide deletion, /=	NO:		L Company	
to first amino acid residue of amino acid sequence  6413  2 885  885  885  885  885  885  885  8	l	1		
amino acid	1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
meino acid aequence  6413  2 885  REFECCIONAL / PODESIBLE NUCLEOTISE de deletion,		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence  Codon, /-possible nucleotide deletion, Possible mucleotide deletion, Sequence  BERECAGRASAIRMEDLESYMBERTISEAPATMOSETWISUTIT RELATED PROGUVERED ALICHARECHIKINES LIGATINGETWISUTIT RELATED PROGUVERED ALICHARECHIKINES LIGATINGETWISUTIT RELATED PROGUVERED ALICHARECHIKINES LIGATINGETWISUTIT RELATED PROGUVERED PROGUMENT SEAPATMOSETWISUTISES GRAVILLOTRUS ROJGEVER TIBLE PROGUMENT SEAPATMOSET VARYES COMMISSION OF THE PROGUMENT SEAPATMOSET VARYES COMMISSION OF THE PROGUMENT SEAPATMOSET VARYES COMMISSION OF THE PROGUMENT SEAPATMOSET VARYES COMMISSION OF THE PROGUMENT SEAPATMOSET VARYES COMMISSION OF THE PROGUMENT SEAPATMOSET VARYES COMMISSION OF THE PROGUMENT SEAPATMOSET VARYES COMMISSION OF THE PROGUMENT SEAPATMOSE COMMISSION OF THE PROGUM		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence  Codon, /-possible nucleotide deletion, -possible nucleotide insertion  REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REGERCALLER REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REGERCALLER REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REGERCALLER REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REGERCALLER REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REGERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REGERCAGNASIMMEDLEFYNDENTISEAPATMERTWEVTHIEN REGERCAGNASIMMEDLEFYNDENTISEAPATMERTWETH PYERAVAGLEGAGSGERREGNENTWINGENGERCERTWENTHIENBENDENTYNDENTISEAPATMERTWETH REFERCAGNASIMMEDLEFYNDENTISEAPATMERTWETH REGERCAGNASIMMEDLEFT REGERCAGNASIMMET REGERCAGNASIMMET REGERCAGNASIMMET REGERCAGNASIMMET REGERCAGNASIM REGERCAGNASIM REGERCAGNASIM REGERCAGNAS		residue of	amino acid	N=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence		amino acid	sequence	
6413 2 885 HEPRCAGRASIAMMOLDEPYMDENT ISRAPATMETEWSIVELY RICHT PROGUCEPADILATARK CHRISTORY LOGATEDATORY REAL BYATTOKOP DISPASSATION OF WATCH THE CHRISTORY LOGATEDATORY REAL BYATTOKOP DISPASSATION OF WATCH THE CONTROL OF THE CHRISTORY OF THE CHRI				
RRITGIPAGYCEVERALLATARKCHIKINGEPLEGATPARKEYS BYATYGKOPONSEYSTSJ.PUGDITOPUDDUM_HISPEPKWYPSCGG GKVVLDQTGSKOYGFVWEPTSLEDQKRALTECGANGLGSKEVE LSVAIPKASRVKPVEYSGMYSYSYNYYYQYQYYQYYXAQWOYDG GSYSTSTPQYGTTQSTWGYTEEVGDDALEDDMQLDATKANKEY GSYSTSTPQYGTTQSTWGYTEEVGDDALEDDMQLDATKANKEY MEGSEBLIJDALDCIMGPLDTYSSETPAMM  EGRAALLFAREPCCEPKPEPGARSSRATTGGFESPGMATSIGV SPSVLGGVPBAKKNGSPERNYILIREVEYQGPEPEVVKDCHAK LKERLANARYSPERPCLERKHEPASSRATTGGFESPGMATSIGV SPSVLGGVPBAKKNGSPERNYILIREVEYQGPEPEVVKDCHAK LKERLANARYSPERPCLERKHEPASSSAYGGWAGAFBYKWYQV VICEGREGGVPHASKGCFMADTOMYTHOVPMINGLFCVVAAPGC PTY  1168 PVXOMGSHRRACGIGCEANAGGGBEPRGRASSVAGWGGAPGC FYY  1168 PVXOMGSHRRACGIGCEANAGGGBEPRGRASSVAGWGGAPGC FYY  1168 PVXOMGSHRRACGIGCEANAGGGBEPRGRASSVAGWGGAPGC FYY  1168 PVXOMGSHRRACGIGCEANAGGGBEPRGRASSVAGWGGAPGC FYY  1168 PVXOMGSHRRACGIGCEANAGGGBEPRGRASSVAGWGGAPGC FYY  1168 PVXOMGSHRRACGIGCEANAGGGBEPRGRASSVAGWGGAPGC FYY  1168 PVXOMGSHRRACGIGCEANAGGGBEPRGRASSVAGWGGAPGCAPACH KKRCGVVSGPYIVYHLODLOILEDWTITRAMATIGPHRVCTEP PVXLERHILIANABERGBLIJTOHEKAMPIGGPTGAV  1171NHDEVWFRRPDGSKSKLYISQLOKGKYSIKHS  6416 410 1519 ETAPADLEITRACHVILISRTSINGSVTGEMAPSLITQGITCBACC AVYKINRCYGNOGTYSTRISTMSVTGCTGARAGGCPTSAV  1171NHDEVWFRRPDGSKSKLYISQLOKGKYSIKHS  6416 410 1519 ETAPADLEITRACHVILISRTSINGSVTGEMAPSLITQGITCBACC AVYKINRCYGNADGITSETRSGILQDLALAAAGGGRSYSCILISH ALLGCAPAGAPGARACACACACACACACACACACACACACACACACACACA	6472		DOE	.1
6414 1 538 RGGRALLPHREPPCCEPERGPARESSRATEGERSPORALTSCOCKAL  6414 1 538 RGGRALLPHREPPCCEPERGPARESSRATEGERSPORALTSCOCKAL  6415 2 1168 PVROMOSHREPOCKALEROSSRATEGERSPORATSCOCKAPOR VICEORAGE POR VICEORAG	0413	1 2	663	•
6414  6414  1 538  6628ELIDALDCIMOPTORY TRANSVERY SENT SYNONY TO TO THE ADMINISTRATION OF THE ADMINISTRATION O		j		
6414 1 518 RIGHT REPRESENTATION OF THE PROPERTY OF THE PROPERY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY		ł.		
6414 1 538 REGRANLI-WERRPFCCRPROPAREPSERATEGRESPEGATSIGV SFSV-SIGVY BRAKINAGERENTY ILREVYBOQRERESVINOCHAV LKERELANAEV SPERMPOLTRELSEN TORLK-KREYDEK YRMVQV VICEGREGGVPRASERGFRIADTINT-HUVFMORSELFAND LKERELANAEV SPERMPOLTRELSEN TORLK-KREYDEK YRMVQV VICEGREGGVPRASERGFRIADTINT-HUVFMORSELFCVVAAPGC PTY  6415 2 1168 FVROMGSHERACGIGCERAGGGEEPERGRASSVAGWVGAFRAP FIRAVAGIGACERAKGGGKERFRIADTINT-HUVFMORSELFCVVAAPGC PTY  FIRAVAGIGACERAKMPV-ISKORKEKTINHEBUSVDVA ENRGSSSEDEDTESSSVERGIGDS RANDERCERRENGELDENGN LEKOFTDIKUDIV-KKELSQUADALIGEV TARKABEPLEDLATJOE NMOIPTIVAGI YRELCLESVKNKYBCEIQASRQHCESEKLILIJD TVQSELBEKTRRIBEDRIST TOT SILAMDELGSRKRERDFFRP PVELKKHLISBARSEBRITY TORGWITSCHTTISHER TORGHTENAT LEKOFTDIKUDIV-KKELSQUADALIGEV TARKABEPLEDLATJOE NMOIPTIVAGI YRELCLESVKNKYBCEIQASRQHCESSKLILIJD TVQSELBEKTRRIBEDRIST TOT SILAMDELGSRKRERDFFRP PVELKKHLISBARSEBRITY TORGWITSCHT TIT SILAMDELGSRKRERDFFRP PVELKKHLISBARSEBRITY TORGWITSCHT TIT SILAMDELGSRKRERDFFRP PVELKKHLISBARSEBRITY TORGWITSCHT TIT SILAMDELGSRKRERDFFRP PVELKKHLISBARSEBRITY TORGWITSCHT TIT SILAMDELGSRKRERDFFRP PVELKKHLISBARSEBRITY TORGWITSCHT TIT SILAMDELGSRKRERDFFRP PVELKKHLISBARSEBRITY TORGWITSCHT TORGWIT			]	
MEGSERLINDALMOCHINOPLIDTYSSELTRAM   1		1		
6414 1 538 RGGRALLPWERPECCEPREQPARESSEATFGERSEGMATSIGV SFSVSIGVPBAEKNAGEPENTYILRPVFQQRFPESVAKCCHAV LKBELANARYSPEBRPQLITHILSENIKOKLKEMSFDEYMAVQV VIGEORGEGVPMASKCFMIDADTINYTHDVFMMOSLFCVVAAPGC FYY  6415 2 1168 FVROMGSSHRRACGIGCERKAGGGEBPEGKASSVAGWVGAFRAP FIRANVAGLGAGGGKRERGMBVSIKGRASSVAGWVGAFRAP FIRANVAGLGAGGGKRERGMBVSIKGRASSVAGWVGAFRAP FIRANVAGLGAGGGKRERGMBVSIKGRASSVAGWVGAFRAP KERGSSSEDEDTKSSSVSEDGDS RADDEDCERRECLDEMSN LERGFTDLKOQLYKERLSQVDAKLAGVIAGKAPEKLEPLATLQE MMOITERVAGITYBELGLESVKNNYKEGIQASRHCHEEKLLLYD VONGLERKTRILBEDRESDTITSELHANDELGSKRKKRSDFFFPD KKKPGVVSGFYLYVHLQDLDIEDMTTIREAMATLGFRUKTEP FYKLERHLBISARSEBRILYTOGBWYIRGGTICIDEKDBCCTSAV ITTINIDEWWRRPPOGSKSKLYJSQLGKGKYSKHGE FIRADLETPAGPVLLSRATSSTMSVTGGKMAPSLTQEILGHL GLASKTAMAGTLETTRITFLARSVDKADQRLLBATTGGCVDRSAL VDVLINNSREGRQLISRNFQERTQDLMKSLQAALSGNIERIVM ALLQTTAQFDAQRELTTALKASDSAVDVAIBILATTTPOFQLGCL AVYKINFQVERVUGTSETSGTIQULLLALAKGBYSGGIUTY ALLQTTAQFDAQRLETALKASDSAVDVAIBILATTTPOFQLGCL AVYKINFQVERVUGTSETSGTIQULLLALAKGBYSGGIUTY NLAEQOVQALQRAEGGBREETWYPY-TORIPERLIKVPDQYGRS TGGELEERAVOMRHGDAQVALGLASVINKSTYPAGKHGAGL ETEPNYQVLIRILISRCSTDLLSINGSDLINKSINDERTYPAGKHGALQ ETEPNYQVLIRILISRCSTDLLSINGSDLINKSINDERTYPAGKHGALQ ETEPNYQVLIRILISRCSTDLLSINGSDLINKSINDERTYPAGKHGALQ ETEPNYQVLIRILISRCSTDLLSINGSDLINKSINDERTYPAGKHGALQ ETEPNYQVLIRILISRCSTDLSINGSDLINKSINDERTYPAGKHGALQ ETEPNYQVLIRILISRCSTDLSINGSDLINKSINDERTYPAGKHGALQ ETEPNYQVLIRILISRCSTCAVY AGIELLHQKLELPDNVSGEPGMSFCLACVSAPLQFMASALPIWA AHTMREKETIMKNIRVA AGIELLHQKLELPDNVSGEPGMSFCLACVSAPLQFMASALPIWA AHTMREKETIMKNIRVA AHTMREKETIMKNIRVA AHTMREKETIMKNIRVA PERPERPENGERGDDHILMSSSSPSQMFPMRPQAARGGRINGG TYSRFOTLBEGRERIGEDDHILMSSSSPSQMFPMRPQAARGGRINGG TYSRFOTLBEGRENIGEDDHILMSSSSPSQMFPMRPQAARGGRINGG TYSRFOTLBEGRENIGEDDHILMSSSSPSQMFPMRPQAARGGRINGG TYSRFOTLBEGRENIGEDDHILMSSSSPSQMFPMRPQAARGGRINGG TYSRFOTLBEGRENIGEDDHILMSSSSPSQMFPMRPQAARGGRINGG TYSRFOTLBEGRENIGHDLINGSDLIKTVINGSDRIX VLUGHDNINKHKINGDPGGILIJKHADTROVSTRANGSTRINGSDKY VLUGHDNINKHKINGDPGGILIJKHADTROVSTRROVSTRANGSTRINGS NQELLKSMVRSIKMBVSGPOWARLICKGSSSTSTROW PRINKHKKENNICHDERSTLIKTGR		1	ĺ	GSYSYSYPQYGYTQSTMQTYEEVGDDALEDPMPQLDVTEANKEF
SFSVEIGUPERAKKNAGIPERTYTILRPUPOQREPESVVEICHAV LKRELANARYSPERMPQLTKHLSENIKOHLKENGPYKNVUVQV VIGERGEGVPRASKCPMDADTONTHUPMINDSLFCVVARPOV VIGERGEGVPRASKCPMDADTONTHUPMINDSLFCVVARPOV PYY  6415  2 1168 FVRONQSSHRRACGIGCERRAGGEEPRGRASSVAGWVGAPRAP FIRANAGIGAGSGKRRCKMMPV:ISRGDKKETINHIDEMSUDYA BENEGSSENDENTSSSVSERGDORSAMUDDECHMECLDEWSH LEKQPTOLKOQLYKERLSQVDAALGEVIAGKADEVLEPLATIGE MMOIPTKVAGIYVELCI-SVUKNYKEGIGASKRKEKDPFWP KKRPGVVSGPYLVYHLQDLDILEDMYTIRRAHATIGPHKRYTEP PVKLEKHLEISRARBERGRILYDGBWINGOYICIDEKROCFTSAV ITTINIDEVWFKRPDOSKSKUTISQLOKOKYSIKHE  6416 410 1519 EIRPADLISIPACPYVLISRRTSSTMSVTGGEMAPSLIQDELISHL GLASKKARAMGTLGTLRTPIAFSVDKDAORILARATIGGUNGAT ITTINIDEVWFKRPDOSKSKUTISGLOKOKYSIKHE GLASKKARAMGTLGTLRTPIAFSVDKDAORILARATIGGUNGAT ALLQPTAQPDAQELRTALKASDSAVDVAISILARATIGGUNGAT ALLQPTAQPDAQELRTALKASDSAVDVAISILARATIGGUNGAT ALLQPTAQPDAQELRTALKASDSAVDVAISILARATIGGUNGAT ALLQPTAQPDAQELRTALKASDSAVDVAISILARATIGGUNGAT AVKINIPQVBAVDGITSSTSTGGILQDLLIALAKGGRIDSYGLOKA ALLQPTAQPDAQELRTALKASDSAVDVAISILARATIGGUNGAT AVKINIPQVBAVDGITSSTSTGGILQDLLIALAKGGRIDSYGLOKA KGDCOSALLALCRAEUM ALLQPTAQPDAQELRTALKASDSAVDVAISILARATIGDELICHAVOORGA CETEPHYQULIK ILISCKSTDLISI BRAPRIKKEKSKILVSSLQDAV KGDCOSALLALCRAEUM  6417 1 845 RESSPOLWSELEERAGGGEGNASSINARMINNFPATAFVIACVLE LISTYMAASICTDFWYENSEPVQENNSGILIKSINDEPIDBAD EKTYNDALPRINGTVUGUMRRCTIPKNRWYSPPETRSFOVVT KCUSTTLTRQPMSKVDFORNNSGIDLISRTIMRCPELBFVVSIL GIMCGRALIGLOXICGESKYPTLATGIHLAGLGLTIGSVSCTV AGEIELHIGKLEDDWISGSPECLACVSARDLOPMASALPTWA AHTINKENTIMKAYKVA AHTINKENTIMKAYKVA AHTINKENTIMKAYKVA AHTINKENTIMKAYKVA TPAPPPPPPCCGIAGGGPAKKYGGNILARQCHIPTTQGRABLVQ YPDCCSSSGNI LGEDDHILMQSSP SOMPHMRQADEGRRGGOT TYSRPQTLBIGERFFLFNPYLITRRRIEVSGLALARGERDAKT VLIQMINDHAKHQDPGQPLY ILMNAHTQCATTOLAGNISH PSDPVTYPTILESLUMKEELESLENBEGDHASTVANDKOPPP MARSISTGGLOKEORGONISKSILDENGENBASTTANDEVOHHBIV PNILWWYPTELLALLEPYTPILLIPKTRITISGVKSTHCORPP STUWECKKTPGGPUL RIMINKKGRINDDORPHSQUARDARVKKRIPPHONEDSUKY VLIQMINDHAKHQDPGQPLY ILMNAHTQCYTUWRRCHIPPHALQKSDNSP NGELIKSWSISI ORIGONOPHSQUALLIPKTRICHTRKRONIKENDSLYKEN NLEUGARRTVATIMOGHAAVWHGYKVHGRINIKEND		i		MEQSEKLYDALMOCHWQPLDTVSSEIPAMM
LIKERLANDAEVS PERMPOLTKHLISENI KOKLKEMSPERYKNVUVU VIGEOREGUPMASRCFWDADTDNYTHOUPMINDSLECVUVAPGO PYY  1168 PVROMOSSHRACGLÄCERARGGGEBERGRASSVAGWVGAPRAP PVROMOSSHRACGLÄCERARGGGEBERGRASSVAGWVGAPRAP PVROMOSSHRACGLÄCERARGGGEBERGRASSVAGWVGAPRAP PVROMOSSHRACGLÄCERARGGGEBERGRASSVAGWVGAPRAP ENGGSSKIDENTESSSVEBUGDSSRMDBDCERREMIGLDENSN LEKOPTOLKOLVKERLISCUVAKLOVITAGURE VILLYD TVORELBERIRRIEDHSI DITSBLIMNDBLOGRKKKROPPWPB KKRPGVVSGPYTVYMLQDLÖLLBOMTTIKANATLGGHRVKTEB PVRLIKRHLHISARSBERGRIYYDGBYTRGQTI CIDKORCTSAV ITTINIBDSWYKRPDGSKSKLYJSQLOKAPSLINGBRUSTSAV ITTINIBDSWYKRPDGSKSKLYJSQLOKAPSLINGBRUSTSAV TITINIBDSWYKRPDGSKSKLYJSQLOKAPSLINGBRUSTSAV TITINIBDSWYKRPDGSKSKLYJSQLOKAPSLINGBRUSTSAV ALLQPTAGPDAQBERTALVSBVANDVATERLARGTPSPORTSAL ALLQPTAGPDAQBERTALVSBVANDVATERLARGTPSQLESAV ALLQPTAGPDAQBERTALVSBVANDVATERLARGTPSQLESAV ALLQPTAGPDAQBERTALVSBVANDVATERLARGTPSQLESAV ALLQPTAGPDAQBERTALVSBVANDVATERLARGTPSQLESAV ALLQPTAGPDAQBERTALVSBVANDVATERLARGTPSQLESAV ALLQPTAGPDAQBERTALVSBUNDVATERLARGTPSQLESAV ALLQRAGNENGANDVATERLARGTPSVANDVATERLARGTPSQLESAV ALLQRAGNASSLAVANDATERLARGTPSVANDVATERLARGTPSQLESAV ALLQRAGNASSLAVANDATERLARGTPSVANDVATERLARGTPSQLESAV ACCENTALALVANDVATERLARGTPSVANDVATERLARGTPSVANDVATERLARGTPSOLDAV KGDOSBALLALCARBUM EKTYDALLARTNOTUCLIBERCTIT PLYMAMINSPPERTSSPOND EKTYNDALLARTNOTUCLIBERCTIT PLYMAMINSPPERTSSPOND KCUSPTLTEQPMSKPODPONINGSIDLLARTNOCOPLILIPUSA GENCPALLIGICACTICESLYPTLATGILAGCTLGSVSCTV AGIBLHCKLELPDNVSGEPONSPCLACVSAPLQFMASALPTWA AHTBREVTTIMKAYRVA  6418 2 662 TRTEPRREPPELGAAVEKAGARSTSTPAGASPAAAVQADPPPPAH TPAPPPPPPCGGTACHGEPAAFYGYDNLORGPITTQBABLIVG YPPCKSSSGNIGEDPHILMSGSSPSOMPFWRPQAAFGRRORQ TYSRPOTLBERSPLENPYLTRKRETEVSHALALTERQVIT MPC NEMMKKKENNINGKPPVSGSSPSOMPFWRPQAAFGERGUT TYSRPOTLBERSPLENPYLTRKRETEVSHALALTSPGVKTNICDRPP STOWMCKKENNINGKPPVSGSSPSOMPFWRPQAAFGERGUT TYSRPOTLBERSPLENPYLTSLVANKELESLIBBERGRORD TYSRPOTLBERSPLESLIBBERGERGUT VICINIMINIKHTOTOGOPLIT LIBERGUTGUT. LIBERGUTGUT. PRILIVALEGUT. LIBERGTUT. LIBERGUTGUT. LIBERGUTGUT. LIBERGUTGUT. LIBERGUTGUT. LIBERGUTGUT. LIBERGUTGUT. LIBERGUTGUT. LIBERGUTGUT. LIBERGUTGUT. L	6414	1	538	RGGRAALLPWRRFPCCRPRPQPARPSSRATPGPRSPGMATSIGV
LIKERLANDAEVS PERMPOLTKHLISENI KOKLKEMSPERYKNVUVU VIGEOREGUPMASRCFWDADTDNYTHOUPMINDSLECVUVAPGO PYY  1168 PVROMOSSHRACGLÄCERARGGGEBERGRASSVAGWVGAPRAP PVROMOSSHRACGLÄCERARGGGEBERGRASSVAGWVGAPRAP PVROMOSSHRACGLÄCERARGGGEBERGRASSVAGWVGAPRAP PVROMOSSHRACGLÄCERARGGGEBERGRASSVAGWVGAPRAP ENGGSSKIDENTESSSVEBUGDSSRMDBDCERREMIGLDENSN LEKOPTOLKOLVKERLISCUVAKLOVITAGURE VILLYD TVORELBERIRRIEDHSI DITSBLIMNDBLOGRKKKROPPWPB KKRPGVVSGPYTVYMLQDLÖLLBOMTTIKANATLGGHRVKTEB PVRLIKRHLHISARSBERGRIYYDGBYTRGQTI CIDKORCTSAV ITTINIBDSWYKRPDGSKSKLYJSQLOKAPSLINGBRUSTSAV ITTINIBDSWYKRPDGSKSKLYJSQLOKAPSLINGBRUSTSAV TITINIBDSWYKRPDGSKSKLYJSQLOKAPSLINGBRUSTSAV TITINIBDSWYKRPDGSKSKLYJSQLOKAPSLINGBRUSTSAV ALLQPTAGPDAQBERTALVSBVANDVATERLARGTPSPORTSAL ALLQPTAGPDAQBERTALVSBVANDVATERLARGTPSQLESAV ALLQPTAGPDAQBERTALVSBVANDVATERLARGTPSQLESAV ALLQPTAGPDAQBERTALVSBVANDVATERLARGTPSQLESAV ALLQPTAGPDAQBERTALVSBVANDVATERLARGTPSQLESAV ALLQPTAGPDAQBERTALVSBVANDVATERLARGTPSQLESAV ALLQPTAGPDAQBERTALVSBUNDVATERLARGTPSQLESAV ALLQRAGNENGANDVATERLARGTPSVANDVATERLARGTPSQLESAV ALLQRAGNASSLAVANDATERLARGTPSVANDVATERLARGTPSQLESAV ALLQRAGNASSLAVANDATERLARGTPSVANDVATERLARGTPSQLESAV ACCENTALALVANDVATERLARGTPSVANDVATERLARGTPSVANDVATERLARGTPSOLDAV KGDOSBALLALCARBUM EKTYDALLARTNOTUCLIBERCTIT PLYMAMINSPPERTSSPOND EKTYNDALLARTNOTUCLIBERCTIT PLYMAMINSPPERTSSPOND KCUSPTLTEQPMSKPODPONINGSIDLLARTNOCOPLILIPUSA GENCPALLIGICACTICESLYPTLATGILAGCTLGSVSCTV AGIBLHCKLELPDNVSGEPONSPCLACVSAPLQFMASALPTWA AHTBREVTTIMKAYRVA  6418 2 662 TRTEPRREPPELGAAVEKAGARSTSTPAGASPAAAVQADPPPPAH TPAPPPPPPCGGTACHGEPAAFYGYDNLORGPITTQBABLIVG YPPCKSSSGNIGEDPHILMSGSSPSOMPFWRPQAAFGRRORQ TYSRPOTLBERSPLENPYLTRKRETEVSHALALTERQVIT MPC NEMMKKKENNINGKPPVSGSSPSOMPFWRPQAAFGERGUT TYSRPOTLBERSPLENPYLTRKRETEVSHALALTSPGVKTNICDRPP STOWMCKKENNINGKPPVSGSSPSOMPFWRPQAAFGERGUT TYSRPOTLBERSPLENPYLTSLVANKELESLIBBERGRORD TYSRPOTLBERSPLESLIBBERGERGUT VICINIMINIKHTOTOGOPLIT LIBERGUTGUT. LIBERGUTGUT. PRILIVALEGUT. LIBERGTUT. LIBERGUTGUT. LIBERGUTGUT. LIBERGUTGUT. LIBERGUTGUT. LIBERGUTGUT. LIBERGUTGUT. LIBERGUTGUT. LIBERGUTGUT. LIBERGUTGUT. L			ļ	SFSVGDGVPRAEKNAGEPENTYILRPVFOORFRPSVVKDCIHAV
6415 2 1168 FVRQWQSSHRRACGLGCEARAGGGEBERGRASSVAGWVGAPRAP FIRANVACLGAGSGKRRCMMPY-ISRGDKKETHHIBMEUDYJA BRIGGSSEDBUTYRSSVSEDGDSSAMDBOCERRRINGCLBHSIN LEKQFTDLKDQLVKERLSQUDAKLQEVLAGKAPBYLEPLATTQE NMQIPTKVAGI YRRCLG-BSVKNKYBCEIQASRQHCESEKLLIYD TVQSELBEKIRRIEBDRISIDITSBILMDBLQSRKRKDPFWPD KKKPGVVSGYPTIVMLQDLDLLBUMTTIRKAMATLGGBRUKTEN PVRLIERHLBSARBEGGILYDOBKTLGGLOGSKORKENDPFWPD KKKPGVVSGYPTIVMLQDLDLLBUMTTIRKAMATLGGBRUKTEN PVRLIERHLBSARBEGGILYDOBKTLGCIONGKYSIKB FPRVLIERHLBSARBEGGILYDOBKTLGCIONKYSIKB  6416 410 1519 EIAPADLE IBRACAPULLSBATSSTBSVTGGRADSLTQGETLSHL GLASKTAAWGTLGTLRTPLNPSVDKDAQRLLRAITCQGVDRSAI VDVITNRSREGRQLISENTSSTBSVTGGRADSLTQGETLSHL ALLQTTAQFDAGELRTAKASBOSAVDVAB EILARTTPPQLOBCL AVYKINFQVBAVDGITSSTGGILDGLLLALAKGGRDSYSGILDY NLAEQDVQALQRABGESBRETWVVFYTORPHLIRVFDQVGRS TCGELEEAVQNRFHGDAQVALLGLASVINNTPLYFADKHQALQ ETBPYQVLIRILISRCETDLLSIRABFRKKPGSLYSSLQDAV KGDCOSALLALCRABUM KGDCOSALLALCRABUM KGDCOSALLALCRABUM KGDCOSALLALCRABUM EKTYNDALPRYNGTVULWRCHITPKNMINYSPPBRTSSFDVVT KCVSPTLTEQFBMEKFVDPGNINSGIDLLRTYLWRCQFLLPFVSL GIMCGGAILGLCACICESLFPTIATGIHLLAGLCTIGSVSCTV AGIBLHGKLELPDNVSGEFOMSFCLACVSAPLQFMASALFIWA AHTMIRETTIMAYRVA AHTMIRETTIMAYRVA AHTMIRETTIMAYRVA AHTMIRETTIMAYRVA FORMSKKENNINGKPVSGSPSGVMGGTKKRAPGBLEBGRABGLTIN PSPDPVTVPTLSPLVVMKELESLLBREGGLACVSAPLQFMASALFIWA TPRPPPPPPGGGAAVGKAGASSTSTPAGASPAAVQADPPPPAH TPRPPPPPGGGAAVGKAGASSTSTPAGASPAAVQADPPPAH TPRPPPPPGGGAAVGKAGASSTSTPAGASPAAVQADPPPAH TPRPPPPPGGGAAVGKAGASSTSTPAGASPAAVQADPPPAH TPRPPPPPGGGAAVGKAGASSTSTPAGASPAAVQADPPPAH TPRPPPPPGGGAAVGKAGASSTSTPAGASPAAVQADPPPAH TPRPPPPPGGGAAVGKAGASSTSTPAGASPAAVQADPPPAH TPRPPPPPGGGAAVGKAGASSTSTPAGASPAAVQADPPPAH TPRPPPPPGGGAAVGKAGASSTSTPAGASPAAVQADPPPAH TPRPPPPPGGGAAVGKAGASSTSTPAGASPAAVQADPPPAH TPRPPPPTGGAAVGKAGASSTSTPAGASPAAVQADPPPAH TPRPPPPTGGAAVGKAGASSTSTPAGASPAAVQADPPPAH TPRPPPPTGGAAVGKAGASSTSTPAGASPAAVQADPPPAH TPRPPPPTGGAAVGKAGASSTSTPAGASPAATQACTDSLGBHL TPRPPPPPTGGAAVGKAGASSTSTPAGASPAAVQADPPPAH TPRPPPPTGGAAVGKAGASSTSTPAGASPAAVQADPPPAH TPRPPPTGAAVGATASCGAAVGKAGASSTSTAGASSTAVATAGATGAGAAVGAATGATGAGAAVGAATGAGAAVGAATGAGAAVGAATGAGAAV		i	'	
6415 2 1168 FYYROWQSSHRRACGIGCEARAGGGEPERGRASSVAGWVGAPRAP FIBAVAGIGAGSGKRRKMKMPYERGOKKETHHIDEMEVDYA ENGSSSSEDENTESSSVERGORSSAMDEDCERREMECLDEMEN LEKOPTOLKOQLYKERLEJOVAKLOGVIGARGKETHHIDEMEVDYA ENGSSSSEDENTESSSVERGORSSAMDEDCERREMECLDENSIN LEKOPTOLKOQLYKERLEJOVAKLOGVIGARGKETHHIDEMEVDYA TVOSKLEREKIRLEDRISE DITTERLAMPATLGERKRKKDPFMPD KKKPGVVSGPYIVYMLQDLDILEDWTTIRKAMATLGPHRVKTEP PVILLERHHIBARSEEGRILYDGBWYIRGCTIGARGKETSBKLLLTYD TVOSKLEREKIRLEBERBER DITTERLAMPATLGPHRVKTEP PVILLERHHIBARSEEGRILYDGBWYIRGCTIGARGKTSICHEN EARACHAUCHTEN PROVINCIA STATEST STATE		1	l	
6415 2 1168 FYRONGS SIRRACGIGCERANGGGERPRGRAS SYAGWYGAPEAP PIBAAVAGIAGSGGKRRGMINPYSISRGKKETNHIDEMSVDYA BNGGSSKDEDTESSSVSEDGDBSZMDDBDCERRRMECLDEMSN LERGFTDLEDGLYKERIGGVDARLOEVIAGRAPSYLEPLATIOE NMGIPRYKVAGITYRELG-ESVANKYREGAPSCHESKLLLYD TVOSKLERKIRRLERDRHSIDITSKLMNDBLOERKRRKDPFWPD KKKPGVVSGPYIVYMLQDLDILEDMTTIKAMATLGPHRVKTEP PVILERHIBISARSBERGRIYYDGRWITROGTICIDKRORCPTSAV ITTINBEWWRRPDGSKSKLIVISQLOKGKYST KHS  6416 410 1519 EIAPADELEISRNISTSTSVSVGGKMAPSLTORILSHL GLASKYAAMGTICTIRRPINFSVDKOAQRLIRAITTGGUDRSAI VDVLITNSREQRQLISRNSPOERTQOLMKSLQAALSGNLERIVM ALLQPTAGFDAQBLRTALKASDSAVDVAIBILLATRTPOLDECL AVYKINFQUEAVOGITSETSGILQDLLLALAKGGRDSYSGILDY NLAEQDVOALORABGSSREETWVPYTIRFBHILIRVPDYORS TGGELEEAVQNRFHGDAQVALLGLASVIKNTPLIFADKLHOALO BTEPNYQULIBILISRGSTDLLSIRAERDRHYFHIJENDYDYORS TGGELEEAVQNRFHGDAQVALLGLASVIKNTPLIFADKLHOALO BTEPNYQULIBILISRGSTDLLSIRAERDRHYFHATAFVILACULS KRYNDALFRINGIVGIMRRCCTITIFKNHMYSPPERTRSFDVVT KCVSPTLITRGPMBRFVDPORNSSGILNKSIMDEFISDBAD EKTYNDALFRINGIVGIMRRCCTITIFKNHMYSPPERTRSFDVVT KCVSPTLITRGPMBRFVDPORNSSGILNKSIMDEFISDBAD EKTYNDALFRINGIVGIMRRCCTITIFKNHMYSPPERTRSFDVVT KCVSPTLITRGPMBRFVDPORNSSGILNGAPPTATAFVILACULS GLMCPGALIGICACICRSLYPTIATGILHLAGLCTIGSVSCYV AGIBLHGKLELPDNVSGEPGSPSCLACVSARPLJFMASALFINA AHTMRKEYTIMKAYRVA  6418 2 662 TKTRPRRPPGGGAAVGRAGARSTSTPAGASBAAAVQADPPPPAH TRAPPPPPPCGGAAVGRAGARSTSTPAGASBAAAVQADPPPPAH TRAPPPPPPCGGAAVGRAGARSTSTPAGASBAAAVQADPPPPAH TRAPPPPPPCGGAAVGRAGARSTSTPAGASBAAAVQADPPPPHA TRAPPPPPPCGGAAVGRAGARSTSTPAGASBAAAVQADPPPPHA TRAPPPPPPCGGAAVGRAGARSTSTPAGASBAAAVQADPPPHA TRAPPSPPPPCGGAAVGRAGARSTSTPAGASBAAAVQADPPPHA TRAPPSPPPCGGAAVGRAGARSTSTPAGASBAAAVQADPPPHA TRAPPSPPPCGGAAVGRAGARSTSTPAGASBAAAVQADPPPHA TRAPPSPPPCGGAAVGRAGARSTSTPAGASBAAAVQADPPPHA TRAPPSPPPCGGAAVGRAGARSTSTPAGASBAAAVGADPPPAH TRAPPSPPPCGGAAVGRAGARSTSTPAGASBAAAVGADPPPHA TRAPPSPPPCGGAAVGRAGARSTSTPAGASBAAAVGADPPPHA TRAPPSPPPCGGAAVGRAGARSTSTPAGASBAAAVGADPPPHA TRAPPSPPPCGGAAVGRAGARSTSTPAGASBAAAVGADPPPHA TRAPPSPPPCGGAAVGRAGARSTSTPAGASBAAAVGADPPPHA TRAPPSPPPCGGAAVGRAGARSTSTPAGASBAAAVGADPPPHA TRAPPSPPCGGAAVGRAGARSTSTPAGASBAAAVGADP		ł	,	
FIRANAGIGAISGKRRROMMPVISKADKKETNHHIDEMEUDYA ENRGSSEDEDTESSSVEDIGDSSMDDEDCERRRMECLDEMSN LEKQFTDLKOQLYKERLSQVDAKLQEVTAGKAPEYLEPLATIQE MMGIRTKVAGIYRBLCLESVKNKYKGETQASRQHCESBKLLLIYD TVQSKLERKERIRLEBERBSDTTSTSHADGGKKRKKDEPYNEPLAKTQE KKKPGVVSGPYIVYMLQDLDILEDWTTIRKAMATLGPHRVKTEP PVKLEKHHEISARSBEGRIKYDDGBWYTRQTICIDKIDKCPTSAV 1TTINIDESWWKRPDGSKSKLYISQLGKKYSIKHS 6416 410 1519 EIAFADLETPACAPVLLSRRTSSTMSVTGGEMAPSLTQBILSHL GLASKYAMAGGTGTTLRFTDHSVDKOALKARATTGCPHRVKTEP PVKLEKHHEISARAGGTGTTLRFTDHSVDKOALKARATTGCDRSAI VDVLTNRSREQRQLISRNPQERTQQDLMKSLQAALSGNLERIVM ALLQTTAGPDAQBLKTALKASDSAVDVAIELLARTTPPCLOECL AVYKNHFQVEAVDGITSETSGLIQDLLALAKGGRDSYSGIDY NLAEQDVQALQRABGPSRETWYVYTQRFFEHIRVFDOYGRS TCGCLEESAVQNRFHGBOAVVALGLASVRYPILYPADALHQALQ ETEPNYQVLIRILISRCSTDLLSIRAFKKFGKSLYSSLQDAV KGDCOSALLALCRABUM KGDCOSALLALCRABUM KGCOSALLALCRABUM EKTYNDALFRYNGTVGLWRRCTTIPKMWYSPPERTBSFDVVT KCVSPTLTRQWMEKFVDFONNSSGILMKSTWDEPTSDEAD EKTYNDALFRYNGTVGLWRRCTTIPKMWSYPPERTBSFDVVT KCVSPTLTRQWMEKFVDFONNSSGILMKSTWDEPTSDEAD EKTYNDALFRYNGTVGLWRRCTTIPKMWSYPPERTBSFDVVT KCVSPTLTRQWMEKFVDFONNSSGILMKSTWDEPTSDEAD EKTYNDALFRYNGTVGLWRRCTTIPKMMSYPPERTBSFDVVT KCVSPTLTRQWMEKFVDFONNSSGILLKGTTLJACGTGLSDFPVSL GIMCRGALIGLCACICESLYPTTATGTHHLAGLCTIGSVSCTV AGISLLMGKLELPDNVSGFGCASFCLACVSAPLQFMSSALFVWA AHTMRKEYTLMKAYRVA AHTMRKEYTLMKAYRVA AHTMRKEYTLMKAYRVA AHTMRKEYTLMKAYRVA AHTMRKEYTLMKAYRVA AHTMRKEYTLMKAYRVA AHTMRKEYTLMKAYRVA TPAPPPPPPCGGIACHGEPAKFYGDMLORQPIPTTQQRABILVQ YFDCXSSGSNIGEDPDHIADGSSPSQWFPMMRPQAAPGRRGRG TYSRFQTILEBERELINPYLTKRRRLEVALLALTERQVKIW WFQ NRRMKNKKENNKDKPPVSRQEVKDGETKKBAQELEEDRAEGLTN PSDPVTVPYLSPLVWKKLESLLENBGDEATTVADFVOHIP IV FWILVWYPRRLDLPSNLPGLILISBEHCHKYKKIPTRQRSLYMFI LPSSLVALGRRINDIDAPKSKNAYDRLTPSQVKSTINCCRPP STGVMECRKTFGBPYL  6419 1973 PREPREVERGDALTGRAFTGLEBHL PSDPVTVPYLSPLVUKKLESHCKYKSI PRHCMSEDSKY VLLQHIMDNMILHQDFGQPLYILIMARTQKYRWHLLQKSDNSF NOELLKSMVSI KNNDVYOPMSQTLETTLNKCPHFKRQRSLYRBT LFLSLVALGRRINDIDAPKSKNAYDRLTPSQVKSTINCCRPP STGVMECRKTFGBPYL  6420 207 1187 RINIDKNGTGVGGOSVPYMICLITHLERNFGUEQLEDYLNFAN VLLWVETFULLILLIPYFTILLYLTITLHIVKRKNVLKPAYSK NLMDGGA	GATE	<del>  3</del>	1160	
ENGCSSIDDENTESSSVERUGDSSAMDDENCERRAMECLDEMSN LEKOFTOLKOLLYKERLSQUDAKLQEVIAGKAPEYLEPLATLQE NMOIRTKVAGIYRELCLESVKNYIKEGIQASRCHCESEKULLYD TVQSKLEBEKIRRLEEDRESIDITSELMMDELQGEKRKROPPWHO KKKPGVOSEPTIVVMLQDLDILEDMTTRKAMATLGFHEVETEP PVKLERHLEISABSERGRLYYDGEWYIRGGTICTDKKDRCFTSAV ITTINHDEVWFRRPDGSKSKLYISQLQKGKYSIKHS  6416 410 1519 EIAFADLEITACAPVLLSRATSSTESVTGGKMAPSLTQSILISHL GLASKYAANGTLGTLRTPLANESUDKDAQRLLRAITGGUDASIA UDVLTMESERGRQLISENFOERTQOURASIA UDVLTMESERGRQLISENFOERTQOURASIA UDVLTMESERGRQLISENFOERTQOURASIANERIVM ALLQTAQPDAQBLRTALKASDSAVDVAIBILARTPOPQLOECL AVYKHRQVEAVDGITSETSGILQDLLLALAKGGRDSYSGILDY NIAEQUVQALQRABGESREETWVPYTQREFEILIRVPDQYQRS TGGELEEAVQRRFHGDAQVALLGLASVIKNTPLIYFADKLHQALQ ETSPHYQVIIRILISECTETULSI IRRKFKFKGKISISSLQDAV KGDCOSALLALCRAEDM  6417 1 845 RGESRVLWSELEGEACGAGGNASSINARMDNRPATAFVIACVLE LISTIYMAASIGTDFWYEYRSFVQBNSSDLINKSIWDEFISDRAD EKTYNDALFRINGTVGLWRRCCTTIPKNMENYSPRETESFDVVT KCVSPTLTERQFWBKFVDFORNHSGIDLIRTYLWRCQFFLDFVSL GLMCFGALLIGLCACICESLYPTIATGTHHLAGLCTLGSVSCYV AGIELLHQRLELPDNVSGEFCNSFCLACVSAPIPKDFPSLEFFUS GLMCFGALLIGLCACICESLYPTIATGTHHLAGLCTLGSVSCYV AGIELLHQRLELPDNVSGEFCNSFCLACVSAPIPKASALFINA AHTNRKEYTIMKAYRVA  6418 2 662 TRTEPRRPPGGGAAVGKAGGASTSTPAGASPAAVQADPPPPAH FARPPPPPPCGGAAVGKAGGASTSTPAGASPAAVQADPPPPAH FARPPPPPCGGAAVGKAGGASTSTPAGASPAAVQADPPPPAH FARPPPPPCGGAAVGKAGGASTSTPAGASPAAVQADPPPPAH FARPPPPPCGGAAVGKAGGASTSTPAGASPAAVQADPPPPAH FARPPPTLISHEREPPVLTRRRRIEVSTALGATDSIGLEBIL PSPDPVTVPYLSPLVWKELESLLENEGDHAITVADPVOHHPIV FNNLWWYRRIADLESKILDSRHCLKYSKIPHCMSEDSKY VLIQMIMNNMILHQDDGQPLYLINMATTQCATDSIGLERHL PSPDPVTVPYLSPLVWKELESLLENEGDHAITVADPVOHHPIV FNNLWWYRRIADLESKILDSRHCINKTSKIPHCNSEDSKY VLIQMIMNNMILHQDGOQPLYLINMATTQCYTWHILLGKSNISF NOBLIKSMYKSIKNNDVYGPMSQILETINKCPHFKRQRSLYRBT LPISLVALGRRNDTIDLADFKBYKMAYDRTYPSQVKSTINCORPP STGWECKKTFGBPYL  6420 207 1187 RINIDKNGTGVGQOSVPWINICLATHILERNFGVGLEDYLAFAN MANGGARKTVATIMDGERAVMIGYSVIGMBRIPERGPSLLLDWPC ALHGFREKCVSILRSGHLLAISPGGVKRALISDSTYLNVKHERX MANGGARKTVATIMDGERAVHIGYSVIGMBRIPERGDPALLITPYH GAIPDFYYFMAKIFTHLLAISPGGVKRALISDSTYLNVKHERX	0.772	1 4	1100	I .
LEKQFTDLKOQLYKERLSQUDAKLQEVIACKAPEYLEDLATLQE NMQIRTKVAGIYRELCLESVKNKYKGETQASRQHCESKKLLIYD TVQSKLEKERIRLISEDRRISIDITSELMNDELQSRKKRKDPFWPD KKKPGVVSGPYIVYMLQDLDILEDWTTIRKAMATLSPHRVKTEP PVILKEKHLISABSERSGRIYYTOGBETRAGYICIDEKGRCPTSAV ITTINDEWWPKRPDGSKSKIYISQLQKGKYSIKHS 6416 410 1519 EIAFADLEIPACAPULLSRTSSTMSVTGAQALGRAFSTGETISCHAPSLITQEILSHL GLASKYAAMGTLGTLETPIANSVDKDAQRLLRAITQQGVDRSAI VDVLTMRSERGRQLISRNFQRTQDDMKSLQAALSGNLERIVM ALLQJYAQFDAQBELATAKAADSAVDIS ILLATPPOPQLGEL AVYKHNFQVEAVDGITSETSGILQDLLLALAKGGRDSYSGILDY NIAEQDVQALQRAEGPSREETWYPVTYORIPELLIKVFDQYGRS TGGELEERAYQNRFHGDAQVALLGLASVIKNTPLIYEAPDLJGELL AVYKHNFQVEAVDGITSETSGILQDLLLALAKGGRDSYSGILDY NIAEQDVQALQRAEGPSREETWYPVTYORIPELLIKVFDQYGRS TGGELEERAYQNRFHGDAQVALLGLASVIKNTPLIYEAPDLJGELD KGDQSALLALCRAELM  6417 1 845 RGESRVIMSELEGRAGGAGMASSINARMDNRFATAFVIACVLS EKTYNDAJLFRINGTVGLWRRCITIFNMINSSPPRETRSFDVVT KCVSPTLTEQPMSKPVDFVGNINSGIDLLRTYLWRCQPILDFVSL GEMCPGAALIGLCACICRSLYPTIATGILHIJGLGTLGSVSCYV AGIELHICKLELPDNVSGEPCMSFCLACVSAPLGYMASALFIWA AHTMREYTIMRAYKVA AFIELHICKLELPDNVSGEPCMSFCLACVSAPLGYMASALFIWA AHTMREYTIMRAYKVA TTREPREPPGCLGAAVGKAGARSTSTPAGASPAAAVQADPPPPAH TPAPPPPPPCGIACHGEPAKFYGYDNLQRQPIPTTQQBAKLVQ YPDCKSSGINIGEDDDILMDSSSPSQMFPMMRQAAFGRRGRGR TYSFFQTLLEIREFLIFNFYLTIKRIS USSHALALTERQVIK IMFO NRMKNKKINNIDKEPPSRGVKOGETKKEAQBLEEDRABGLIN PGRPRVNIPTLEILEFLIFNFYLTIKRIS USSHALALTERQVIK IMFO NRMKNKKKNINKDKPPVSRGVKOGETKKEAQBLEEDRABGLIN PSPDPYTVPYLSPLVVMKELESLLENGGDEATTVADFVDHHPIV PFINLWYPRICLDLSPINLGGILLASHINKYSKIPHCHSBDSKY VLIQMLMINMKLHQDPGQPLYILMNABTQKYPMVHLLQKSDINSP NQBLIKSMYKSIKMIDMPGROSULEETLINKCPHFKRGRSLYRBI VLIQMLMINMKLHQDPGQPLYILLEENFGVEQLEDYINFAN VLIQMLMINMKLHQDPGQPLYILLEENFGVEQLEDYINFAN VLIQMLMINMKLHQDPGGPLGLHTLEENFGVEQLEDYINFAN VLLWYFRILLILDFYFTIFLLILTITIFLHYKKRNVLKRAYSK NLMDGARKTVATIMDGIRAWWHGYENGHKERLFBGPALITPYH GAPIPTYFMAKIF PLIKGRTCRVAADHPVPKIPGPSLLLDVPC AHLGGREKCVETLINSGHLALISDGVARRALISDBTYNLVMGHRK NLMDGARKTVATIMGGIRAWHGYEVHGMSK LTEBGPALLIDVPC AHLGGREKCVETLINSGHLALLSPGGVARALISDBTYNLVMGHRK		l	ļ	
MMOIRTRVAGIYRELCIRSVENKRYBCEIQASRKRKRDFFWPD TVQSELEEKIRRIEEDRHSIDITSELMDELQSRKKRKDFFWPD KKKPGVVSGPYIVYMLQDIDILEDWTTIRRAMATLSPHRVKTEB PVKLERHLISABSEEGRIYYDGBWYIKGGYICIDKKDECFTSAV ITTINIDEWPKRRPDGSKSKULTJGLGKGKYSIKHE 6416 410 1519 EIAFADLEIPACAFVLLSRATSSTMSVTGGKMAPSLTQEILSHL GLASKTAAMGTILGTLRTFLNSVDKDAQRLIKARITGQGVDRSAI VDVLTRRSERGRQLISRHPQERTGDDLMKSLQAALSGNIERIVM ALLQPTQAGPBAGBLETALKASDSAVDVAIRILATRTPPOLQECL AVYKHNFQVEAVDGITSETSGILQDLLLALAKGGRDSYSGILDY NLAEQDVQALQRAEGPSREETWVPYTQNRPEHLIRVFDQVQRS TGGELEEAVQNRPHGDAQVALLGLASVINNTPLYFADKLHQALQ ETEPNYQVLIRILISRCSTDLLSIRABFRKKPGKSLYSSLQDAV KGDCOSALLALCRAEDM 6417 1 845 RGESRVIMSELEGEAGGAGGGASSINARMDNRFATAFVIACVLE LISTIMAASICTDWYSYRSPVQENSSDLNKSIMDEFISDRAD EKTYNDALFRYNGTVGLWRRCITIPKMMWYSPPERTRSFDVVT KCVSPTLTRQPMSKVVDFGWINSGIDLARTJURCQPFLDPFVSL GMCMPGAALIGLCACICGSSLYPTLATGILHLAGLCITLSSVSCTVV AGIELHIQKLERPDNVSGEPGMSFCLACVSAPLQFMASALFIWA AHTMRKSTIMKAYRVA AHTMRKSTIMKAYRVA AHTMRKSTIMKAYRVA TPAPPPPPPGGIJAANGKAGARSTSTPAGASPAAAVQADPPPPAH TPAPPPPPPGGIJAANGKAGARSTSTPAGASPAAAVQADPPPPAH TPAPPPPPPGGIJAANGKAGARSTSTPAGASPAAAVQADPPPPAH TPAPPPPPPGGIJACHGEPAKFYGYDNLORGPIFTTQQBABLVQ YPDCKSSSGNIGEDDDHLMDSSSSPSQMFPMMPQAAPGRRGRGG TYSRFQTLELEKEFLIFNPYLTRKRRIEVSHALALTERQVKIWFQ NRRMKKKKINNBOKEPVSRGEVKOGETKKRAGLEEDRABGLITN PGEPREVRINDLINGSLIGGBFFGKRAGLEEDRABGLITN PGEPREVRINDLINGSLIGGBFFGKRINGYSFIPHCHSBDSKY VLIQMINDMMKHQDPGGPLYILMMABTQKYPMVHILQKSDNSP NOELLKSMVKSIINMDVYGPUSQLEPTINKCPHFKRORSLYKR VLIQMINDMKHRJOPGGPLYILMMABTQKYPMVHILQKSDNSP NOELLKSMVKSIINMDVYGPUSQLEPTINKCPHFKRORSLYKR LTISLVALGRENIDIDAPDREYKMAYDRUTPSQUSSTHNCORPP STGVMECRKTFGEPYL  6420 207 1187 RMIDKNQTGRVGQDSVPYMICLIHILEENFGUEQLEDYLNFAN VLLWVETPLILLILIPYFTIPLLIKITIPHIVKRRNVLKRAYSE NUMDGARKTVATIMDGIHAAWHGYEVIGMSKIPBGPALILPYH GAPIPYYFMAKIPHINGGIHAAWHGYEVIGMSKIPBGPALILPYH CHAHGEREKCVETILRSGHLLALSPGGVKRALISBGFLLLDVFG				
TVQSELBERIERLERDRISIDITSELMNDELQSRKKRKDPFWPD KKKRFGVVSGPYIVYMLQDLDILEDWTITGET PVKLERHLHSARSEBGRILYTDGBWYIRGQTICIDKDBCPTSAV ITTINIDEWWFRPDGSKSKLYTSQLQKGKYSTKHS  6416 410 1519 EIAFADLEIPACAFVLLSRATSSTMSVTGGKMAPSLTQBILSHL GLASKTAAMGTLGTLRTFLANSVDKDAQRLLRAITGQGVDRSAI VDVLTMRSEBGRQLISRNFQBTQDLMKSLQAALSGNIBRIVM ALLQPTAQFDAQBLRTALKABDSAVDVAIBILATRTPPQLQBCL AVYKINFQVBAVDGITSETSGILQDLLLALAKGRDSYSGILDY NLAEQDVQALQRAEGPSRBETWVVFTQNFBELLRVFDQVGRS TQGLEBEAVONRFHEDAQVALLGLASVIRNFDLYFADKHQDALQ ETEPNYQVLIRILISRCSTDLLSIRAEFRKKPGKSLYSSLQDAV KGDCOSALLALCRABUM 6417 1 845 RESERVINSELEGRAGGAGGASSINARMINRFATAFVIACVLS LISTIYMAASIGTDFWYEYRSPVQENSSDLIKSIMDEPISDBAD EKTYNDALFTRWGTVGLWRRCITIPKNMINSPPBRTBSFDVVT KCVSPFLITRQPMEKFVDFGNINSGIDLLRYJLWRCQFLLPFVSI GLMCPGAALIGLCACICSSLYPTIATGILHLAGLGCTLGSVSCYV AGIELLHQKLELDDNVSGBPGWSFCLACVSAPLQFMASALFIWA AHTMREWTIMMAXRVA AHTMREWTIMMAXRVA 6418 2 662 TKYRPAPPPPPGGIACHGEPAKFYGYDNLQRQPIFTTQQBABLVQ YPDCXSSSGNIGEDPDHLINGSSSPSQMFPWMPQAAPGRRGRG TYSRFQTLSLEBEFLFNFYLIRKRRIEVSBALALFERQVKIWFC NRRMKKENNKDRFPVSRQEVKOGBTKKBQOBLEBDRAEGLIN PSPDPVTVPYLSPLVWKELESILEBEGDATTVADFVDHIPIV FWNLWYFRRDLDSSNIGULSSEHCNRYSKIPHCMSBDSK VLIQMIMNDMKLHQDPGGPLYILMNAHTQXFYMVHILLQKSDNSF NQELLKSWVKSIKMNDIDDAFDRSYKMAYDRITRACPHYRFRRIERDFSLIPFS TSTWHECRRTFGEPYL 6420 207 1187 RMMIDKNQTGGVGQDSVPYMICLIHILERHFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIPLLXITIIFLHILKRCPHFKRQRSLYRBH NLMGGRRKTVATIMGGHAAWHGYBVHGHBKITEBGPALITPYH GAPIPDFYYFMAKIFIHKGRTCRVAADHVPVFRIPGPSLLLDVFG AHGGREKCVETILRSGHLLAISFGGVRRALISDETYNIVKHERR				
KKKPGVVSGPIIVYMLQDILDILEDWTIRKAMATIGPRRVKTEP PVKLEKHLHSARSEBGRLYYDGBWTIRGYIICIDKKDECPTSAV ITTINIDEWWFKRPDGSKSKLYISQLQKGKYSIKHS 6416 410 1519 EIAPADLEIFPACAPVALISRATSSTMSVTGGKMAPSLTQEILSHL GLASKTAAWGTLGTLETPILDSVDKAQRLLRAITGQGVDRSAI VDVUTMRSREQRQLISRNFQERTQQDLMKSLQAALGGNLERIVM ALLQPTAQFDAQELRTALKASDSADVJAIRILATHTPPQLQECL AVYKHNFQVEANDGTISRTGSGLQDLLLALAKGGDSVSGIIDY NLAEQDVQALQRAEGPSRETWVPVFTQRNPEHLIRVFDQXQRS TGQELEEAVQNRRHGDAQVALLGLASVIKNTPLYFADKLHQALQ ETEPPNYQVLIRILISRCETDLLSIRABFRKKFGKSLYSSLQDAV KGDCQSALLALCRABUM 6417 1 845 RGESRULWSELEGEAGGAGGWASSLNARMDNRFATAFVIACVLS EKTYNDALFRYNSTVGLWRRCLTIPKNMEWSPPBRTBSFDVVT KCVSPTLTBQPMSEVDPGONNSGDLMKSIWDEFISDEAD EKTYNDALFRYNSTVGLWRRCLTIPKNMEWSPPBRTBSFDVVT KCVSPTLTBQPMSEVDPGONNSGDLMKSIWDEFISDEAD EKTYNDALFRYNSTVGLWRRCLTIPKNMEWSPPBRTBSFDVVT KCVSPTLTBQPMSEVDPGONNSGDLMKSIWDEFISDEAD EKTYNDALFRYNSTVGLWRRCLTIPKNMEWSPPBRTBSFDVVT KCVSPTLTBQPMSEVDPGONNSGDLMKSIWDEFISDEAD EKTYNDALFRYNSTVGLWRRCLTIPKNMEWSPPBRTBSFDVVT KCVSPTLTBQPMSEVDPGONNSGDLMRSITWDEFISDEAD EKTYNDALFRYNSTVGLWRRCLTIPKNMEWSPPBRTBSFDVVT KCVSPTLTBQPMSEVDPSPCHAGGGAGASSLAPAQADPPPPHH ATHREYTIMKANFVA AHTMREYTIMKANFVA AHTMREYTIMKANFVA  6418 2 662 TRTEPRPPPEPCGGIACHGEPAKFYGYDNLQRQFIFTTQQRABLVQ YPDCKSSGNIGEDPHLMOSSPSQMFPWRPQAAPGARGRG TYSRPQTLBLEKEPILPNYLTRKRIEVSHALALTERQVKIWFO NRRMKKKKSNNIDKPFVSRQEVKGGETKKRAQBLEEDRAGGLIN MARSISTSGPLDKEDTGROKLISTGSLPATLQCATDGLGLEWHL PSPDPVTVPYLSPLVVWKELESLLENGCHAITVADPUHHPIV PNNLWWFFRLDLPSNLGCLILSSBHCKKYSKIPHCMSBDSKX VLIQMINDNMKLHQDPGGPLYILMNAHTQKYPMVHLLQKSDNSP NQELLKSMVKSIKMIDDLAPDKSKMAYDRLTESQVKSTHNCDRPP STGVMSCRKTFGGPYL  FRMILWWFTRILDLPSNLGCLILSSBHCKKYSKIPRHCMSBDSKX VLIQMINDNMKLHQDPGGDPLYLINNAHTQKYPMVHLLQKSDNSP NQELLKSMVKSIKMIDDLAPDKSKMAYDRLTESQVKSTHNCDRPP STGVMSCRKTFGGPYL  FRMILWYFRILDLLPSTIPLLYLTIILHTYRKRNVIKERYSH NLWGGRRKYVATIMGGHBAVHIGYBVHOMERIPBDGPALLIPYH GAIPIDPYYFMAKIPTHLKGTCKVADADHFVFRIPGSLLLDVPG ALHGPREKCVETLRSGHLLAISPGGVRALLSDBTYNIVKSHRR				1
PVKLEKHLHSARSEBGRLYYDGBWYIRGQTICIDKKDECPTSAV				•
ITTINHDEWBYKRPDGSKSKLYISQLQKKYSIKHS				KKKPGVVSGPYIVYMLQDLDILEDWTTIRKAMATLGPHRVKTEP
6416 410 1519 EIAPADLEIPACAPVILSRATSSTMSVTGGKMAPSLTQEILSHL GLASKTAAMGTILGTLRFTLABSUVDKDQRLLRAITGGGVDRSAI UDVITNRSREGQGLISSRIPGERTQDDLMKSLQAALSGRILBRIVM ALLQPTAQPDAQBLRTALKASDSAVDUAIBILATRTPPQLQECL AVYKHHFQVBAVDGITSETTGGILQDLLALAKGGRDSYSGILDY NIALBQDVQALQRAEGPSREETWVPVFTQNRFHLIRVPGYQRS TGQELEBAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHQALQ BTEPNTQVLIRILISRCETDLLSIRABFRKKFCKSLYSSLQDAV KGDCOSALLALCRABUM AGGCOSALLALCRABUM EKTYNDALFRYNGTVGLMRGCTIPKMMEMYSPPERTRSFDVVT KCVSPTITRQPMBEFYDDGCNRSSDLNKSIMDEFISDBAD EKTYNDALFRYNGTVGLMRGCTIPKMMEMYSPPERTRSFDVVT KCVSPTITRQPMBEFYDDGCNRSGLLACVSAPLQFMASALFIWA AHTNRKSYTLMKAYRVA  6418 2 662 TKTEPRPPGLGAAVGKAGARSTSTPAGASPAAAVQADPPPPAH TPAPPPPPGGTACHGEPMSFCUACVSAPLQFMASALFIWA AHTNRKSYTLMKAYRVA  6419 1 973 FGRPRVNFDGLGSAVGKAGARSTSTPAGASPAAAVQADPPPPAH TPAPPPPPPGGGTACHGEPAKFYGYDNLQRQPIFTTQQRABLVQ YPDCKSSSGNIGEDPDHLNGSSSPSQMFPMMRPQAAPGGRRGRQ TYSRFQTLBLEKEFILFNPYLTRKRIEVSHALLLITERQVKI MPQ NRRMKKKRNNKDKPPVSRGVKDGTKKRBQGLIEBDRABGLIN PSDPVTVPYLSLVWKELESLLBNSGDBLATTAQATDSLGLEWHL PSDPVTVPYLSLVWKELESLLBNSGDBLATTADGVUHHPIV FWNLVWYFRRLDLPSNLPGLILSSBCNKYSKIPRICMSBDSKY VLIQMIMDINNKLHQDPSQPLYILMNBATGYYPWHLLQKSDNSP NGELLKSMWSI KUNDVYGTGDLIFTLANCFUFFKRGRSLYBEI LFISLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGERYLL FRANDTENTER 6420 207 1187 RKMIDANGTGGOGOSVPYMICLIHILEBNFGUEQLEDYLNFAN YLLWVFTPLILLILPYFTIFLLYLTIJPHIYKRKNVLKEAYSH NLWDGARKTVATIMOGHAAVWHGYBVHGMSKIPEDGPALIIPYH GAIPIDPYYFMAXIPHLKGRTCXVADHFVPKT PGFSLLLDVYC ALHGPREKCVETLRSGGHLALISPGGVRKALISDBTYNIVWGHRR				PVKLEKHLHSARSEBGRLYYDGBWYIRGQTICIDKKDECPTSAV
GLASKTAAWGTLGTLRTPINFSVDKDAQRLIRAITGQGVDRSAI VDVLTRRSBEQRQLISBNPGERTQQDLMSLQAALSGNLBRIVW ALLQ7TAQFDAGBLRTALKASDSAVDVAIB LLARTTPPGLQECL AVYKHNFQVEAVDGITSETEGILQDLLLALAKGGRDSYSGIIDY NLAEQDVQALQRAEGEPSRETWYPV*TQRNFEHLIRVPDQYGRS TGGELEBAVQNRFHGDAQVALLGLASVIKNFPLYFADKLHQALQ ETEPNYQVLIRILISRCETDLLSIRAEFRKKPGKSLYSSLQDAV KGDCQSALLALCRABDM  6417 1 845 RGESRVLWSSLGEGAGGAGGWASSLNARMDNRFATAFVIACVLS LISTIYMAASIGTDFWYEYRSPVQENSSDLINKSIWDEFISDBAD EKTYNDALFRYNGTVGLWRRCITTPKNMEWYSPPERTRSFDVVT KCVSPTLTBQFMEKFVDPGNNHSGIDLLRTYLWRCQPLLPFVSL GIMCFGALIGLCACICESLYFTLATGILHLAGGCTIGSVSCTV AGIELLHGKLBLPDNVSGEFGWSFCLACVSAPLQFMASALFIWA AHTNRKEYTLMKAYRVA AHTNRKYTLMKAYRVA AHTNRKEYTLMKAYRVA TPAPPPPPPGGGAAVGKAGARSTSTPAGASPANAYQADPPPPAH TPAPPPPPPGGGAAVGKAGARSTSTPAGASPANAYQADPPPPAH TPAPPPPPPGGGAAVGKAGARSTSTPAGASPANAYQADPPPPAH TPAPPPPPPGGGAAVGKAGARSTSTPAGASPANAYQADPPPPAH TPAPPPPPPGGGAAVGKAGARSTSTPAGASPANAYQADPPPPAH TPAPPPPPPGGGAAVGKAGARSTSTPAGASPANAYQADPPPPAH TPAPPPPPPGGGAAVGKAGARSTSTPAGASPANAYQADPPPPAH TPAPPPPPPGGGAAVGKAGARSTSTPAGASPANAYQADPPPPAH TPAPPPPPPGGGAAVGKAGARSTSTPAGASPANAYQADPPPPAH TPAPPPPPPGGAAVGKAGARSTSTPAGASPANAYQADPPPPAH TPAPPPPPPGGAAVGKAGGARSTSTPAGASPANAYQADPPPPAH TPAPPPPPPGGAAVGKAGGARSTSTPAGASPANAYQADPPPPAH TPAPPPPPPGGAAVGKAGGARSTSTPAGASPANAYQADPPPPAH TPAPPPPPPGGAAVGKAGGARSTSTPAGASPANAYQADPPPPAH TPAPPPPPPGGAAVGKAGGARSTSTPAGASPANAYQADPPPPAH TPAPPPPPPGGAAVGKAGGARSTSTPAGASPANAYQADPPPPAH TPAPPPPPPGGAAVGKAGGARSTSTPAGASPANAYQADPPPPHAH PARSISTSGPLDKEPTLTRKRIEVSHALALITERQVINFWINFUN FPANAYNY TPAPPPPPTGGAAVGKAGARSTSTPAGASPANAYQADPPPPHAH PSPDPVTVPYLSPLVWKELESLLENEGDHAITVADFVOHHPIV FNNLWWYFRIDLDESHLEKEPLNPYLIRKRIZGATDSLGEWHL PSPDPVTVPYLSPLVWKELESLLENEGDHAITVADFVOHHPIV FNNLWWYFRIDLDESHLUANHATQWYPWHLLQKSDNSF NOBLLSMWKSIKMOVGPUSGILETLINCCPHFKRQRSLYRBI LFLSLVALGRENIDDIDAFDKSYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGEPYL  6420 207 1187 RKNIDKNQTCGVGQDSVPYMICLIHILERNFGUEQLEDYLNFAN YLLWVFTPLILLILPYFTIFLLYLTIIVHNYKRKNVLKEAYSH NLWDGARKTVATIMOGHAAVWHGYSVHGMSKIPGBGEDPALITPH GAIPIDFYYFMARKIFFHAGGRAUADHYNGHAKUFGBSLEDVNIVNGHRR ALKGPREKCVEILRSGHLLAISPGVVRALISDETY		1		ITTINHDEVWFKRPDGSKSKLYISQLQKGKYSIKHS
VDVLTNRSREQRQLISRNFQERTQQLMKSLQAALSGNLERIVM ALLQPTAQFDAQBLRTALKASDSADVATBILATRTPPPQLQECL AVYKHNEQVEAVOGITSETSGILQDLLJALKAGGRSPYSGILDY NLAEQDVQALQRAEGPSREETWVPYTQRNPEHLIRVFDQYQRS TGGELEEAVQNRFHSDAQVALLGLASVIRNTPLYFADKLHQALQ ETEPNYQVLIRILISRCETDLSIRAEFRKKPGKSLYSSLQDAV KGDCOSALLALCRAEUM KGDCOSALLALCRAEUM  6417 1 845 RGESRYLWSBLEGEAGAGAGWASSLNARMDNRFATAFVIACVLS LISTIYMAASIGTDFWYEYRSPVQENSSDLNKSIWDEFISDRAD EKTYNDALFRYNGTVGLWGRRCITIPKNMENYSSPPERTSBROVYT KCVSPTLTEQFMEKFVDPGNHNSGIDLLETYLWRCQFLLPFVSL GIMCFGALIGLCACICESLYPTIATGILHLAGLCTIGSVSCTV AGIELLHQKLELPDNVSGEPGMSFCLACVSAPLQFMSSALFIWA AHTMREYILMKAYRVA AHTMREYILMKAYRVA  6418 2 662 TKTEPREPPGIGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH TPAPPPPPPPGGGIACHGEPAKFYGYDNLQRQPIPTTQGRAELVQ YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRRGRQ TYSRFQTLELEKEFLFNPYLTRKRIEVSHALALTERQVKIWFQ NRRMKKKKENNKDKPPVSRQEVKUGETKKBAQBLEEDRAEGLIN 6419 1 973 PGRPVNRFDLINSKSILQEFFCTRSIQIPANRSKTAMSKCPIPP MARSISTSGFLDKEDTGROKLISTGSLPATLQGATDSLGLEWHL PSDPVTVPYLSPLVWKELESLLENEGDHATTVADFVDHHPIV FWNLVWYFRRLDLPSNLPGLILSBENCNKYSKIPRHCMSEDSKY VLIQMINDNNKLHQDPGGPLVILMNAHTQKYPMVHLLQKSDNSF NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYRBI LFTISLVALGRENIDIDAFDKSYKMAYDRLTPSQVKSTHNCDRPP STGVMECKKTFGEPYL  6420 207 1187 RRMIDKNQTCGVGQDSVPYMICLTHILEEWFGUEQLEDYINFAN YLLWVFTPLILLILPYFTIPLLYLTIIPHIYKRRNVLKBAYSH NUMDGARKTVATIMDGHAAVHRGYTCKVVADHEVFRIPGGPALIIPYH GALPIDFYYFMAKIFIHKGTTCKVVADHEVFRIPGGFALLIDVFC GALPIDFYYFMAKIFIHKGTTCKVVADHEVFRIPGGFALLIDVFC GALPIDFYYFMAKIFIHKGTTCKVVADHEVFRIPGGFALLIDVFC	6416	410	1519	EIAPADLEIPACAPVLLSRATSSTMSVTGGKMAPSLTQEILSHL
ALLQPTAQFDAQBLRTALKASDSAVDVAIBILATRTPPQLQECL AVYKHRPQVEAVDGITSSTSGILQDLLALAKAGGRSYSGILDY NLAEQDVQALQRBEGPSRETWPVPTQNRPEHLIRVPQDYQRS TGQELEEAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHQALQ ETEPNYQVLIRILISRCETDLLSIRABFRKKPGKSLYSSLQDAV KGDCQSALLALCRABDM  6417 1 845 RGESRVLWSELGGRAGGGGWASSLNARMDNRPATAFVIACVLS LISTIYMAASIGTDFWYBYRSPVQBNSSDLNKSIWDEPISDRAD EKTYNDALPRYNGTVGLWRRCITIPKNMEWYSPPERTBSFDVVT KCVSPTLTBQFMBRKFVDPGNINSGIDLLRTYLWRCQFLLFFVSL GLMCFGALIGLCACLCRSLYPTIATGILHLAGLCTLGSVSCTV AGIELLHQKLELPDNVSGEFGWSFCLACVSAPLQFWASALFIWA AHTNRKSTITMKAYRVA  6418 2 662 TKTEPRPPGLGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH TPAPPPPPCGGIACHGEPAKFYGFONLQRQFIFTTQQRABLVQ YPDCKSSSGNIGEDPDHLNQSSSPSQMPFWRPQAAPGRRGRQ TYSRFQTLBLEKEFLFNPYLTRKRRIBVSHALALTERQVKIWFQ NRRMKWKKNNKDKPPVSRQBVKDGETKKBAGBLEBDRAGGLIN PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADFVDHHPIV PHNLWYFRRLDLFSNLFGLILSBHCNKYSKIPRHCMSGBSKY VLIQMLWDNMAKHQDPGGPLVILMNAHTQKSYMPWHLLQKSDNSF NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYRBI LFISLVAALGRRNTDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGBPYL STGVMECRKTFGBPYL ALHGPREKCVEILRSGHLAUSTRIPCHYRIPGGLALDIFYC GAIPIDFYYFMAKIPIHGRTCKVVADHFVRIPGGELLLDVFC GAIPIDFYYFMAKIPIHGRTCKVVADHFVRIPGGELLLDVFC GAIPIDFYYFMAKIPIHGRTCKVVADHFVRIPGGELLLDVFC GAIPIDFYYFMAKIPIHGRTCKVVADHFVRIPGGELLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRRALISDETYNIVWGHRR				GLASKTAAWGTLGTLRTFLNFSVDKDAQRLLRAITGQGVDRSAI
ALLQPTAQFDAQBLRTALKASDSAVDVAIBILATRTPPQLQECL AVYKHRPQVEAVDGITSSTSGILQDLLALAKAGGRSYSGILDY NLAEQDVQALQRBEGPSRETWPVPTQNRPEHLIRVPQDYQRS TGQELEEAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHQALQ ETEPNYQVLIRILISRCETDLLSIRABFRKKPGKSLYSSLQDAV KGDCQSALLALCRABDM  6417 1 845 RGESRVLWSELGGRAGGGGWASSLNARMDNRPATAFVIACVLS LISTIYMAASIGTDFWYBYRSPVQBNSSDLNKSIWDEPISDRAD EKTYNDALPRYNGTVGLWRRCITIPKNMEWYSPPERTBSFDVVT KCVSPTLTBQFMBRKFVDPGNINSGIDLLRTYLWRCQFLLFFVSL GLMCFGALIGLCACLCRSLYPTIATGILHLAGLCTLGSVSCTV AGIELLHQKLELPDNVSGEFGWSFCLACVSAPLQFWASALFIWA AHTNRKSTITMKAYRVA  6418 2 662 TKTEPRPPGLGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH TPAPPPPPCGGIACHGEPAKFYGFONLQRQFIFTTQQRABLVQ YPDCKSSSGNIGEDPDHLNQSSSPSQMPFWRPQAAPGRRGRQ TYSRFQTLBLEKEFLFNPYLTRKRRIBVSHALALTERQVKIWFQ NRRMKWKKNNKDKPPVSRQBVKDGETKKBAGBLEBDRAGGLIN PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADFVDHHPIV PHNLWYFRRLDLFSNLFGLILSBHCNKYSKIPRHCMSGBSKY VLIQMLWDNMAKHQDPGGPLVILMNAHTQKSYMPWHLLQKSDNSF NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYRBI LFISLVAALGRRNTDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGBPYL STGVMECRKTFGBPYL ALHGPREKCVEILRSGHLAUSTRIPCHYRIPGGLALDIFYC GAIPIDFYYFMAKIPIHGRTCKVVADHFVRIPGGELLLDVFC GAIPIDFYYFMAKIPIHGRTCKVVADHFVRIPGGELLLDVFC GAIPIDFYYFMAKIPIHGRTCKVVADHFVRIPGGELLLDVFC GAIPIDFYYFMAKIPIHGRTCKVVADHFVRIPGGELLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRRALISDETYNIVWGHRR		İ		VDVLTNRSREOROLISRNFOERTOODLMKSLOAALSGNLERIVM
AVYKHNFQVEAVDGITSETSGILQDLLLALAKGGRDSYSGIIDY NLAEQDVQALQRAEGPSRETTWPYFTQRNFEHLIRVFDQYQRS TGQELEEAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHQALQ ETEPNYQVLIRILISRCETDLLSIRAERKKFGKSLYSSLQDAV KGDCOSALLALCRAEUM  6417 1 845 RGESRVLWSELEGEAGGAGWASSINARMDNRFATAFVIACVLS LISTIYMAASIGTDWYEVRSPVQENSSDLNKSINDEFISDRAD EKTYNDALFRYNGTVGLWRRCITIPKNMEWYSPPERTBSFDVVT KCVSPTLTBQFMBKFVDPONHNGSIDLLRTTLWRCQFLLBFVSIL GLMCFGALIGLCACICRSLYPTIATGILHLLAGLCTLGSVSCYV ACTELLHQKLELPDNVSGEPCWSFCLACVSAPLQFMASALFIWA AHTNRKSYTLMKAYRVA  6418 2 662 TRTPRRPDGLGAAVGKAGARSTSTPAGASPAAYQADPPPPAH TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQFIPTTQQRABLVQ YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRRGRQ TYSRFQTLBLEKEFILPNPYLTRKRIEWSHALALTERQVKIWFQ NRRMKKKENNKDRPPVSRQEVKDGETKKBAQELEEDRAEGLIN MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL PSDDPVTVPYLSPLVVWKELESLLENBGDHATVADFVDHHPTV FWNLVWYFRRLDLPSNLVGLILSSBHCNKYSKIPRHCMSEDSKY VLIQMLWDNNKLHQDPGQPLYLIWNAETGXYPWWHLLQKSDNSF NQBLLKSMVKSIKMDVYGPMSQLLETLNKCPHFKRQRSLYRBI LITISLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECKKTGEPYL  6420 207 1187 RKMIDKNQTCGVGQDSVPMICLIHILEWFGUEQLEDYINFAN YLLWVFTPLILLILPYFTIFLLYLTIIPHHYKRRNVLKEAYSK NLWDGARKTVATLWDGHAAVGYEVHGMEKIPEDGFALLIPYH GAIPIDPYYFMAK IF HIKGRTCRVVADHFVFKR PGFSLLLIDVFC ALHGPREKCVEILRSGHLLALSPGGVRRALISDETYNIVWGHRR		İ		
NLAEQDVQALQRAEGPSREETWVPVFTQRNPEHLIRVFDQYQRS TGGELEBAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHQALQ ETEPNYQVLIRILISRCETDLLSIRAEFRKKFGKSLYSSLQDAV KGDCQSALLALCRABIM  6417 1 845 RGESRVLMSELEGEAGGAGGMASSLNARMDNRFATAFVIACVLS LISTIYMAASIGTDFWYEYRSPVQBNSSDLMKSIMDEFISDRAD EKTYNDALFRYNGTVGLWRRCITIPKNMEWYSPPERTBSFDVAD EKTYNDALFRYNGTVGLWRRCITIPKNMEWYSPPERTBSFDVAT KCVSPTLTEQFMEKEVDPONHNSGIDLLRTYLWRCQFFLDFFVSL GLMCFGALIGLCACICRSLYPTIATGILHLLAGLCTIGSVSCYV ACTELLHQKLELPDNVSGEPCMSFCLACVSAPLQFMASALFIWA AHTMRESTLMMAYKVA  6418 2 662 TRTEPRRPPCLGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQPIPTTQQRABLVQ YFDCKSSSGNIGEDPDHLMQSSSPSQMFPWWRPQAAPGRRGRG TYSRFQTLELEKEFLFNPYLITRKRIEVSHALALTERQVKIWFQ NRRMKWKKENNKDKPPVSRQEVKDGETKKEAQBLEEDRAEGLIN NRRMKKKKENNKDKPPVSRQEVKDGETKKEAQBLEEDRAEGLIN PSPDPVTVPYLSPLVWKKELESLLENEGDHAITVADFVDHHPIV PWNLWWYFRRLDLPSNLFGLILSSBHCNKYSKIPHCMSEDSKY VLIQMLWDNMKLHQDPGQPLYILWNAETQKYPMVHLLQKSDNSF NQELLKSMVKSIKMDVYGPMSQILETLINCCPHFKRQRSLYRBI LFISLVALGRENIDIDAPKEYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTTGEPPIL  6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEWFGVEQLEDYINFAN YLLWVFTPLILLILPYFTIFLLYLTIIFHHYKRRNVLKEAYSH NLWDGARKTVATLWDGHAAVGYEVHGMEKIPBGGFSLLIDVFC GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKR PGFSLLLIDVFC ALKGPREKCVEILRSGHLLAISPGGVRRALISDETYNIVWGHRR		<b>i</b> .		1
TGQELEEAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHQALQ ETEPNYQVLIRILISRCETDLLSIRABFRKKFGKSLYSSLQDAV KGDCQSALLALCRABUM KGDCQSALLALCRABUM RGESRVLWSRILBEBAGGAGGWASSINARMDNRFATAFVIACVLS LISTIYMAASIGTDFWYEYRSPVQENSSDINKSIWDEFISDEAD EKTYNDALFRYNGTVGLWRRCITIIRNMYSPPERTBSFDVVT KCVSPTILTBQPMBKFVDPGNINSGIDLLRYYLWRCQFLLPFVSL GIMCFGALIGLCACICRSLYPTIATGILHILAGLCTICSVSCTV AGIBLLRQKLBIPDNVSGEFCWSFCLACVSAPLQFMASALFIWA AHTMRKEYTLMKAYRVA AHTMRKEYTLMKAYRVA  6418 2 662 TRYEPREPGIGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH TPAPPPPPPPCGIACHGEPAKFYGYDNLQRQPIPTTQQRABLVQ YPDCKSSSGNIGEDPDHINQSSPSQMFPMMRPQAAPGRRGRQ TYSRFQTLBLEKEFLFPNYLTKRRIEVSHALALTERQVKIWFQ NRRMKMKKENNKDKPPVSRQSVKOGETKKBAQKLEEDRRAEGLIN 6419 1 973 PGRPRVRNFDLNSKSILQEPFCTRSIQIPANRSKTAMSKCPIFP MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL PSPDPVTVYLSPLVVWKELESLLENEGDHAITVADFVDHHPIV FNNLWYFRRIDLPSNLPGLILSSBHCNKYSKIPRHCMSEDSKY VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSP NOBILKSMVKSIKMNDVYGPMSQILETLINCPHFKRQRSLYRBI LFISLVALGRENIDIDAFKKYMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGEPYL 6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYINFAN YLLWVFTPLILLILPYFTIFLLYLTIIFHIYKRKNVLKEAYSH NLWGGARKTVATLWGGHAAVWHGYEVHGMEKIPEGGPALIIPYH GAIPIDPYYFMAKIFIHKGRTCRVVADHFVFKIFGFSLLLDVPC ALHGPREKCVEILRSGHLLAISPGGVRRALISDETYNIVWGHRR		ŀ		
6417 1 845 REEPNYQVLIRILISRCETDLLSIRABFRKKFGKSLYSSLQDAV KGDCQSALLALCRABUM  RGESRVIWSELEGEAGGAGGWASSINARMDNRFATAFVIACVLS LISTIYMAASIGTDFWYEYRSPVQENSSDINKSIMDEFISDBAD EKTYNDALFRYNGTVGLWRRCITIPKNMHWYSPPERTBSFDVVT KCVSFTLTRQPMEKFVDPGNINNSGIDLLRTYLWRCQFLLPFVSIL GLMCFGALIGLCACICRSLYPTIATGILHILAGLCTIGSVSCYV AGIELLRQKLELPDNUNGEFGWSFCLACVSAPLQFMASALFIWA AHTMRKEYTLMKAYRVA  6418 2 662 TRTEPRPPEGGAAVGKAGABSTSTPAGASPAAAYQADPPPPAH TPAPPPPPPPCGGIACHGEPAKFYGYDNLQRQPIFTTQQRABLUV YPDCKSSSGNIGEDDHILNQSSSPSQMFPMMRPQAAPGRRGRQ YPDCKSSSGNIGEDDHILNQSSSPSQMFPMMRPQAAPGRRGRQ TYSRFQTLBLEKEFFLPNPYLTRKRRIEVSHALALTERQVKIWFO NRRMKNKENNKDKPFVSRQEVKDGETKKEAQBLEEDRAEGLTN FRHVWFRKNKKENNKDKPFVSRQEVKDGETKKEAQBLEEDRAEGLTN PSPDPVTVPYLSPLVWWKELESLLENBEGHAITTVADFVDHHPTV FMNLVWYFRRLDLPSNLPGILISGSHCNKYSKIPRHCMSEDSKY VLIQMLMDNMKLHQDPSQPLYILWNAHTQKYPMVHLLQKSDNSF NQELLKSMVKSIKMNDVYGPMSQILETLNRCPHFKRQRSLYREN LFISLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGEPYL  6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILBENFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIFLLYLTIIFLHYKRKNVLKEAYSH NLWDGARKTVATLWGGHAAVWHGYEVHGMBKIPEDGPALIIPYH GAIPIDFYYFMAKIFIHKGRTCRVVADHFVKIFGFSLLLDVPC ALHGPREKCVEILRSGHLLAISPGGVRRALISDETYNIVWGHRR				
KGDCQSALLALCRAEDM  RGESRVIWSELEGEAGGAGGMASSINARMDNRFATAFVIACVLS  LISTIYMAASIGTDFWYEYRSPVQENSSDLNKSIWDEFISDEAD  EKTYNDALFRYNGTVGLWRRCITIPKNMHYSPPERTESFDVVT  KCVSPTLTEQPMEKFVDPGNHNSGIDLLRTYLWRCQFLLPFVSL  GLMCFGALIGLCACICESLYPTLATGIHHLAGLCTLGSVSCTV  AGIELLHQKLELPDNVSGEPCWSFCLACVSAPLQFMASALFIWA  AHTMRETTIMKAYRVA  6418  2 662 TRTEPRRPPGIGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH  TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQPIPTTQQBABLVQ  YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRGGRQ  TYSRFQTLBLEKERFLFNPYLTRRRIEVSHALALTERQVKIWFQ  NRRMKWKKENNKDKPPVSRQEVKDGETKKEAQELEEDRAEGLIN  6419  1 973 PGRPRVRNFDLWSKSILGEFFCTRSIQIPANRSKTAMSKCPIPP  MARSISTSGPLDKEDTGROKLISTGSLPATLQGATDSIGLEWHL  PSPDPVTVPYLSPLJVWKELESILBNEGDHAITVADFVDHPIV  FWNLVWYFRRLDLPSNLPGLILSSBHCNKYSKIPRHCMSEDSKY  VLIQMLWDNMKLHQDPGQPLYILWNAFTQKYPMVHLLQKSDNSF  NOELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYREI  LFISLVALGRENIDIDAFDKEYKMAYDRLTPSQVKSTHNCDRPP  STGVMECRKTFGEPYL  6420  207  1187 RKMIDKNQTCGVGQDSVPYMICLIHILERWFGVEQLEDYINFAN  YILWVFTPLILLILPYFFIPLYLITIIPHTYKRKNVI,KEAYSH  NLWDGARKTVATLWDGHAAVWHGYKVHGMEKIPEDGPALIIPYH  GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFRIPGFSLLLDVPC  ALHGPREKCVEILRSGHLLAISPGGVRKALISDETYNIVWGHRR		·		***
6417  1 845 RGESRVLWSELEGEAGGAGGWASSINARMDNRPATAFVIACVLS LISTIYMAASIGTDFWYBYRSPUQENSSDINKSIWDEFISDBAD EKTYNDALFRYNGTUGLWRRCITIPKNMIWYSPPERTBSFDVVT KCVSPTLTRQPMEKPVDPGNHNSGIDLLKTYLWRCQFILPFVSI, GEMCFGALIGLCACICRSLYPTLATGIHHLAGLCTIGSVSCTV AGIELHQKLELPDNVSGEPGWSFCLACVSAPLQFMASALPIWA ARTMRKBYTIMKAYRVA  6418  2 662 TRTEPRRPPGIGAAVGAGARSTSTPAGASPAAAYQADPFPPAH TPAPPPPPPPCGGTACHGBPAKFYGYDNLQRQPIPTTQQBABLVQ YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAFGRRGRQ TYSRPQTLBLEKEFLFNPYLTRKRIEVSHALALTERQVKIWFQ NRRMKWKKENNBDKFPVSRQEVKDGETKKEAQBLEEDRAEGITN  6419 1 973 PGRPVRNFDLNSKSILQBFFCTRSIQIPANRSKTAMSKCPIFP MARSISTSGPLDKEDTGRQKLISTGSLPATLQCATDSIGLEWHIL PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADPVDHHPIV FWNLVWYBRRLDLPSNLPGIILSSBHCHKYSKIPHCMSBDSKY VLIQMLWDINMKHQDPGQPLYILWNAHTQKYPMVHLQKSDNSF NQBLLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYRBI LFILSLVALIGRBNIDDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGEPYL  6420 207 1187 RMMIDKNQTCGUQQDSVPYMICLIHILEBWFGUEQLEDYLNFAN YILWVFTPLILLILPYFTPLYLTIJIHHIYKRNVIKEAYSH NLWDGARKTVATILWDGHAAVWHGYEVHGMEKIPBDGPALIIPYH GAIPIDFYYFMAKIFHKGRTCKVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRKALISDBTYNIVWGHRR		1		
LISTIYMAASIGTDFWYEYRSPVQENSSDLNKSIWDEPISDRAD EKTYNDALFRYNGTVGLWRRCITIPKNMHWYSPPERTESFDVVT KCVSPTLTBQPMEKFVDPGNHINSGIDLLRTILWRCQFILIPFYSL GLMCFGALIGLCACICRSLYPTIATGILHILAGLCTIGSVSCYV AGIELLHQKLELPINVSGEPCWSFCLACVSAPLQFMASALFIWA AHTINKEYTLMKAYRVA  6418 2 662 TRTEPRRPPGIGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH TPAPPPPPPPCGGIACHGEPAKFYGYDNLQRQPIFTTQQBABLVQ YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWRPQAAPGRRGRQ YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWRPQAAPGRRGRQ NRRKKKENNKDKPPVSRQEVKDGETKKEAQELEEDRAEGITN NRRKWKKENNKDKPPVSRQEVKDGETKKEAQELEEDRAEGITN MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL PSPDPVTVYYLSPLVWKELESLLENBGDHAITVADFVDHHPIV FWNLVWYFRRLDLPSNLPGLILSSBHCNKYSKIPRHCMSBDSKY VLIQMLWDNNKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF NQBLLKSMVKSIKNNDVYGPMSQILETLNKCPHFRKQRSLYRBI LFLSLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECKKTFGBPYL  6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYINFAN YLLWVFTPLILLILPYFTIFLLYLTIIPLHIYKRKNVLKEAYSH NLWDGARRTVATLWDGHAAVWHGYBVHGMRKIPBDGPALIIPYH GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRKALISDETYNIVWGHRR	CA37	<del> </del>	046	
EKTYNDALFRYNGIVGLWRRCITIPKNMEWYSPPERTRSFDVVT KCVSPTLTEQFMEKFVDPGNHNSGIDLLRTYLWRCQFLLPFVSL GIMCFGALIGLCACLCRSLYPTLATGILHILAGLCTIGSVSCYV AGIELLHQKLELPDNVSGEPGWSFCLACVSAPLQFMASALFIWA AHTMRKEYTIMKAYRVA  6418 2 662 TRTEPRRPPGIGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQPIPTTQQRABLVQ YPDCKSSSGNIGEDPDHLNQSSSPSQMFFWMRPQAAPGRRGRQ TYSRFQTLELEKEFLFNPYLTRKRRIEVSHALALTERQVKIWFQ NRRMKKKENNKDRFPVSRQEVKDGETKKEAQBLEEDRAEGLIN 6419 1 973 PGRPVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL PSPDPVTVPYLSPLVWKELESLLENEGDHAITVADFVDHHPIV FWNLVWYFRRLDLPSNLFGLILSSHCNKYSKIPRMSEDSKY VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF NOBILKSMVKSIKMDVYGPMSQILETLNKCPHFKRQRSLYREI LFLSLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGEPYL 6420 207 1187 RRMIDKNQTCGVGQDSVPYMICLHILEEWFGUEQLEDYLNFAN YLLWVFTPLILLIPYFTIPLLYLTIIPLHYKRKNVLKEAYSH NLWDGARKTVATLWDSHAAVWHGYEVHOMEKIPEDGPALIIPYH GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIRGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR	0411	1 *	045	· ·
KCVSPTLTEQFMEKPVDPGNHNSGIDLLETYLWRCQFLLPFVSL GLMCFGALIGLCASLYPTLATGILHILAGLCTIGSVSCYV AGIELLHQKLELPDNVSGEFGMSFCLACVSAPLQFMASALFIWA AHTMRKEYTIMKAYRVA  6418 2 662 TRTEPREPPGLGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH TPAPPPPPPPCGGIACHGEPAKFYGYDNLQRQPIFTTQQBABLVQ YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRGRQ TYSRFQTLELLEKEFLPNYLLTRKRRIEVSHALALTERQVKIWFQ NRRMKKKENNKDKPFVSRQEVKDGETKKEAQELEEDRAEGLIN 6419 1 973 PGRPVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADFVDHHPIV FWNLVWYFRRLDLPSNLPGLILSSBHCNKYSKIPRHCMSBDSKY VLIQMLWDDMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF NOBLLKSMVKSIKMDVYGPMSQILETLNKCPHFKRQRSLYREI LFISLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGBPYL 6420 207 1187 RRMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIPLLYLTIIPLHYKRKNVLKEAYSH NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPEDGPALIIPYH GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR				
GLMCFGALIGLCACICRSLYPTIATGILHILAGLCTIGSVSCYV AGIELLHQKLELPDNVSGEPGWSFCLACVSAPLQFMASALFIWA AHTMRESTTIMKAYRVA  6418  2 662 TRTEPRRPPGLGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQPIPTTQQRABLVQ YPDCKSSSGNIGEDPDHLNQSSSPSQMFFWMRPQAAPGRRRGRQ TYSRFQTLELEKEFLFNPYLTRKRRIEVSHALALTERQVKIWFQ NRRMKWKKENNKDKPPVSRQEVKDGETKKEAQELEEDRAEGLIN 6419  1 973 PGRPRVRWFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIPP MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADPVDHHPIV FWNLVWYFRRLDLPSNLPGLILSSBHCNKYSKIPRHCMSBDSKY VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYREI LFLSLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGEPYL  6420  207  1187 RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH NLWDGARTTVATLWDGHAAVWHGYEVHGMEKIPBBGPALIIPYH GAIPIDFYYFMAKIPIHKGRTCKVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR	i			
AGIELLHQKLELPDNVSGEPGWSFCLACVSAPLQFMASALPIWA AHTMRKEYTIMKAYRVA  6418 2 662 TRTEPRRPPGLGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH TPAPPPPPPPCGGIACHGEPAKFYGYDNLQRQPIPTTQQBASLVQ YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRGRQ TYSRFQTLELEKEFLFNPYLTTKRRIEVSHALALTERQVKIWFQ NRRMKWKKENNKDKPPVSRQEVKDGETKKEAQELEEDRAEGLTN  6419 1 973 PGRPRVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP MARSISTSGPLDKEDTGRQKLLSTGSLPATLQGATDSIGLEWHIL PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADFVDHHPIV FWNLVWYFRLDLPSNLPGLILSSBHCNKYSKIPRHCMSBDSKY VLIQMLWDNMKLHQDPGQPLYLLWNAHTQKYPMVHLLQKSDNSF NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYREI LFLSLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGEPYL  6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIPLLYLTIIPHIYKRKNVLKEAYSH NLWDGARKTVATLMDGHAAVWHGYEVHGMEKIPBBGPALIIPYH GAIPIDFYYFMAKIPIHKGRTCRVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR		ł		· · · · · · · · · · · · · · · · · · ·
AHTMRKETTIMKAYRVA  AHTMRKETTIMKAYRVA  6418  2 662 TRTEPRRPPGIGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH TPAPPPPPPCGIACHGEPAKFYGYDNI_ORQPIFTTQQBABI.VQ YPDCKSSSGNIGEDPDHINQSSSPSQMFPWMRPQAAPGRRGRGY TYSRFQTLBLEKEFLFNPYLTRKRRIEVSHALALTERQVKIWFQ NRRMKWKKENNKDKFPVSRQEVKDGETKKBAQBLEEDRABCGLTN  6419 1 973 PGRPRVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSIGLEWHL PSPDPVTVTYI.SPLVVWKELESLLENBGDHAITVADFVDHHPIV FWNLVWYFRRLDLPSNLPGLILSSBHCNKYSKIPRHCMSEDSKY VLIQMLWDNMKLHQDPSQPLYILWAAHTQKYPMVHLLQKSDNSF NQBLLKSMVKSIKMNDVYGPMSQILETINKCPHFKRQRSLYRBI LFI.SLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGEPYL  6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGUEQLEDYLNFAN YLLWVFTPLILLILPYFTIPLLYLTIIPLHIYKRKNVLKEAYSH NLWDGARKTVATLWDGHAAVWHGYBVHGMBKIPBBGPALIIPYH GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR		1		
6418 2 662 TRTEPREPPGIGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQPIPTTQGRABLVQ YPDCKSSGNIGEDPDHLNQSSSPSQMFFWMRPQAAPGRRGRQR TYSFPQTLELEKEFLFNPYLTRKERIEVSHALALTERQVKIWFQ NRRMKKKENNKDRPPVSRQEVKDGETKKEAQBLEEDRAEGLIN 6419 1 973 PGRPRVRNPDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADFVDHHPIV FWNLVWYFRRLDLPSNLPGLILSSHCNKYSKIPRHCMSEDSKY VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF NOELLKSMVKSIKMDVYGPMSQILETLNKCPHFKRQRSLYREI LFLSLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGEPYL 6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGUEQLEDYLNFAN YLLWVFTPLILLILPYFTIPLLYLTIIPLHYKRKNVLKEAYSH NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPEDGPALIIPYH GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR				
TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQPIFTTQQRARIVQ YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRRGRQ TYSRFQTLBLEKEFLEMPYLTRKRRIEVSHALALTERQVKIWFQ NRRMKWKKENNKDRFPVSRQEVKDGETKKBAQBLEEDRAEGLTN  6419 1 973 PGRPVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL PSPDPVTVPYLSPLVWKELESLLBNEGDHAITVADFVDHHPIV FWNLVWYFRRLDLPSNLPGLILSSBHCNKYSKIPRHCMSBDSKY VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF NQBLLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYRBI LFISLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGBPYL  6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH NLWDGARRTVATLWDCHAAVWHGYEVHGMEKIPBDGPALIIPYH GAIPIDFYYFMAKIPIHKGRTCKVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWCHRR		L		I
YFDCKSSSGNIGEDPDHLNQSSSPSQMFFWMRPQAAPGRRRGRQ TYSRFQTLELEKEFLFNPYLTRKRRIEVSHALALTERQVKIWFQ NRRMKWKKENNKDRFPVSRQEVKDGETKREAQBLEEDRAEGLIN 6419 1 973 PGRPRVRNPDLNSKFILQEFFCTRSIQIPANRSKTAMSKCPIFP MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADFVDHHPIV FWNLVWYFRRLDLPSNLPGLILSSBHCKKYSKIPRHCMSBDSKY VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF NQBLLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYRBI LFISIVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGBPYL 6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN YLLWVFTPLILLILPYFIFLLYLTIIPLHIYKRKNVLKEAYSH NLWDGARRTVATLWDCHAAVWHGYEVHOMEKIPBDGPALIIPYH GAIPIDFYYFMAKIPIHKGRTCKVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWCHRR	6418	2	662	TRTRPRRPPGLGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH
TYSRFQTLELEKEFLFNPYLTRKRRIEVSHALALTERQVKIWFQ NRRMKMKKENNKDKPPVSRQEVKDGETKKEAQELEEDRAEGLIN  6419 1 973 PGRPVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIPP MARSISTSGPLDKEDTGROKLISTGSLPATLQGATDSIGLEWHL PSPDPVTVPYLSPLVWKELESLLENEGDHAITVADPVDHHPIV FWNLVWYFRIDLPSNLPGLILSSEHCNKYSKIPRHCMSEDSKY VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYREI LFLSLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGEPYL  6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIPLLYLTIIFLHIYKRKNVLKEAYSH NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPBBGPALIIPYH GAIPIDFYYFMAKIPIHKGRTCKVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR				TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQPIFTTQQBABLVQ
TYSRFQTLELEKEFLFNPYLTRKRRIEVSHALALTERQVKIWFQ NRRMKMKKENNKDKPPVSRQEVKDGETKKEAQELEEDRAEGLIN  6419 1 973 PGRPVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIPP MARSISTSGPLDKEDTGROKLISTGSLPATLQGATDSIGLEWHL PSPDPVTVPYLSPLVWKELESLLENEGDHAITVADPVDHHPIV FWNLVWYFRIDLPSNLPGLILSSEHCNKYSKIPRHCMSEDSKY VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYREI LFLSLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGEPYL  6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIPLLYLTIIFLHIYKRKNVLKEAYSH NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPBBGPALIIPYH GAIPIDFYYFMAKIPIHKGRTCKVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR				YFDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRRGRO
NRRMKWKKENNKDRPPVSRQEVKDGETKKBAQBLEEDRAEGLTN  6419 1 973 PGRPRVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSIGLEWHIL PSPDPVTVPYLSPLVVWKELESLLENBEGDHAITVADFVDHHPIV FWNLVWYFRRLDLPSNLPGLILSSBHCNKYSKIPRHCMSEDSKY VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHILLQKSDNSF NQBLLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYRBI LFLSLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGEPYL  6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIPLLYLTIIPHIYKRKNVLKBAYSH NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPBDGPALIIPYH GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR			]	
6419 1 973 PGRPRVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL PSPDPVTVPYLSPLVVWKELESLLBNBGDHAITVADFVDHHPIV FWILVWYPRRLDLPSNLPGLILSSBHCNKYSKIPRHCMSBDSKY VLIQMLWDIMWSLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF NQBLLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYRBI LFLSLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGEPYL 6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILBEWFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIPLLYLTIIPLHIYKRKNVLKPAYSH NLWDGARKTVATLWDGHAAVWHGYBVHGMBKIPBGGPALIIPYH GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR				
MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSIGLEWHIL PSPDPVTTPYLSPLVVWKELESILENEGHAITVADFVDHHPIV FWNI,VWYFRELDLPSNLPGILISBECCKKYSKIPRHCMSBDSKY VLIQMLWDDMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF NOBILKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYREI LFISLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGBPYL  6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIPLLYLTIIPLHIYKKNVLKEAYSH NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPEDGPALIIPYH GAIPIDFVYFMAKIFIHKGRTCKVVADHFVFKIFGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR	6419	1	973	A
PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADFVDHHPIV FWNLVWYFRRLDLPSNLPGLILSSBHCNKYSKIPRHCMSBDSKY VLIQMLWDNMKLHQDFGQPLYILWNAHTQKYPMVHLLQKSDNSF NQBLLKSMYKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYRBI LFLSLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGBPYL  6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILERWFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH NLWDGARKTVATLWDGHAAVWHGYEVHGMRKIPBDGPALIIPYH GAIPIDFYYFMAKIPIHKGRTCKVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDBTYNIVWGHRR	V 2.1.7		,,,,	
FWNLVWYFRRLDLPSNLPGLILSSEHCNKYSKIPRHCMSEDSKY VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF NQBLLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYRBI LFLSLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGBPYL  6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH NLWDGARKTVATLWDCHAAVWHGYEVHOMEKIPBDGPALIIPYH GAIPIDFYYFMAKIPIHKGRTCKVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWCHRR		]		<b>)</b>
VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF NQBLLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYRBI LFISIVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGBPYL  6420 207 1187 RKMIDKNQTCGVGQDSVPMICLIHILEENFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH NLWDGARTVATLWDGHAAVMHGYEVHGMEKIPBDGPALIIFYH GAIPIDFYYFMAKIPIHKGRTCKVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR		]		4
NOBLLKSMVKSIKNNDVYGPMSQILETLNKCPHFKRQRSLYRBI LFLSLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGEPYL  6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPBDGPALIIPYH GAIPIDFYYFMAKIFIHKGRTCKVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR			1	
LFLSLVALGRENIDIDAFDKBYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGBPYL  6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEENFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIPLLYLTIIFLHIYKRKNVLKEAYSH NLWDGARKTVATLWDGHAAVWHGYEVYHOMEKIPEDGPALIIPYH GALPIDFYYFMAKIFIHKGRTCKVVADHFVFKIFGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR				• · · · · · · · · · · · · · · · · · · ·
STGVMECRKTFGEPYL  6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIPLLYLTIIFLHIYKRKNVLKEAYSH NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPEBGPALIIPYH GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR				
6420 207 1187 RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIFLLYLTIIPLHIYKRKNVLKEAYSH NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPEDGPALIIPYH GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR				LFLSLVALGRENIDIDAFDKEYKMAYDRLTPSQVKSTHNCDRPP
YLLWVFTPLILLIDPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPBDGPALIIPYH GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR				STGVMECRKTFGEPYL
YLLWVFTPLILLIDPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPBDGPALIIPYH GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR	6420	207	1187	
nlwdgarktvatlwdghaavwhgyevhgmekipedgpaliipyh gaipidfyyfmakifihkgrtcrvvadhfvfkipgfsllldvfc alhgprekcveilrsghllaispggvrbalisdetynivwghrr		,		
GAIPIDFYYFMAKIPIHKGRTCRVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVRBALISDETYNIVWGHRR		i		
ALHGPREKCVEILRSGHLLAISPGGVREALISDETYNIVNGHRR				
, ,		·		, <del></del>
GFAQVAIDAKVPIIPMFTQNIREGFRSLGGTRLFRWLYEKFRYP			•	
				GFAQVAIDAKVPIIPMFTQNIREGFRSLGGTRLFRWLYEKFRYP

Deginning location corresponding to first amin acid amino acid residue of amino acid amino acid amino acid sequence sequ		T TO THE TOTAL TOT	I to all about and	I Amine agid cogrant containing gignal montide
No.   mucleotide   corresponding   to first   saino acid   residue of   saino acid   residue of   saino acid   sequence   security   saino acid   sequence   security   saino acid   sequence   sequ	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cocation   Corresponding   Co first   amino acid   amino acid   cridue of   caldue of	1			
to first anino acid residue of anino acid residue of anino acid sequence    Perfoline, Geditamine, N-Angairaje,   Perfoline, Geditamine, N-Valine,   Sescrine, T-Threonine, V-Valine,   Manino acid   Sequence	NO:	l .		
to first anion acid arcidus of anion acid arcidus of anion acid acid residus of anion acid sequence  Sescrie, T-Threonie, V-Valline, M-Tryptophan, Y-Tyxosine, X-Unknown, *estop codon, /-possible nucleotide deletion, V-possible nucleotide dissertion) REPRYOGE PVILETYING PYNDOTITARELARCHANOQALID HIGH TOWN OF THE PROVING PYNDOTITARELARCHANOQALID HIGH TOWN OF THE PROVING PYNDOTITARELARCHANOQALID HIGH TOWN OF THE PROVING PYNDOTITARELARCHANOQALID HIGH TOWN OF THE PROVING PYNDOTITARELARCHANOQALID HIGH TOWN OF THE PROVING PYNDOTITARELARCHANOQALID HIGH TOWN OF THE PROVING PYNDOTITARELARCHANOQALID HIGH TOWN OF THE PROVING PYNDOTITARELARCHANOQALID HIGH TOWN OF THE PROVINCE PYNDOTITARELARCHANOQALID HIGH TANKING PYNDOTITARELARCHANOQALID HIGH TOWN OF THE PROVINCE PYNDOTITARELARCHANOQALID HIGH TOWN OF THE PROVINCE PYNDOTITARELARCHANOQALID HIGH TOWN OF THE PROVINCE PYNDOTITARELARCHANOQALID HIGH TOWN OF THE PART OF THE PART OF THE PYNDOTITARELARCHANOQALID HIGH TOWN OF THE PART OF THE PART OF THE PYNDOTITARE PYNDOTITARELARCHANOQALID HIGH TOWN OF THE PART OF THE PART OF THE PYNDOTITARELARCHANOQALID HIGH TOWN OF THE PART OF	1	1		
amino acid reidue of amino acid sequence whypophan, Y-Tyrosing, X-Wabknown, *-stop Codon, /-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclectide deletion, V-possible nuclear d	İ			
residue of amino acid sequence (Codon, *-possible nucleotide deletion, codon, *-possible nucleotide deletion, codon, *-possible nucleotide deletion, codon, *-possible nucleotide deletion, codon, *-possible nucleotide deletion, codon, *-possible nucleotide insertion)  FARMYGEPWIRE/FLODIEYPURGITE/FURGIERE/FREE/REKTENAVQALID INDRIEDER/FURGIERE/FU				
amino acid sequence Codon, /-possible nuclectide insertion) PAPMYGGFPVKLRTIGSD   PYDPQUTREKLARKYKNAVQALID   REREITORINSALLERFH   REREITORINSALLERFH   FAPMYGGFPVKLRTIGSD   PYDPQUTREKLARKYKNAVQALID   REREITORINSALLERFH   FAPMYGGFPVKLRTIGSD   PYDPQUTREKLARKYKNAVQALID   REREITORINSALLERFH   FAPMYGGFPVKLRTIGSD   PYDPQUTREKLARKYKNAVQALID   REREITORINSALLERFH   FAPMYGGFPVKLRTIGSD   PYDPQUTREKLARKYKNAVQALID   REREITORINSALLERFH   FAPMYGGFPVKLRTIGSD   PYDPQUTREKTYKNASIPALIDARG   FAPMYGGFPVKLRTIGSD   PYDPQUTREKTYKNASIPALIDARG   FAPMYGGFPVKLRTYLLARS   FAPMYGGFPVKLRTYLLARS   PYDRAMATILISPAGRCCM   FAPMYGGFPPFGIUMPGTGGGLERWALLARG   FAPMYGGFPVKLRTYNGGVKLRTYKNGWARATILISPAGRCCM   FAPMYGGFPPFGIUMPGTGGGLERWALLARG   FAPMYGGFPVKLRTYNGGVKLRTYKNGWARATILISPAGRCCM   FAPMYGGFPPFGIUMPGTGGGLERWALLARG   FAPMYGGFPVKLTYNGGVKLRTYKNGWARATILISPAGRCCM   FAPMYGGFPVKLTYNGGVKLRTYKNGWARATILISPAGRCCM   FAPMYGGFPVKLTYNGGVKLRTYKNGWARATILISPAGRCCM   FAPMYGGFPVKLTYNGGVKLRTYKNGGVKLRGARIGAMGATA   FAPMYGGFPVKLTYNGGVKLRTYKNGGVKLRGARIGAMGATA   FAPMYGGFPVKLTYNGGVKLRGARIGAMGGTSGSFWFI   FARMYGRAYTHYGGYMALYATTYKYYPPEHABOUTNYCCHA   FAPMYGGFYVTYTAYATARIKANKYGGBFVKLTYKGGVKLGARAIGAMGGTSGSFWFI   FARMYGRAYTHYGGYMALYATTYKYYPPEHABOUTNYCGFPKNGT   FARMYGGFTVGTFWGGTFTGGGSMLTTFLGGTTMKYGGNE   FAPMYGGKGFFFYKLTYTTKAYFFFTAGTFTLGGTTMKYGGNE   FAPMYGGFTYFTKAYFFTYGGTMLYYTTKYYPPHABOUTNYCGFPKNGT   FAPMYGGFTYFTKAYFFTAGTTTTKAYFFTAGTTKAYFTKAYFFTAGTTKAYFTTKAYFTAGTTKAYFTTKAYFTTAGTTKAYFTTAGTTTTKAYFTAGTTKAYFTTAGTTTTKAYFTTAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	İ		1	)
Sequence   Sequence   Septimic file   Sequence   Septimic file   Septimic fi	l			
FAPPWIGG PYMERTYLGOP 1 PYDDOLTBEELARKT KNAVQALID	· ·	1	sequence	
RIBERT DESIGNATION		sequence		1 - •
1844   362   WALSLENDPREWSINGLISPIPISVULRESPRANSSPAVILRASE	i	ł ·		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
YOMSLESSADELGSPOLEGUGOLTEVPARRAATTLILEPSAGRCY DEPWILTAVEGLAPDGY TILRSAURGEGGALPGHARPYRADITGE LDLERAPALGGSPAGLEPMGLLWALEPEKFLVYKDVYKDVYKPTUAT VELGULDGENDDDICKILLQTREERTIFJPOWTREFVEYVERVROTG LEFPPERGEPFEG VOWNGTGGGGLEVRASLAGGRAVWALLAYT HYBDLEKTMETHLEV FERAMWILLSTREWKGPVGFLGLISEGG ELCLSMASFILEGT TAMVINGSCHEWRGST IPVERRASTELFUG ODDENNESSFYRABACKELGAMERKEGILFFOHYLEPVGVNR MEIKVITGOYADI VOVINSPLEGEPDQKSF IPVERRASTELFUG ODDENNESSFYRABACKELGAMERKEGILFFOHYLEPVGVNR MEIKVITGOYADI VOVINSPLEGEPDQKSF IPVERRASTELFUG ODDENNESSFYRABACKELGAMERKEGICHFOHYLEPVGVNR MEIKVITGOYADI VOVINSPLEGEPDQKSF IPVERRASTELFUG ODDENNESSFYRABACKELGAMERKEGICHFOHYLEPVGVNR MEIKVITGOYADI VOVINSPLEGEPDQKSF IPVERRASTELFUG ODDENNESSFYRABACKELGAMERKEGICHFOHYLEPVGVNR MEIKVERGEFT IN GGGEPRAHMAQVDAMKOLGOTFFRIKILG GREGTIPSKY PLCRASLHANLOGSP II WGGGPRAHMAQVDAMKOLGOTFFRIKILG GREGTIPSKY HOLLUVOCOPSINILRKOGIHKGDEVALTYMMI PELVVAMLACAR IGALHSI VYRAGFSESSLCER ILDSCSLLITTDAFYRGEKLIMI. REALDBALGKORKOFFVRCCI VVRHIGARBIGMOSTSGSPP I KRSCPIVQISMIQGILMWHELMQEASHGKEERHCDABRIGHTIL ITTSSTIGK ROWNINTOGYTULMWHELMQEASHGKEERHCDABRIGHTIL ITTSSTIGK ROWNINTOGYTULMWHELMQEASHGKEERHCDABRIGHTIL ITTSSTIGK ROWNINTOGYTULMWHELMQEASHGKEERHCOLDEN WINCH WINTHKVUCAQRCP LVDTFMOTTETGGHMLTPLFGGTTMKEGSAT FPPFGGVARAI MINSSGRELGERGGYLVRKOPHTAVGENTHUNGSH REPTTYPKK PROLYPYGGGCQRDQDGYWHTGRICHTVYORHE REPTTYPKK PROLYPYGGGCQRDQDGYWHTGRICHTVYORHE REPTTYPKK PROLYPKGGCQRDQDGYWHTGRICHTVYORHE REPTTYPKK PROLYPKGGCQRDQDGYWHTGRICHTVYORHE REPTTYPKK PROLYPKGGCQRDQDGYWHTGRICHTVYORHE REPTTYPKK PROLYPKGGCQRDQDGGYWHTGRICHTVYORHE REPTTYPKK PROLYPKGGACHDABRICHTVYORHE REPTTYPKK PROLYPKTYLDLICHDAWICHTVYORHE REPTTYPKK PROLYPKTYLDLICHDAWICHTVYORHENT REPTTYPKK PROLYPKTYLDLICHDAWICHTVYORHINKOH REPTTYPHOLYPKTYLDLICHDAWICHTVYORHINKOHH REPTTYPHOLYPKTYLDLICHTVYORHENT REPTTYPKK PROLYPKTYLDLICHDAWICHTVYORHINKOHH REPTTYPHOLYPKTYLDLICHTVYORHINGHTHAN TORYTOGGGGGGGGWYTHTOGGGCGGGGGGGGWGYTHOGGGCGGGGGGGGWYTHTOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				
DEVURIAVRIGAPEQPYTLIRASIADBEKGALFQAHAPKRADITIGE LDLERAPALGSPAGERMEILLANALEPPERPELVERVERDEVELGE VELLEVIAGEDPDOSCILLOTTEREXPILAGIGSPAVMALAYY NYEDLEKTMETHILEYPERAMYLLISHEVERGAVMALAYY NYEDLEKTMETHILEYPERAMYLLISHEVERGAVMALAYY NYEDLEKTMETHILEYPERAMYLLISHEVERGAVMALAYY NYEDLEKTMETHILEYPERAMYLLISHEVERGAVMALAYY NYEDLEKTMETHILEYPERAMYLLISHEVERGAVMALAYY NYEDLEKTMETHILEYPERAMYLLISHEVERGAVMALAYY NYEDLEKTMETHILEYPERAMYLLISHEVERGAVIALOTPHIKIGE GREGTIPSEV  GODHINNKSEPYANBACKELQAHGREKEQIICTPERGYTEPPYF PLCRASLIAHLOSPIT HORGEBERHAMAQUDABLOFFFIKHLIG GREGTIPSEV  GREGTIPSEV  GREGTIPSEV  GREGTIPSEV  181  2133  EGERLSWPOEPWGIDIAKEPYMKTPCPGPEPERNPOVTKOKEFFIE HINKGARTHICKNUJDBUNHEKKLIDKUAFYWERNEDGETTQITY HQLLUQVCQPSIVILRKQGIHKGDRVAIYHMITERLOTTY HQLLUQVCQPSIVILRKQGIHKGDRVAIYHMITERLOTTY HQLLUQVCQPSIVILRKQGIHKGDRVAIYHMITERLOTTY KELADBALQKCQEKGFFVRCCIVVKEHGARBIGAMOSTSGEPFI KRSCPTVQISMOGOLDHAWELMQSADGAUESPENGDABDPLFILI YTSGSTGKPKGVVHTVGGYHLYVATTEKYVPDFHABOVENCTAD IGMITGHSYVTYGPLANGATSULPSETTYDTYPHABOVENCTAD IGMITGHSYVTYGPLANGATSULPSETTYDTYPHABOVENCTAD IGMITGHSYVTYGPLANGATSULPSETTYDTYPHABOVENCTAD IGMITGHSYVTYGPLANGATSULPSETTYDTYPHABOVENCTAD IGMITGHSYVTYGPLANGATSULPSETTYTYYGHER REPTTYPKKPGPTYTYGPLANGATSULPSETTYGATHOKGGSTUNDBA WLHYHUVUAQAGCPTUDTFMQTTGGAMLITHLGATTHKGGSGT PPFFGAAPATALINSGKRIBGEBABGYLVPKGPHICIMSTYCHBIR REPTTYPKKPGYTYTGGANGAUPROGODGYYWITGTDDMIANSGHL LSTAEVESALVEHEAVARAAVGHHEPYKGGCLYCFYTCOCHH FSPILITEBLKKQTREKIOPATHOTYCHGAMONINKARA RIANNAHICOCTIOQULESHABASHETAHNICKTSULDEBARGP FLANABDADLOMENSTVADEPSVISHLESHRICLTIQ KRIANDADLOMENSTVADEPSVISHLESHRICLTIQ GREGGEGOGOVWVANAHRHYGWATLOGLIDSHNICKYBANNIKARA RIANNAHHICOCTIOQULESHABASHETAHNICKTSULPSHICKANIKANI GERGGGOGOVWVANAHRHYGWATLOGLIDSHNICKANIKANIKANA RIANDAHLGULTAVALASHUSHANIKANIKANIKANIKANA RIANDAHLGULTAVALASHUSHANIKANIKANIKANI GERGGGGIDHAWATCASULPSHICKANIKANIKANI GERGGGGIDHAWATCASULPSHICKANIKANIKANI LLITEBLEHYREBLQTKCANIPHALAWANDOLPDAQOKFIRIMANIKANI KOMENERJEHIPENGARGATANITIKANDIT LLITEBLEHYREBLQTKCANIPHALAWANDOLPDAQOKFIRIMANIKANI REGGGGIDHAWATCASULPTANIKANIKANI REGGGGIDHAWATCASULPTANIKANI	6421	1844	362	1 - ·
DIJERRAPALGOSPAGLERMSLIAMALEPRELVERLVERLVERLDER VELEVIDLENDERGENCELTERRYPELPEVERRUERUS VELEVIDERUGENES LEFTERPEPPPPFIVIDMPGTGGGLLEVRASLLAGKGPAVMALAYY MYEDLE KTMETTHLEV FERAMIYLLSHEW KOEVGILLISKGG ELCISMASFILKGIT TANUVINGSVANGGGILRVERGETLEPVGVMA BEYLKVIKOGYADUTUVINSPLEGEPDUSS FI PVERRASTELFIVO ODDENNESS FYRABRACKELQAMGREKGGILFERGY LEPEYF PLCRASLHANUGSP I I WGGEPRAHAMAQVDAWKOLOTFFIKHLG GREGOTI PSEV  6422 181 2133 EGENLSWFQEFWGILAKEPVWKTPCPGPPFLENNPUVKKGKIFLE WMKGATTHICKNULDENWEKKLGIKORAFYWKGHAPGTTTY HQLLVUVCOPSMULKKGGIKKGDRVALYWHIP DELVVANLACAR I GALHSI VYAGFSSESLCERILDSSCGLLITTDAFYRGEKKUMI. KELADBAQUKCQEKGFPVCCIVWHIGARGHOSTTOSPEY KRSCPDVQI SHNQGIDIAWHELMQEAGHCEPSHOCANDUSTGSEPT KRSCPDVQI SHNQGIDIAWHELMQEAGHCEPSHOCANDUSTGSEPT KRSCPDVQI SHNQGIDIAWHELMQEAGHCEPSHOCANDUSTGSEPT KRSCPDVQI SHNQGIDIAWHELMQEAGHCEPSHOCANDUSTGSEPT KRSCPDVQI SHNQGIDIAWHELMQEAGHCEPSHOCANDUSTGSEPT KRSCPDVQI SHNQGIDIAWHELMQEAGHCEPSHOCANDUSTGSING KRSCPDVQI SHNQGIDIAWHELMQEAGHCEPSHOCANDUSTGSING KRSCPDVQI SHNQGIDIAWHELMQEAGHCEPSHOCANDUSTGSING KRSCPDVQI SHNQGIDIAWHELMQEAGHCEPSHOCANDUSTGSING KRSCPDVQI SHNQGIDIAWHELMQEAGHCEPSHOCANDUSTGSING KRSCPDVQI SHNQGIDIAWHELMQEAGHCEPSHOCANDUSTGSING KRSCPDVQI SHNQGIDIAWHELMQEAGHCEPSHOCANDUSTGSING KRSCPDVQI SHNQGIDIAWHELMQEAGHCEPSHOCANDUSTGSING KRSCPDVQI SHNQGIDIAWHELMQEAGHCEPSHOCANDUSTGSING KRSCPDVQI SHQGIDIAWHELMQEAGHCEPSHOCANDUSTGSING KRSCPDVA SHQGIDIAWHELMQEAGHCEPSHOCANDUSTGSING KRSCPDVA SHQGIDIAWHELMQEAGHCEPSHOCANDUSTGSING KRSCPDVA SHQGIDIAWHELMGA SHANDUSTGSING SHNAANNIKANA RIAMNPHOCOTLQQULRSHASHETANDU CKTSVLIDEHAGRE FERRANDADLICANDERSTORM SHORT SHOW SHOWAND SHOW		ŀ		
UNLEWINGENDED GRALLOGTERERYELD POVERREPUREDWORTS LEFPERGEPRGET UNDMITTICEGULETYREALLAGIGERAVMALAYY NYEDLERTMETHILEY PERAMNYLLSHPEVKOPCUGLIGISKOG ELCLISMASFILKGI TRAVUTNOS VARUGSTURKUETLEPUGNER HELKURING VARUAUTUNINSELERPOQKS EI PUGRALBETUGHING ODDHNINKSEYTANBACKELQAHGREKOG I CUPERGETTEPUGNE HELKURING PATHAMON DAN DE HAMMON DAN DE HER PROBENDEN DE THOUTH PELCHASILBALVOS PI HORDE PRAHAMON DAN DE THE PETER P	l		1	
LFLPPBEGPPGI UDMPTTGGGLLEYGALLAGGGRAVMALAYY NYBOLDKYMETHLIKYPERSANNYLLSHPAVGOVGLLGISGG ELCLSMASFLKGI TAAVVINGSVANVGGTLRYKGETLPPUGVINR NEIKVYKOG YADLVUDUSSPLEGFDQKSFI PURBASSFILEIVAG GERGTPSEV  ODDENNKESPFYMBACAKIQAANGRURGQI CICYPSTCHYLEPPYP PLCRASLHALNGSPI I WGGEPRAHMAQVDAWKOLQTFPHKILG GRESTPSEV  GGROTPSEV  GGROTPSEV  GGROTPSEV  LGRISHPSEV  EGRISHFOEWGDLAKEPYWETPCROPPLRYNDUVKKKLFIE MMKKARTHI CYNVLDRUNGEKLGDKUVAFVYBCRBEDGETTQITY HOLLVOVCOPSNVLRKQGIHKGDRVAIYMPHI PELVVANLACAR IGALHSIVPAGFSSESLCERILDSSCSLLITITAFRGEKUMI. KERADBALQKCQEKGPPVGKINJVATTEKYDPHREDUVRCHA IGHITCHSVYTYGFLANGATSVLPSGIPTYPDVNKHSUNCHA IGHITCHSVYTYGFLANGATSVLPSGIPTYPDVNKHSUNCHA IGHITCHSVYTYGFLANGATSVLPSGIPTYPDVNKHSUNCHA IGHITCHSVYTYGFLANGATSVLPSGIPTYPDVNKHSUNCHA IGHITCHSVYTYGFLANGATSVLPSGIPTYPDVNKHSUNCHA IGHITCHSVYTYGFLANGATSVLPSGIPTYPDVNKHSUNCHA IGHITCHSVYTYGFLANGATSVLPSGIPTYPDVNKHSUNCHA REPETTYPKKPPGYYATGDCQRDQDGYWTTGRIDIMINVSCHL LSTAKVESALVEHEAVARAAVVGHBEVFURGSCILVEYCTLCOGHT FSPKLTEBELRQIRKKIG HATPDYTQNAFGLPKTINSGKIMBRV LKHLAQNDEDDGMSTVADPSVISHLPSHRCLTIQ  6423  614  1237  ANLÆETPRIDEPTVLIJVINDSNOTTSIPBETFKDITGLEVLINLS KNGIBFIDBHAPKKVABTLQTLOISDNRIGGSHCKTSGKIMBRV LRILAQNDEDDGMSTVADPSVISHLPSHRCLTIQ GRAGGGGGDVWVVAHRRMTLKQTKOGSTGRGGFTRISGKIMBRV LRILANDAMHCOCTLQVLUSMASNINETANDVICKTSVLDEHAGRP FINAANDADLCHLPKKTTDYAMLVTMFCWFTMVISYVVYYVRQN QBOARRHLEYLKSILPSRGKKADERDDISTVV  6424  1 1188  KRYSWFVARMWICSCULPRKYGNFDILKLFTRGGSGGMGYPRI GGGGGGGGDVWVVAHRRMTLKQLKUNGVPRRANSKISLA MNKGMGHKFLKHIERTRQLLFVNOIGOPGLSSTROYARSKISLA MNKGMGHKFLKHIERTRQLLFVNOIGOPGLSSTROYARDGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	l	'		
NYEDLEKTMETLIHLEKYERANNYLLSHPEVUGDUGLISLISKIG ELCLSMASFIKGITAAVVINGSVANVGGTLEYVGGTLEVUGNE REIKVITKOGYADIVDVINSPERGEPDGRSTIPVBRAESTFLFLVG ODDENNKSEPYAMBACKRLQARGRRRQ1ICYPETCHYEPPYF PLCRASLHANUGSPI IWGGPPRRRBODDAWKGLOTFFHRILG GREGTTPSKV  GREGTTPSKV  EGERLSWFOEPWGDIAKEPYWKTPCPGPPLRYNPDVYKKKIFIE MKGATTPICYNUDENVERKGLEDKVAPYWEGSEPGETTQITY HQLLVUVQOPSINILEKGLEDKVAPYWEGSEPGETTQITY HQLLVUVQOPSINILEKGLEDKVAPYWEGSEPGETTQITY HQLLVUVQOPSINILEKGLEDKVAPYWEGSEPGETTQITY HQLLVUVQOPSINILEKGLEDKVAPYWEGSEPGETTQITY HQLLVUVQOPSINILEKGERVALTYMENIERGERVALTYMENIERGERVANLAKACA IGAHSIVVAGFSSESLGERILDSSCSLITTIDAFYRGEKUNI. KELADBALQKOPKGFPVWCCIVVKELIGRASIGMGDSTSGSPPI KRSCPIVQI SINNQGIDLWHRIMSINGALGMGDSTSGSPPI KRSCPIVQI SINNQGIDLWHRIMSINITELDARJAVALCAP IGHTCHSVYTYGELANGATSVLPREI PYVORIBRUSIVOKYK VTKPYTAPTAIRLLMKFGDEPVTKHSRASLQVUGTVUSED INDEA MIAWHRVVGAQRCE JVOTFWGTETGGHMITTELDARJAVENCHEP PFFGVARAILNESGERLEGGERGEVIVVFUQWGINERGILVGWHCIAN LSTARVESALVEHEAVARAVVOHPPEWSECLVCFVTLCOCHT FSPRLIFBELKKQIREKIGP LATPDYIQNAFGILFYTKSGKINRV LRKTAQNBURLGOTTLQVULKRAAVVOHPPEWSECLVCFVTLCOCHT FSPRLIFBELKKQIREKIGP LATPDYIQNAFGILFYTKSGKINRV RKTATADAPADADLCHLEFKTTYANLUTHFOGFTMVISAVVYYVQON QUARRHLEFILKSLFSRGKKADEPDDISTVV  6423 614 1237 ANLKETPRDLPPRTVLLYLDSNQTTSTPNETFKDLHQLRVLNLS KNGIBP IBBHAFKCVARTLQTIJDLSNNRQSVHKNARNILKARA RANNWHICOCTLQVULKRASSNETELANVICKTSVLDEHBGRP FLANAADDADLCHLEFKKTTYANLUTHFOGFTMVISAVVYYVYQON QUARRHLEFILKSLFSRGKKADEPDDISTVV  6424 1 1188 KKSYMWAAMWEGSVLKYMSYSTIDKLRLFTRGSGGGGFTRD GGRGGKGDVWVAAHNRSTLKQLKDRYPRKYVYYVYYVQON QUARRHLEFILKSLFSRGKALDEPDISTVV  6424 1 1188 KKSYMWAADAATVELKSHTERGKALDAVNOHDHAGKSSLLSC VSHARFALADAATVATTKREKGTKYDLLAVNOHDLAGFILKSLL LKGSKKKWBIPYPVUSISTTENKKI IGELSKKRNDEILLYAGGGI GGKLLTNFLPLKGGRRITHLDLKALIADVUSUPSPRARSSLLSC VSHARFALADAATVATTKERGCTGRASSLLSC VSHARFALADAATVATKTERGTGGLEKHTMSTLYKANGLAVANGGL GGKLLTNFLPLKGGRRITHLDLKALIADVUSUPSPRARSSLLSC VSHARFALADAATVATKTERGTGGLEKHTMSTLYKNALA KNKGMEHKFLIKHTEKTRQLLFVVNISSTRAWNINGHLANGAGGLERGERVSSLLGKENGGELLTATTKRDLI LLITKRILEVKREGGGGGRAVTATARFGTFTSFSPEPTLEDIR HREGOGGSGGRAVGGGETRGDTGGGLTAA		<b>i</b>	Ì	· · · · · · · · · · · · · · · · · · ·
RICLISMASFILIGITAAVVINGSVANVGGTLRYKGETI.PPUVINN NRIKYTKOTYADIYDULNSPILIGPOORS I PPURRASTIFLIVO QDDHNINKSFYANBACKRIQARIGRIKOPI ICTYPETCHYIEPYP PLCRASILHAINGSBI I WGGEPRAHBAQOVDAWKQLQTFPHKHIGG GREGTTPSEV  6422 181 2133 EGRILSWFQEFWGDI IAKEFYWKTPCPGPPLRYNDUTKKKLFIRE WKGATTHI CYNLVLDRIVHKKLGDKUAPYWGGEPGETTQITY HQLLVOVCQPSIVILIKKQGTHKGDRVATYMPHI PELVYAMILACAR IGALHSI VPAGPSSESLICER ILDSSCSLILITTDAPYRGEKIJMI. KELDBALQKQEKGPPVRCCIVVKHIGRARIGMGDSTSQSPPI KRSCPDVQI SWNQGI DILWWHELMQBAGDECEPRICABPLET ILI YTSSSTGRE KROVHTVSGGTMINTVATTEK XVTVPPHAREUVENCTAN IGHITCHSYVTYGELAMGATSVLPEGIPTYPDVUKKUSIVKIX VTKEYTAPTARILIMKYGEDEPVTHSRASLQVLGTVGEPIRPEA HJWHRVUCAQRCD TUDTFWQTETGSHMITPLEGATTMKGSGTHER HJWHRVUCAQRCD TUDTFWQTETGSHMITPLEGATTMKGSGTHER REPTTYPKK PPGYVYTGDCQDCDQDGYWHITGRIDMMAVSGHL LSTARVESALVEHEAVARAAVVGHPIPVKGBCLYCFVTLCDGHT FSPRLIEBELKRQIREKIGG IATEPYTQNARCLFYCFVTLCDGHT FSPRLIEBELKRQIREKIGG IATEPYTQNARCLFYCFVTLCDGHT FSPRLIEBELKRQIREKIGG IATEPYTQNARCLFYCFVTLCDGHT RANDADLCHLDKKTTDYAMLTWFGGFFWVISSCHIRRV LRIAQNDEDDGMSTYADPSVISHLPSHRCLITO ORDARRHLEYLKSLESGRKYLWFJNGCSYHRANIKARAN RIGHEFIDBHAPKCVAETLQTI.DISDNRTQSYHRANIKARAN RIGHTCHTQCTQOLVARMSNIHETAHVICTCSVLDEHJGGR FINAANDADLCHLDKKTTDYAMLTWFGGFFWVISSYVYYYVQN ORDARRHLEYLKSLESGRKYAMSNIHETAHVICTCSVLDEHJGGR FINAANDADLCHLDKKTTDYAMLTWFGGFFWVISSYVYYYYYVQN ORDARRHLEYLKSLESGRKKRENDENTHAVICTCSVLDEHJGGR GGRGGGDWWVAHRRWTLAQLADYTPRRFPVARAVICTCSVADLEGLISGGT WSHAVEALADATTTIKRPCLIKKMNDDILTDAQGGE GGRGLUTHFIPLKGGKRITHIOLKLIADVGUPSPARGKSSLISG VSHAVEALADATPTTIKRPLKGKINTSDFTRAGRISGISGKSCHINKSSILAGA MNKGMGHKPLHHIRSTRQLLFVVNOLISGGCLSSHOVPATAPETTI LLTKELRIYREBLQTKVPALLAVNKMDLPDAQDKFHELMSQLQDH KOPTHHIPSKRNIPPSRAVRPQHITT BIANTYTSKDIIT LLTKELRIYREBLQTKVPALLAVNKMDLPDAQDKFHELMSQLQDH KOPTHHIPSKRNIPPSRAVRPQHITT BIANTYTSKBILT LUGGTKAVAYAVATPFVPPQHTMQLICKTCRSI DEQANOGRDANLHKKQLIALMISDJTMSSTEPPSKEDNVINGKRE REGEDDARVAACKEPPPHHTTDHAVGEGITVANTADSTFRORE REGEDDARVAACKEPPPHHTTDHAVGEGITVANTADSTFRORE REGEDDARVAACKEPPPHHTTDHAVGEGITVANTADSTFRORE REGEDDARVAACKEPPPHHTTDHAVGEGITVANTADSTFRORE REGEDDARVAACKEPPPHHTTDHAVGEGITVANTAD	Í			
RIKUYTKOGYADIUDVIANSPLEGDOKSSIIPURRASSTELFLIVE QDDHNMKSBYYANBACKRLQAHGRKRQJICYPETGHYIEPYF PLCRASIANJIGSBIIWGGEPRARDARQVDAMKQLQTFFHKIIG GRESTITSKV  GRESTITSKV  BISHLSWFQEPWGDIAKEPYWKTPCPGPPLRYNPDVTKKKLFIE WMKGATTHICYNVLDRNVERKILGDKVAFYWGGEPGETTQITY HQLLUVOVOPSNUR,RKQGIHKGEDVAIYWGGEPGETTQITY HQLLUVOVOPSNUR,RKQGIHKGEDVAIYWFDLAVARALACAR IGALHSIVFAGFSSESLCERILDSSCSLLITTDAFYRGEKLVNI, KELADBALQKCQEKGPPVRCCIVVIRIIGRABIGMGDFSQSPFI KRSCPIVQI SINNQGIDLAWHKIMQBAGBKGEPBRCDAEDPLFII, YTSGSTGKEKGVWITVGGYMLYVATTEKTVPDPWRRUMSIVOKYK VTKYTAPTAIRLIMKKGDBEVTHSRASILQVICTVQEPINPEA HJMYHRWCAQRCE JUVDFWOTTSTGGHIDLOATPHMKEDBAT PPPFGVAPAILMESGERLEGEAEGYLVFKQPWFGIMRTVYGNHE RPETTYFKKPPGYYVTGDCQCRDDGSYWITGRIDDMINSGHIL LSTARVESALVEHEAVARAVOWHPHEVRGKCLYCCTVTLCOCHT FSPRLITBELKRQIREKIGP IATPDYIQNAFGLFYKTRSKIHRRV LKKIAQNBUDGJSVSTHLGTHARAVOWHPHEVRGKCLYCCTVTLCOCHT FSPRLITBELKRQIREKIGP IATPDYIQNAFGLFYKTRSKIHRRV KRKIACNDUBGJSWSTHLAUSHANDARDLORGTSVRUNGKRINKVSHINK RIGIEPIDEHAFKGVASTLVCILDSNQITSITPBETFKDLAQLEVINIG  6423 614 1237 ANLKETPROLPFFTVILLYLDSNQITSITPBETFKDLAQLEVINIG KRKIACNDUBGJSWSTHLAUSHANDARDLORGTSVRUNGKNIKANAFNILKARA RIANNWHCOCTLQQVIRSMASNBETHAVICKKTSVIDEHGGR FIANAANDADLCNLDKKTTDYAMLVTHFGRFTMVISVYVYVYQG QDAARRIBETILKSIJFERGVKADBFDDLISVG VSHARVALADVATATTICKLRYPKRPVAGVANSKYLSA LKGSKGKDWEIPYPVGISVTDENGKI IGELNKRNDRILVAQCGL GGKLLTNH-PJKKGJRRITHLDLKALADVGULGFFRAKSSLLSC VSHARVALADVATATTICKLRYPKRIVSVADLPGLIRGAR MNKGMGHKELBHIEKTRQLLFVUDIGSGLGSHTYATFTTIKT LLTKRIBLIVKRBLGTYRDALAVNNOMLDADQKFRHSIMSQLADN KOPLHLFERNNI PERTVERQHI TE ISAVTGGGIEBLIKNCIKKSI, DBQANQBNDALHKKOLLINLWIJDTMSSTEPSKEHAVTTSKMDI I LUKGTILVAVAVATYPFVTPALRKVCLPFVPATMKQLERVVKMER CRGSLVJUGGSGGRYLDATARKGFTASSTEPSKEHAVTTSKMDI I LUKGTILVAVAVATYPFVTPALRKVCLPFVPATMKQLERVVKMER WRGOVBGSAKYTIGGSGDATVIJAANKGFTAVSKELAVTSKMOFILITG LUKGTIJVAVAVATPFVTPALRKVCLPFVPATMKQLERVVKMAR WRGOVBGSAKYTIGGSGGFTREDTGGGEDTAAAFGRFSFSPEPETLEDIR KRCCTSMINGGSGGRITGDTGGGEDTAAAFGRFSFSPEPETLEDIR KRCCTSMINGGSGGRITGDTGGGEDTAAAFGRFSFSPEPETLEDIR LKHSPARARGRWOPHOPRINLIALAUGLAGELABLFONKTOGEPE PQUKSPRERAALQEEISDVLTYLVALAAARCRVDLPFL		1		•
ODD-INNESS PYANBACKRLQAHORKRPQI I CYPPTCHYTEPYF   PLCRASHALIVGSP I I WGGEPRAHAMAQVDAWKQLQTFFHKHLG   GRBSTTPSKV	Ť		1	
FICKASIAHAIVGSPIIWGGEPRAHAMAQVDAWKQLQTFFHKHLG GREGTIPSKY  GREGTIPSKY  BGERLSWFQEFWGDIAKEFYWKTPCPGPPLRYNFDVTKGKIFIE WMKGATTNICYNYLDRWHEKKLGDKVAFYWEGDEGETTQITT HQLLVQVCQPSNLTRKGGVATYMMTDERLVVAHACAR IGALHSIVPAGFSSESICERILDSSCSLLTTDAFYRGEKLVNI. KELADBALQKCQERGFFVRCCIVVKHIGRARIGHGDSTSQSPI KRSCPDVQISNNQGIDLWHEKMQDSAGDECEPSNCDARDPLFII YTSGSTGKPKGVVHTVGGYMLTVATTFKYVPDFHABDVFNCTAD IGWITCHSVTYTGFLAWRATSULPRGIVPDDVRIMSULVKYK VTKFYTAPTAIRLIMKFGDBEVTKHSRASLQVIGTVGEPINPBA WLMWHRVVGAQRCDIVDTWQTTTGGHUTTLPLGATPHKPGSAT PPFFGVAPALIMESGEELBGEABGGVACPWHGCHITCYTCHH EPFTTYFKKPPGYYTGDGCQRDQDGYWTTGRIDDMINVSGHL LSTARVESALWEHREVARAAVVGHPBCKGLYCPVTLCGHT FSPRLTEELKQIREKIGPIATPDYIQNAPGLPKTRSKIMRV LRKIAQNDEDLGDMSTVADPSVISILEFSHKLITIQ  6423 614 1237 ANLKEIFRILPRHAFKGVASTLQTLOLSDNRIGSVERGLYCPVTLGGHT FSPRLTEELKQIREKIGPIATPDYIQNAPGLPKTRSKIMRV KNGIFFIDBHAFKGVASTLQTLOLSDNRIGVERGLYCPVTLGGHT FSPRLTEELKQIREKIGPIATPDYIQNAPGLPKTRSKIMRV KNGIFFIDBHAFKGVASTLQTLOLSDNRIGVERGLYCPVTLGGHT FSPRLTEELKQIREKIGPIATPDYIQNAPGLPKTRSKIMRV KNGIFFIDBHAFKGVASTLQTLOLSDNRIGVERGLYCPVTLGGHT FSPRLTEELKQIREKAGPIATARVTCKTSVLDEHGGR FINAANDADLCNLPRKTTDYAMLVTMPCWPTMVISYVYYVQN QBDARRHLBYLKSLPSSQKKADEPDDISTVV QBDARRHLBYLKSLPSSGKKADEPDDISTVV GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	l		1	· ·
GRBOTIPSKY  GRBOTIPSKY  BERNISWFQEFWGDIAKEFYWKTPCPGDPLRYNFDVTKGKLFIR  WMKGATTNICYNVLDRAVHEKKLGDKVAFYWECNEPGETTQITT  HQLLVQVCQFSNVLRKGGIHKGDRVATYMENIELVVAMLACAR  IGALHSIVPAGFSESSLCERILDSSCSLLITTDAFYRGERGKINNI.  KELADRALQKCQBKGPPVRCCIVVKHLGRARIGMGDSTSQSPPI  KRSCPDVQISWNQGIDLMWHELMQEAGDESPENCDARDFLFIL  YTSGSTGKRKGVVHTVGGYMLYVATTFKYVPDPHABDVFMCTAD  IGMITGHSYVTYGFLAMGATSVLPKGIPTYDDVRKWSIVDKYK  VTKFYTAFTARLLMKVGDEPVTKHSRASLQVLGTVGGF INPEA  WILMYHRVVGAQRCDIVDTFWGTTEGSHLTPLEGAFPMKPGSAT  PPPFGVAPAILMESGEKLBEGBAEGYLVFKQDWFOTHRTVYGNHE  RPFTTYFKKPPGYYVTCDGCQRDQDGYWHTGRIDDMINVSGHL  LSTAEVESALVEHERVARAAVVGHPHPVKGECLYCFVTLCOGHT  FSPKLTEBELKKQIRKKIGPTATDFJUGAFDKFKTSGTHRRV  LRKIAQNDHDLGDMSTVADPSVISHLPSHRCLTIQ  ANLKEIPRDLPPFTVLLYLDSNQITSIPMFKUGIQLEVLNLS  KNGIBFIDBHAFKGVARTTQTLDLSDNRIGSVHKNAFNNLKARA  RIANNWHCDCTLQQUIRSHASHHETARNVICKTSVLDEHAGRE  FLANANDADLCKLDRKTTDYAMLVTH-GWFTMVISYVVYVQN  QBDARRHLSYLKSLPSRQKKADBFDDISTVV  GGRGGKGGVWVVAHNNMTIKQLKNYFPRRFVAGSGGKGFPRL  GGRGGKGGVWVVAHNNMTIKQLKNYFPRRFVAGSGRMSKISA  LKGSKGKGWVVVAHNNMTIKQLKNYFPRRFVAGSGNSKISA  LKGSKGKGWVVVAHNNMTIKQLKNYFPRRFVAGSGNSKISA  MKKGMGHKPLKHIERTRQLLFVVDISGPJGSHTQNTAPGETI  LLTTRIBLINKELLTRELGTRALLANNNSDLDDAQDFFHILMSQLG,  GGKLLTNFP,LEGGRRITHLHLLKLADGUGSPHYGRSSLLSC  VSHAKPALADVAFTTLKBELGKIMSDPKQISHTQNTRAPFTIT  LLTTRIBLINKELLTRERLGKLANNSDHDDAQDFFHRIMSQLQNP  KDPTHFFRRMNIPPRTVEPQHIIPISAVTGEGIBELKNCIRKSI,  DBQANQBNALHKKYLLKIMISGINTSGPSKAHVIPASFPVNSLQKSNMGFILTG  LWGGTIVAVYAVATPFVTPALRKUCLPPVDFMKDGLISNNGFILTG  CRRSLIVDIGSGDGRIVIAAAKKGFTAVGYELMPMLWYNSRYRA  WRBCVHGSAKYYIGDLAKVTPSQYSNVVIFGYDMALQSFRGRF  KRPCTSMHPQLPIQA  6426  30  565  SRGAAVGGSVAGGETRGDTGGEDTAAPGRFFSPPTLEDIRE  LHAFFARADMOFHQPRILLLALUGEWGSLAELPMINKTDGERE  PQUHSPRERAALQESLSDVLITIVALAARCRVDLPLAVISKDDI  BRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCLSTGOT  ST	l	ĺ	ł	
6422 161 2133 EGENLSWFQEFWGDIAKEFYWKTPCPGPFLRYNFDVTKGKLYIE WMKGATTNICYNVLDENVHERKLGDKVAFYWEGNEPGETTQITY HQLLVOVCOPSNVLHRKGLGHKGDEVATYMPMTPELVVAMLACAR IGALHSIVPAGFSSESLCERILDSSCSLLITTDAFYRGEKLNI. KELADRALOKCQEKKEPYWCCIVWLTARTHEVYDFHADDVFWCTAN IGHTIGHTUTGSFYTTGEFLANGATSVLFEGARIGANGSTSQSPPI KRSCPDVQISWNQGIDLWHELMQEAGDECEPEMCDAEDPLFIL YTSGSTGKERGVHTVGGYMLTVATTEKYVTPDHADDVFWCTAN IGWITGHSYTTGEFLANGATSVLFEGIPTTPDWARLSJUDKYK WITKFYTAPTAIRLAMKFGDEPVTHSRASIQVLGTVGGDINBPA MIWYHRVUGAQRCDIVDTFWOTETGGIMTDILGATPMKPGSAT PPFFGVAPAILMSSGERLSGEARGTLVFKQPWFGIMRTVYGNHE RPFTTYFKKFPGYYVTGDGCQRDQDGYFWITGRIDDMLNVSGHL LSTAEWSALVKHEWADAPAVVGHPKKGCLYCFVILCDGHT FSPKLTERIKKQIRKKIGD LATPDYIQNAGGIPKTRSGKIMRRV LRKIAQNDHDLGDMSTVADPSVISHLFSHRCLITIQ AMLKEIFRDLPPETVILIVLDSNOJTSIPMEIFKDLHQURVLNIS KNGIEFIDHAFKGVAFTLQTLDLSDNRIQSVHKAFNNLKARA RIANNWHCCCTLQQVLSSMASSHETAHNVICKTSTYLDEHAGRF FINAANDADLCALPKKTTDYAMLVTMCGWFTWISTYVQNA QBOARRHLEYLKSLESRQKKADEPDISTYULDEHAGRF FINAANDADLCALPKKTTDYAMLVTMCGWFTWISTYVYYVRQN QBOARRHLEYLKSLESRQKKADEPDISTYULDEHAGRF FINAANDADLCALPKKTTDYAMLVTMCGWFTWISTYVYYVRQN QBOARRHLEYLKSLESRQKKADEPDISTYULDEHAGRF FINAANDADLCALPKKTTDYAMLVTMCGWFTWISTYVYYVRQN QBOARRHLEYLKSLESRQKKADEPDISTYULDEHAGRF FINAANDADLCALPKKTTDYAMLVTMCGWFTWISTYVYYYRQN QBOARRHLEYLKSLGSRQKKULDRYPTWISTYVOYTYRQN CGGKGKGGDWWVAINNWTLKQLLANDTYGCHFTWISTYVYYYRQN LKGSKGGMSUDWVAINNWTLKQLLANDTYGCHFTWISTYVYYYRRQN LKGSKGGMSUDWVAINNWTLKQLLANDTYGCHFTWAGGSGCMGYPRI GGKGKGGDWVVAINNWTLKQLLANDTSOMPAGKSSLLSC VSHAKPAJADAPFTTLKPELGKIMYSDRQLSVADLPGLIEGAH MNKGMGMKPIKHIERTRQLLEVVUDISGPQLSSHTOYRTAPETTI LLITKILEUVREKQTRPALLANNWOLPDAQDKFREMMYSKALL CRGSLVDIGSGGGRIVIAAAKKGPTAVTGSGIEELKNCIRKSL CRGSLVDIGSGGGRIVIAAAKKGPTAVTGSGIEKHVVKMIR REGVHBSAKYTISLMKVTTSQUSNVVILPGPQMMLQLEKKLE RELEDDARVTACRFPPFWHTTDHTGGIDTWATGTGFTWVWTMAR WRGVHBSAKYTISLMKVTTSQUSNVVILPGYQMMLQLEKKLE RELEDDARVTACRFPPFWHTTDHTGGIDTWATGTGFTWVWTMAR REGVHSHSAKYTISLMKVTTSQUSNVVILPGPQMMLQLEKKLE RELEDDARVTACRFPPFWHTTDHTGGGIDTWATATAGTPTGRE KRPCTSHHFQLFUD WRRYPAHLARSSSRKYTELPHGAISEQQAVGPADIPCDSTGQT NRRYPAHLARSSSRKYTELPHGAISEQQAVGPADIPCDSTGQT NRRYP	l	•		
WMKGATTNICYNVLDENVERKICDKVAPYWEGNEGGTTQITY   HQLLVOVCQPSNVLRKQGIHKGDRVAIYMPMIPELVVAMLACAR     IGALHSIVPAGFSSESLCERILDSSCSLLITTDAPYRGEKLVNI.     KELADRALQKCGKKGFPVRCCIVVKHIGRABIGMGDSTSQSPPI     KRSCPDVQISWNQGIDLWHHELMQEAGDKCEPBNCDARDPLFII.     YTSGSTGKRKGVVHTVGGYMLYVATTFKYVFDPHABDVFNCTAD     IGMITCHSYVTYGFLAMGATSVLPEGIPTYPDVNRLWSIVDKYK     VTKYYTAPTAIRLLAKKFGDPDVTHSRASIQVLGTVCGBINPFA     WLWHRVUGAQRCDIVDTFWQTETGGIMLTPILDGATPMKPGSAT     PPFFTYPKKRPGYYVTGGCQRDQDGYFNITGRIDDMLNVSGHL     LSTABVESALVEHEAVARAAVVGHPHPVKGSECLYCFYVILCOGHT     FSPRLITSBLKKQIRKKIGGINATPYIQNAGGIPKTVGGHK     FSPRLITSBLKKQIRKKIGGINATPYIQNAGGIPKTRSGKIMRRV     LRKIAQNDHDLGDMSTVADPSVISHLPSHRCLTIQ     ANLKEIPRILPPFTVLLILDSNQITSIPMEIFKDLHQIKKNIS     KNGIEPFIDHPFTVLLIVLDSNQITSIPMEIFKDLHQIKKNIS     KNGIEPFIDHRAFKGAFTLQTILDSNQITSIPMEIFKDLHQIKKNIS     KNGIEPFIDHRAFKGAFTLQTILDSNQITSIPMEIFKDLHQIKKNIS     KNGIEPFIDHRAFKGAFTLQTILDSNQITSIPMEIFKDLHQIKKNIS     KNGIEPFIDHRAFKGAFTLQTILDSNQITSIPMEIFKDLHQIKKNIS     KNGIERFIDHRAFKGAFTLQTILDSNQITSIPMEIFKDLHQIKGGRAFNLKARA     RIANNPHCCCTIQQVLRSMASNHETAHNVICKTSVLDEHAGRP     FIRADANDADLCLLPKKTTDYAMUVMPGNIQSVHTNANLXANG     GENGKIGTHAFLPLKGQRRITHLDLKLLADVGUCHYANIS     LKISKGEGMBIPPVGJSVTDENKKI IGEINKENDRILVAQGGI     GENGKLITHT-PLKKQKRITHLDLKLLADVGUCHPPNACKSSLLSC     VSHAKPALADVAPATTARPTITKPLKKHYHSPPKQISVADLEGLI KSGAH     MNKGMGHKPLKHIERTRQLLPVVDISGPQLSSHTQYRTAPETTI     LLITKBLKYKBLQYKPALLANNMOLPDAQDKPRIKINGIKNINGHLIFFRINN DENTVEPQHITHYSPOTTUSPOTTARVTITKENCIKKSI, DEQANDRIDALHKKQLALANNMOLPDAQDKPRIKINGIKNIVKMIL, DEQANDRIDALHKKQLALANNSTEPPSKHAVTTSKMDI I     LAMEGGGGIPLETTLKBELGYKTCLPFVPATMKQIERNVVKMIR     KREEDDARVYACKFPPPHWTPDHITTSCLPPVPMITTSCHYTHT     KREEDDARVYACKFPPPPHWTPDHYTGGGIDTWATDASTFRGER     KREEDDARVYACKFPPPPHWTPDHYTGGGIDTWATDASTFRGER     KREEDDARVYACKFPPPPHWTPDHYTGGGIDTWATDASTFRGER     KREEDDARVYACKFPPPPHWTPDHYTGGGIDTWATDASTFRGER     KREEDDARVYACKFPPPPHWTPDHYTGGGIDTWATDASTFRGER     KREEDDARVYACKFPPPPHWTPDHYTGGGIDTWATDASTFRGER     KREEDDARVYACKFPPPHWTPDHYTGGGIDTWATDASTFRGER     KREEDDARVYACKFPPPHWTPDHYTGGGDATVA	<u> </u>	<u></u>		
HQLLVQVQCPSNYLRKQGIHKGDRVATYMEM TEBLVVAMLACAR IGALHSIVPAGFSSESLCERIIDSSCSLTITTDAFYRGEKLVNI. KELADRALQKCQEKGFPVRCCIVVKHIGRARIGMGDSTSQSPFI KRSCPDVQISWNQGIDLWHISLMQEAGDKCEPBNCDARDFLFIL YTSGSTGKKRGVVHVTGGYMLYMTGYPDHADDVWCTAD IGWITGHSYVTYGGYMLYMTGYPDHADDVWCTAD IGWITGHSYVTYGGYMLYMTGYPDHADDVWCTAD IGWITGHSYVTYGGYMLYMTGYPDHADDVWCTAD IGWITGHSYVTYGGYMLYMTGYPDHADDVWCTAD IGWITGHSYVTYGGYMLYMTGYBDYWNGUNGTWRYDYGDHE WLWHRWUGAQRCF YDVDTFWQTTETGGMLTPLPGGHATPWGORD PPFFGVAPAILMESGERLEGERGUTLVPKQFWIGTMRTVYGNHE RPETTYFKKPPGYYVTGDGCQDDQGYYHTTGGIDDMLNVSGHL LSTAREVESALVEHEAVREARAVVGHPHFVKGCLIKCFVTLCDGHT FSPKLTEBLKKQIRKKIGPLATPDYIQNAFGLFKTGCDMLNVSGHL LSTAREVESALVEHEAVREARAVVGHPHFVKGCLIKCFVTLCDGHT FSPKLTEBLKKQIRKKIGPLATPDYIQNAFGLFKTGCDWLNVSGHL LSTAREVESALVEHEAVREARAVVGHPHFVKGCLIKCFVTLCDGHT FSPKLTEBLKKQIRKKIGPLATPDYIQNAGCHKTGLIKTGFUKGKTMRV LRKIAQNDHDLGDMSTVADPSYISHPSHRCLTIQ GRIADFTADLSTARDVICKTSVLDEHAGRF FLANANDADLCALPKTTDYAMLVTMFGFTMVIGKTRANLKARA RIANNWHCCCTLQVLLESMASHRETHANVICKTSVLDEHAGRF FLANANDADLCALPKTTDYAMLVTMFGFTMVISYVYYYVRQN QEDARRHEFLYLSGLESGRCKADBTFYPAGHTANVICKTSVLDEHAGRF FLANANDADLCALPKKTTDYAMLVTMFGFTMVIGVYYYVRQN QEDARRHEFLYLSGLESGRCKADBTFYPAGHTANVICKTSVLDEHAGRF FLANANDADLCALPKKTTDYAMLVTMFGFTWAGSGCMGYPRL GGGGGGGOVWVAINRWTLKQLLADKTPTGFFTRAGSGCMGYPRL GGGGGGGGOVWVAINRWTLKQLLADKTPTGFTRAGSGCMGYPRL GGGGGGGGOVWVAINRWTLKQLLADKTPTGFTRAGSGCMGYPRL GGGGGGGGOVWVAINRWTLKQLLADKTPTGFTRAGSGCMGYPRL GGGGGGGGGVVVAANTROLPDAQVKFRENDLIVAQGGG GGKLLTNFF,PLKGQKRITHLDLKLLADVGLVGFPRACKSGLLSC VSHAKPAJADYAPTTLKPBLGKIMYSDFQUSSHVYVARAFSFTLYAG KKVSWFVAAWHCSCVLFRKYGNFTLADKLUSTADGLGERIKNCIKKSI, DRQANQENDALHKKQLLNLWISDTMSDEPPSKHAVTTSKMDI I LLTTRILEVRENG TREPTVEPQHI TEDVPATMKGURKNCIKKSI, DRQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDI I LLTTRILEVRAM TERPTVEPQHATPATATGGLERIKNCIKKSI, DRQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDI I CRGSLVDIGSGGGRIVLAAAKKGPTAVGYELNPHLVWYSKRYA WRRGVEGSGAFYISDLWKMTR KRRYPANLAAKGFTAVGGGETAAPGFFSFSPEPTLEDIR CRGSLDDARVTACRFPPPRWTPDHATCGGDTTWAATDASTFGRE KRPCTSMHFQLIFIG LHABFFAABRUNGGFTOFRNALAARCRUDLPLAVLSKMDI NERRYPAHLARSSSRKYTELPHGAISEDQAVGPADI P	6422	181	2133	
IGALHSIVPAGFSSESLCRILIDSCSCILITIDAFYROGEKUNI.  KELADBALQKOQEKGPPVRCIVVKHIGRABIGMGDSTSQSPPI  KRSCPDVQISMNGGIDLWHEILMQENGBCCPEMCDARDELPIL  YTSGSTGKP KGVVHTVGGYMLYVATTFKYVPDFHABDVFNCTAN  IGWITGHSYVYYGPLANGATSVEIPTPYPVARLMSIVDKYK  VTKYTAPTAIRLLMKVGDBPVTKHSRASLQVLGTVGEPINPBA  WIMYHRVUGAQRCPIVDTFWQTETGHHHITELPGATPMKPGSAT  PPPFGVAPAILMSGEKLESGERAGYLVPKQWPWGTMTYVGNHE  RPPTTYPKKPPGYYVTGDGCQRDQDGYYWITGRIDDMLNVSGHL  LSTAEVESALVEHEAVARAAVVGHPPVKGBCLYCFVTLCGHT  FSPRLITEBLKQUTEKLIGP LATPDYIQNAPGLPKTRGGKTMRV  LRKIAQNDHDIGDMSTVADPSVISHLPSHRCLITIQ  6423 614 1237 ANLKEIPRDLPFTVLLYLDSNQITSIPNEIFKDLHQLRVLNLS  KNGIEFIDHHAFKGVASTLGTLDLSDNRIQSVHKNAFNNLKARA  RIANNPHHCDCTLQQULSRMASHBETAINVICKTSVLDEHAGRP  FLANANDALCHLPKHTTDYANLVTMPGHPTWVISVVVYVRQN  QEDARRHLEYLKSLPSRQKKADEPDDISTVV  (GERGKGDDWYVAHRWTHIKGHLFVTGGSGGMGYPRL  KKVSWPVAANVHCSCVLPKKYCNFIDKLFTRGSGGMGYPRL  GGKGLGDWYVAHRWTHIKGLKDRYPKRPVASVGANSKISA  LKGSKGKDWBIPVPVGISVTDENGKIIGELNKENDRILVAQCGL  GGKLLTMFIPLKGQRRIHLBLKLLADVLGFPNAKKSELLSC  VSHAKAPALADJAFTTLRPBLKGIMSDFRQISVADLPGLIEGAR  MNKGMGHKPLKHLEFTRQLLFVVDISGFQLSSHTQYRTAPSTTI  LLTKKBLQTKPRALLAVNNODLPDAQDKFHELMSQLQNP  KDPLHLFERNNIPERTVERCHLIPISAVTGSGIBELKNCIRKSL  CRGSLVDIGSGGGIPLETLIKBSQSRFVLIPASFEVNSLQKSNWGFILTG  CRGSLVDIGSGGGTIVIAAAKKGPTAVGYEINPULWYSEYRA  WREGVHGSAKYYISDLAKVYPSQYSNVVIFGUPOMIQLEKKLE  KRECTISMHFQLETIQA  RELEDDARVIACRFFPPHHTTPDHVTGEGIDTVWAYDASTFRGE  KRPCTISMHFQLETQA  GRAGPFRAALQEELSDVLITIVALAARCRYDLPLAKSKERLE  LHABFAARRDWEQFHQPRNLLLALVGEVGELABLFQNKTDGEPG  PQGHSPRERAALQEELSDVLITIVALAARCRYDLPLAVSCHNID  BRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT  ST	1	]	}	1
KELADRALQKCQEKGPPVRCCIVVKHIGARSIGMSDETSQSPPI KRSCPDVQISWNQGIDLWHELMQEAGBECPERCDARDPLFIL JTSGSTGKPKGVVHTVGGYMLYVATTFKYVPDPHABDVFWCTAD IGWITGHSYVTYGPLANGATSVLFRGIPTYPDVRRLWSIDVKYK VTKFYTAPTAIRLLMKFGDBPVTKHSRASLQVLGTVGEPINPEA MLWYHRVVGAQRCPIVDTWQCTTGGHHLTPLPGATTMKPGSAT FPFFGVAPAILNESGEELBGEAGGTLVFQWPGTMRTVYGNHE RPPTTYPKKPPGYYVTGDGQCQRDQDGYYWITGRIDDMLNVSGHL LSTAEVESALVERIEAVARAAVVGHPHPVKGECLYCFYTLCGHT FSPKLITERLKKQIREKIGPLATPDTYQNAFGLPKTRSGKIMRRV LRKLAQNBHHLGDMSTVADPSVISHLPSHRCLITQ LRKLAQNBHHLGDMSTVADPSVISHLPSHRCLITQ KRGIPFIDHAPKGVARSTLQTILDLSDNRJGSVHKNAPNNLKARA RLANDHCCCTLQVLRSMASHBTANNVICKSVLDEHIGGR FLNAANDADLCNLPKKTTDYAMLVTMPGWFTMVISYVVYVRQN QBOARRHLEYLKSLSPSRQKKADEPDDISTVV  6424  1 1188 KKSWPVAAMVECSCVLPKKYCNPTDKLRLETTGGSGGMYPRL GGEGGKGGDVWVVAHNRMTLKQLKDRYPKRFVAGVGANSKISA LKGSKGKDWBIPPVVGISVTDENGKIIGEKHKKNDRILVAQGGL GGKLLTWFLPLKGQKRIHHLDLKLIADVGLUSPPRACKSSLLSC VSHAKPAIADVAFTTLKPBLGKIMYSDPKQISVADLPGLIEGAH MNKGMGHKPLKHIERTRQLLFVVDISGFPRACKSSLLSC VSHAKPAIADVAFTTLKPBLGKIMYSDPKQISVADLPGLIEGAH MNKGMGHKPLKHIERTRQLLFVVDISGFPRIEMSQLQNP KDPLHLPFRNNIPPRTURPQHIIPISAVTGBGIBELKNCIRKSL DBQANQSNDALHKKQLLHUNSDLPDAQDKFBLMSQLQNP KDPLHLPFRNNIPPRTURPQHIIPISAVTGBGIBELKNCIRKSL DBQANQSNDALHKKQLLHUNSDLPDAQDKFBLMSQLQNP KDPLHLPFRNNIPPRTURPQHIIPISAVTGBGIBELKNCIRKSL DRGGGGTPLETIKBESGGRHPLAFSFFWSKEJCKSMWFPLLTG LVGGTLVAVYAVATPPVPPALRKVCLPPVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGPTAVGYEINPWLWYSRYRA WRBGVHGSAKPYISDLMKVTPSQYSNVVIFGVPQMMQLEKKLE RELEDDARVIACRFPPPHWTPDHVTGEGIDTVWAYDASTPRGRE KRPCTSMHFQLFIQA  6426 30 565 SRGAAVGGMSVAGGETRGOTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAABRDWBQFHQPRILLALAUGEVGELABLFQWKTDGEPG PQGMSPRERAALQEELSDVLITIVALAARCRUDLPLAVLSKMDI WRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT ST			i	
RRSCHDVQISMRQGIDLWMHELMQEAGBKCEPBMCDARDPLFII YTSGSTKKPRGVVHTVGGYMLYVATTFKYVPDFHABDVFNCTAD IGM TTGHSYVTYGFLANGATSVLPEG PTTYPDVNRLMSIVDKYK VTKFYTAPTATRLIMKFGDBPVTKHSRASLQVLGTVGEPINFBA WLWYHRVVGAQRCPIVDTFWQTETGGHMLTPLPGATPMKPGSAT PPFFGVAPATLIMBSGBELEGEBGSYLVFKQFWRGIMKTVVGNHE RPPTTYPKKPPGYYVTGDGCQRDQDGYWTTGRIDDMINVSGHL LSTARWESALVAHERAVBARAVVGHPBVKGECLYCFVTLCOGHT FSPKLTBELKKQIREKIGP LATPDYIQNAPGLPKTRSGKIMRRV LRKTAQNGHDLGDMSTVADPSVISHLFSHRCLTIQ ANLKEIPRDDPBFTVLLVIDONTSIPMET FKNLHQLRVLNIS KNGIBFIDHAPKGVABTLQTLDLSDNRIQSVHKNAFNNILKARA RIANNPHCCCTTLQQVURSMASHBETANNICKTSVLDEHAGRP FINNANDADLCDLPKKTTUSYMLVTMFGWFTMVISYVYYVRON QBDARRHLBYLKSLPSRQKKADBEPDLSTVV QBDARRHLBYLKSLPSRQKKADBEPDLSTVV KKVSWPVAAWHCSCVLFRKYGNFIDRLRFTRGGSGMYPRL GGSGGKGCDWVVAHNRMTLKQLKDRYPRRFVAGVGANSKISA LKGSKGKWBIPYPVGISVTDENGKI IGEINKKNDRILVAQGGI. LKGSKGKWBIPYPVGISVTDENGKI IGEINKKNDRILVAQGGI. LKGSKGKWBIPYPVGISVTDENGKI IGEINKKNDRILVAQGGI. LKTHLPLKGQKRI IHLDLKLLADVGLVGPPNAGKSSLLSC VSHAKPALADVAFTTLKPELGKIMYSDFKQISVADLGGLEGAH MNKGMGHRPLKHIBSTRQLLFVUDISGPQLSSHTQVRTAFBETTIL LLTKREBLYRBELQTKPALLAVNRMDLPDAQDKFHBI MSQLQNP KDPHLHFERNI PERTVEPQHI IP ISAVTGEGI BELKNCIRKSL DBQANQBNDALHKKQLLIM ISDTMSSTEPPSKHAVYTSKMDII LVGGTLVAVVAVATPFVTPALLKVCLPFVPATMKQIENVVKMLR CRRGSLUDIGSGDGRIVIAAAKKGFTAVGYELMPBLVWYSSTRA WRBGGGGI PLETIKKBESGSFHUJASFEWALJQKSNWGPLITG CRGSLUDIGSGDGRIVIAAAKKGFTAVGYELMPBLVWYSSTRA WRBGYGGSAKY ISDLMKYTFSQYSNVI FSVPQMMULGEKKLB RELEDDARVIACRFPPPHWTPDHVTGBGI DTVWAYDASTFRGRE KRPCTISMHFQLPIQA  6426 30 565 SRGANVGGMSVAJGGEI RGDTGGRDTAAPGRFSFSPPEPTLEDI RR LHABFAABRDWBOFHQPRNILLLALVGEVGBLABLFQNKTDGEPG PQGMSPRERAALQBELSDVLIYIJVALAARCCRUDLPLAVISKMDI WRRYPAHLARSSSRKYTELPHGAISEDQAVGPADI PCDSTGQT ST		Ì	1	
TYSGSTGKPKGVUHTVGGYMLYVATTEKYVPDFHABUVFMCTAD  IGMITGHSYTYYGFLANGATSVLJFEGTFYPDVDNRLWSIVDKYK VIKFYTAPFIARLIMKFUBDEVITHSRASLQVLGTVGEPINPBA WLWYHRVUGAQRCPIVDTFWGTETGEIMLTPLDGATPMKPGSAT PPFFGVAPAILNESGEBLEGEAEGYLUFKQFWPGIMRTVYGNHE RPFTTYPKKPPGYVTCTGGCQRDQDGYYMITGRIDMLNVSGHL LSTABVESALVEHEAVARAAVOGHPHPVKGECLYCFVTLCDGHT FSPKLTEBLKKQIREKIGPIATPDYIQNAPGLPKTRSGKIMRRV LRKIAQNDHDLGDMSTVADPSVISHLFSHRCLTIQ  6423 614 1237 ANLKEIFPDLPPTVLLYLDSNQTTSIPNEIFKULHGLRVLNLS RIGHTPDHAPRGVARTLQTLDLSDNRIQSVHKNAFNNLKARA RIANNPHHCDCTTLQQUIRSMASNHETAHNVICKTSVLDEHAGRP FINAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVQN QBDARRHLEYLKSLPSRQKKADEPDDISTVV GGSGGKGGDWWVAHNRMTLKOLKDRYPRRFFVAGVGANSKISA LKGSKGKDWBIPVPVGISVTDENGKIIGELNKENDRILVAQGGL GGKLLTWFLPLKGGKRITHDLKLLADVGLUGFPNAGKSSLLSC VSHAKPATADYAFTTLKPBLGKIMYSDFKQISVADLFGLIEGAM MNKGMGHKPLKHIERTRQLLFVVDISGFQLSVHTQNRTAPBTTI LLTTKBLSLYKRBLQTKPALLAVNKMDLPDAQDKFHBLMSQLQMP KDYLHLFSKNNIPERTVEFQHITPISAAVTGGIBELKNCTRKSL DBQANQENDALHKKQLINLMISDTMSSTEPPSKHAVTTSKMDII LVGGTLVAVVAVATPFVPPALRKVCLPPVPATNKQIENVVKMLR CRGSLVGUGSGGGRIVIAAAKKGFTAVGYELNPWLVWMSRYRA WRBGVHGSAKYISDLAKVTPSQYSNVVIEGVPQMMLQLEKKLE RELEDDARVTACRPPPPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSHHFQLIPIQA  6426 30 565 SRGAAVGGMSVAGGEIRGDTGGRDTAAPGRFSFSPEPPTLEDIRR LHABFAABRUWGPHQPRILLLALVGUGGELAELFQWKTDGEPG PQGMSPRERAALQBELSDVLIYLVALAARCRVDLPLAVLSKMDI WRRYPPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST				
IGWITGHSYVTYGPLANGATSVLPRG 1PTYPDVARLWSIUDKYK VTKYTAPTAIRLIMKRUDBEVTKHSRASIQVLGTVGEPINPBA WLWYHRVUGAGCPIVDTFMQTETGGINLIPPLPGATPMKPGSAT PPPFGVAPAILNESGERLEGEAEGYLVPKQPWPGIMRTVYGNHE RPETTYYKKPPGYYVTGGCQRDQDGYMITGRIDDMINVSGHL LSTARVESALVGHERAVARAAVGHPRPVKGCLYCFVTLCGGHT FSPKLTEBLKKQIREKIGP 1ATPDYIQNAPGLPKTRSGKIMRRV LRKIAQNGHDLGDMSTVADESVISHLFSHRCLTIQ  6423 614 1237 ANLKEIPPDLPBFTVLLYLDGOVITSIPMEIFKOLHQLRVLNIS KNGIEFIDBHAFKGVAFTLQTLDLSDNRIQSVHKNAFNNILKARA RIAMNPHCCOTTLQQVIRSMASNHETHANVICKTSVLDEHAGRP FLNAANDADLCHLDKHTTDYAMLVTMFGWFTMVISYVYYVRQN QEDARRHLEYLKSLPSRQKKADEPDDISTVV  6424 1 1188 KKYSWPVAAWMCSCVLPRKYGNFIDKIRLFTRGSGGMGYPRI GGGGGGGGDWWVAHNRMTLKQLKDKYPRKRFVAGVGANSKISA LKGSKGKUMEIPVPVGISVTDENGKIIGEINKENDRILVAQGGL GGKLLTWFLPLKGQKRIHHLDLKLIADVGLVGPPNAGKSSLLSC VSHAKPAIADVAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH MNKGMGHKPLKHIERTRQLLFVVDISGFQLSSHTQVRTAFETTI LLTKRLEIVKBELQTKPALLAVNRMDLPDAQDKFHBIMSQLQNP KDPHBLFRNNN IEBTVEPCHIFJISAVTGEGIBELKNCITKSL DBQANQKNDALHKKQLLINLWISDTMSSTEPPSKHAVTTSKMDII CRRGSLVDIGSGGGIPLETLKEBSQSRHVLPASFEVNSLQKSNWGFLLTG CRRGSLVDIGSGGGRIVLAANKKSPTAVGEHIPWLWWYSRYRA WREGVEGSAKFYISDLMKVTPSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPPPHWTPDHVTGBGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA  6426 30 565 SEGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAFFAABRUWROPHQPRNLLLALALAGRGFSFSPEPTLEDIRR LHAFFAABRUWROPHQPRNLLLALALAGRGFSFFSPEPTLEDIRR LHAFFAABRUWROPHQPRNLLLALAURARCRUDLPLAVLSKMDI MRRRYPPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST	ļ	ļ	i	
VTKFYTAFTAIRLIMKFGDEPUTKHSRASLQULGTVGEPINPEA WIMWHRVVGAQRCDIVDTFWGTETGGHNITDLFGATPMKPGSAT FPPFFGVAPAILNESGERLEBGERAEGTLUPKQPWFGINRTVYGNHE RPPTTYPKKPPGYYVTGGCQRDQDGYYWITGRIDMLNVSGHL LSTABVESALVEHEAVARANVGHPHPVKGECLYCFVTLCDGHT FSPRIJTEELKRQIRRKIGPIATPDTYQNAFGLPKTRSGKIMRRV LRKIAQNDHDLGDMSTVADPSVISHLPSHRCLTIQ  6423 614 1237 ANLKEIPRDLPFRTVJLYLDSNGITSIPREIFKDLHQLRVLNLS KNGIFFIDBHAPKGVABTLQTLDLSDNRIQSVHKNAFNNLKARA RIANNPWHCDCTLQQVLRSMASNHETAHNVICKTEVLDEHAGRP FINAANDADLCNLPFKTTDYANLVTMFGWFTHVISVVYYVRQN OBDARRHLEFLKSILPSGKKADEPDLISTVV  6424 1 1188 KKVSWFVAAMVHCSCVLPRKYGNFIDKLRLFTRGGSGGMGYPRL GGEGGKGGDVWVVAHNRRTLKQLLKRYPPKRFVVAGVGANSKISA LKGSKGKUWBIPTVFGKISTVDRNGKIIGEINKKNDRILVAQGGL GGKLLTNFLPLKGQKRIIHLDLKLIADVGLVGFPNAGKSSLLSC VSHAKPATADVAFTTLKPELGKIMKSDFKQISVADLPGLIEGAH MNKGMGHRHKJKRIBERTGLFVVDISGFGLSSHTQVRTAPETTI LLTKELRLYKEBLQTKPALLAVNKMDLPDAQDKFHBLMSQLQNP KDPLHLFFKNNIPERTVSRPQHIIPISAVTGGGIBELKNCIRKSL DBQANQSRBDALHKKGLLAHLSDTMSSTEPPSKHAVTTSKMDLI LUGGTLVAVVAVATPFVTPALKVCLPFVPATMKQIENVVKMLR CRGSLVDIGSGDGRIVIAAAKKGPTAVGYELNPWLVYSRYRA WRBGVHGSAKYYISDLMKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPPPHWTPDHVTGGGIDTVWAYDASTFRGRE KRPCTSMHPQLDIQA  6426 30 565 SRGAAVGGMSVAGGEIRDTTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAASROWSOPHOPRNLLLALVGEVGELAELPQNKTDGGEP PQGHSPRERAALQEELSDVLIILVALAARCRUDLPLAVLSKMDI MRRRYPAHLARSSSKKYTKLPHGAISEDQAVGPADIPCDSTGQT ST	ł	ł		· · · · · · · · · · · · · · · · · · ·
### ### ##############################	İ	<i>.</i>		
FPFFGVAPAILMESGERLEGEAEGYLVFKQPWGIMRTVYGNHE RPETTYPKKPPGYYVTGDGCGYDGYYWITGRIDDMINSCHL LSTABVESALVERHEAVAEAAVGHPHPWKGECLYCFVTLCOGHT FSPKLTEBLKKQIREKIGPIATPDYIQNAPGLPKTRSGKIMRRV LRKIAQNDHDLGDMSTVADPSVISHLPSHRCLTIQ RNLEFPRDLPPBTVLLYLDSNQITSIPNEIFKDLHQLRVLNLS KNGIEFIDBHAPKGVASTLQTLDLSDNRIQSVHKNAFNNI.KARA RIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRP FINAANDADLCHLPKKTTDYAMUVTMPCWFTMVISYVVYYVRQN QBDARRHLEYLKSLPSRQKKADEPDISTVV GGBGGKGGDVWVAHNRMTLKQLKDRYPRRPVAGVGANSKISA LKGSKGDWBIPVVGISVTDENGKIIGELMKENDRILVAQGEL GGKLLTNFI,PLKGQKRIIHIDLKLLADVGLVGFPRAGKSSLLSC VSHAKPAIADVAFTTLKPBLGKIMYSDFKQISVADLPGLIEGAH MNKGMGHKFLKHIERTRQLLFVVDISGPQLSSHTQYRTAFETTI LLTKBLRIYKBBLQTKPALLAVNRMDLPDAQDKFHBLMSQLQNP KDFLHLFEKNNIPBRTVBFQHIIPISAVTGBGIBELKNCIRKSL DBQANQBNDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII LWGGTLVAVYAVATPFVTPALRVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA WRBGYHGSAKYYISDLWKVTPSQYSNVVIFGYPQMMLQLEKKLE RELEDDARVIACRFPPPHWTPDHVTGBGIDTVWAYDASTFRGRE KRPCTSMHFQLFIOA KRPCTSMHFQLFIOA KRPCTSMHFQLFIOA KRPCTSMHFQLFIOA KRPCTSMHFQLFIOA KRPCTSMHFQLFIOA KRPCTSMHFQLFIOA KRPCTSMHFQLFIOA KRPCTSMHFQLFIOA KRPCTSMHFQLFIOA KRRPTSMHFQLFIOA KRRPTSMHFQLFIOA KRRPTSMHFQLFIOA				
RPETTYPKKPPGYYVTGDGCQRDQDGYYWITGRIDDMLNVSGHL LSTABVESALVEHEAVAERAVVGHPHPVKGBCLYCFVTLCDGHT FSPKLITEBLKKQIREKIGP LATPDYI QNAPGLPKTRSKKIMRRV LRKIAQNDHDLGDMSTVADPSVISHLPSHRCLTIQ 6423 614 1237 ANLKEIPRDLPPSTVLLYLDSNOJTSIPNET FKDLHQLRVLNIS KNGIEFIDBHAPKGVAETLQTLDLSDNRIQSVHKNAFNNIKARA RIANNPWICDCTLQQVIRSMASNHETAHNVICKTSVLDEHAGRP FLNAANDADLCHLPKKTTDYAMLVTMPGWFTMVISYVVYYVRQN QEDARRHLEYLKSLPSRQKKADEPDDISTVV GGBGKGGDVWVVAHNRMTLKQLKDRYPRKPVAGVGANSKISA LKGSRGKOWRIFVPVGISVTDBNKIIGEINKRNDRILVAQGGL GGKLLTNFLPLKSGKRIIHLDLKLLADUGLVGFPNAGKSSLLSC VSHAKPATADVAFTTLKPBLGKIMYSDFKQLSVADLPGLIEGAH MNKGMGHKPLRHIERTRQLLFVVDISGPGLSSHTQYRTAPETTI LLTKRLRIYREBLQTKPALLAVNKMDLPDAQDKFHEIMSQLQNP KDFHHLFRKNNIPERTVEPCHITFISAVTGGSIBELKNCIRKSL DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII LAMBGGGIPLETTKRESGSRHVLPASFEVNSLQKSNMGFLITG LVGGTLVAVYAVATPPVTPALRKVCLPPVPATMKQIENVVKMIR CRRGSLVDIGSGDGRIVIAAAKKGPTAVGYBLNWILVMYSTYRA WRBGVHGSAKYYISDLMKVTPSQYSNVVIFGYPQMMLQLEKKLE RELEDDARVIACRFPPPHHTPDHVTGEGIDTVWAYDASTPRGRE KRPCTSMHFQLFIOA KRPCTSMHFQLFIOA KRPCTSMHFQLFIOA KRPCTSMHFQLFIOA KRPCTSMHFQLFIOA KRPCTSMHFQLFIOA KRPCTSMHFQLFIOA KRPCTSMHFQLFIOA KRPCTSMLFQLFIOA KRRPTSPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST				
LSTARVESALVEHEAVAEAAVVGHPHPVKGECLYCFVTLCDGHT FSPKLITEBLIKQIREKIGP LATPDYI QDAPGLPKTRSGKIMRRV LRKIAQNDHDLGDMSTVADPSVISHLPSHRCLIIQ  6423 614 1237 ANLKEIPRDLPPETVLLYLDSNQITGIPMEIPKDLHQLRVLNLS KNGIEFIDBHAFKGVAETLQTLDLSDNRIQSVHKNAFNNLKARA RIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRP FINNANDADLCKILKTTDYANLVTMFGWETMVISYVVYYVRQN QEDARRHLEYLKSLPSRQKKADEPDDISTVV  6424 1 1188 KKYSMPVAAMVHCSCVLFRKYGNFIDKLRIFTRGGSGGMGYPRL GGEGGKGGDVWVAHNRMTLKQLKDRYPRKRFVAGVGANSKISA LKGSKGKDWBIPYPVGISVTDENGKI IGEINKRNDRILVAQGGL GGKLLTNFLPLKGQKRIHLDLKLIADVGLVGFPNAGKSSLLSC VSHARPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH MNKGMGHKFLKHIERTRQLLFVVDISGFQLSSHTQYRTAPETTI LLTKRIRIVREBLQTKPALLAVNKMDLPDAQDKFHRIMSQLQNP KDPLHLFEKNMIPERTVBPQHIIPISAVTGEGIEELKNCIRKSL DBQANQENDALHKKQLLINLWISDITMSSTEPPSKHAVTTSKMDII LUGGTIVAVYAVATPFVTPALRKVCLPFVPATMKQIEMVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA WRBGVHGSAKFYISDLMKVTFSQYSNVVIEGVPQMMLQLEKKLE RELEDDARVIACRFPPPHMTPDHVTGEGIDTVWAYDASTPRGRE KRPCTSMHFQLFIQA  6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAARRDWRGFHQPRINLLALVGEVGELAELFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT		1	1	•
FSPKLTEBLKKQIREKIGPIATPDYIQNAPGLPKTRSGKIMRRV LRKIAQNDHDLGDMSTVADPSVISHLPSHRCLTIQ  ANLKEIPRDLPPETVLLYLDSNQITSIPNEIPKDLHQLRVLNLS KNGIEFIDBHAPKGVABTIQTLDLSDNRIQSVHKNAFNNLKARA RIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRP FIANANDADLCNLPKKTTDYAMLVTMPGWFTMVISYVVYYVRQN QBDARRHLEYLKSLPSRQKKADEPDDISTVV  6424 1 1188 KKYSWPVAAMVHCSCVLFRKYSMFIDKLRILFTRGSGGGMYPRL GGEGGKGGDWVVAHNRMTLKQLKDRYPRKFVAGVGANSKISA LKGSKGKOWBIPVPVGISVTDSNGKIIGEINKRBDRILVAQGGL GGKLLTNFLPLKGQKRIIHLDLKLLADVGLVGFPNAGKSSLLSC VSHARPATADYAPTTLKPBLGKIMYSDPKQISVADLPGLIEGAH MNKGMGHKPLKHIERTRQLLFVVDISGFQLSSHTQYRTAPETTI LLTKBLRLYKEBLQTKPALLAVNKMDLPDAQDKFHBLMSQLQNP KDFUHLFEKNMIPERTVEPQHIIPISAVTGEGIBELKNCIRKSL DBQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII  6425 1850 1144 LAMESGGGIPLETLKBESGSRHVLPASFEVNSLQKSNWGFLLTG LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRCSLVDIGSGDGRIVIAAAKGFTAVGYELMPWLVWYSRTRA WRBGVHGSAKFYISDLWKVTPSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACKFPPPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA  6426 30 565 SRGARVGGMSVAGGEIRGDTGGDTAAPGRFSFSPEPTLEDIRR LHABFAABRDWRGFHQPRULLALVGEVALDELFQWKTDGEPG PQGWSPRERAALQEELSDVLIYAVALAARCRVDLPLAVLSKMDI NRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT ST	İ			17 17
LRKIAQNDHDLGDMSTVADPSVISHLPSHRCLTIQ  6423 614 1237 ANLKEIPRDLPPETVILIJDSNQTTSIPNEIPKDLHQLRVLNLS  KNGIEFIDBHAPKGVAETLQTLDLSDNRIQSVHKNAFNNLKARA RIANNPWHCCCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRP FLNAANDADLCNLPKKTTDYAMLVTMPGWPTMVISYVVYYVRQN QBDARRHLEFILKSIPSRQKKADEPDDISTVV  6424 1 1188 KKVSWPVAAMVHCSCVLPRKYCRPIDKLRLFTRGGSGGMGYPRL GGEGGKGGDVWVVAHNRMTLKQLKDRYPRKRFVAGVGANSKISA LKGSKGKDWRIPVPVGISVTDENGKIIGELNKENDRILVAQGGL GGKLLTNFIPLKGGKRIIHLDLKLIADVGLVGFPPNAGKSSLLSC VSHAKPAIADVAFTTIKPBLGKIMYSDPKQISVADLPGLIBGAH MNKGMSHKPIKHIERTRQLLFVVDISGPGLSSHTQVRTAPBTII LLTKKLRLYKBELQTKPALLAVNKMDLPDAQDKFHBLMSQLQNP KDPHALFFRNNIPERTVBPQHITPISAVTGGGIBELKNCIRKSL DBQANQSNGALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII LVGGTLVAVYAVATPFVTPALRKVCLPPVPATMKQIENVVKMLR CRGSLVDIGSGDGRIVIAAAKKSPTAVGYELNPWLVWYSRYRA WREGVHGSAKFYISDLMKVTFSQVSNVVJFGVPQMMLQLEKKLE RELEDDARVIACRFPPPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHPQLPIQA  6426 30 565 SRGAAVGGMSVAGGEIRGDTGEDTAAPGRFSFSPEPTLEDIRR LHABFAABRUWBOPHQPRNLLLALVGEVGELARLFQNKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST	i			1
6423 614 1237 ANLKETPRDLPPRTVLLYLDSNQITSIPNEIFKDLHQLRVLNIS KNGIEFIDBHAFKGVABTLQTIJLSDNRIQSVHKNAFNNLKARA RIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLJDEHAGRP FINAANDADICNLPKKTTDYAMLVTMPGWFTMVISYVVYYVRQN QEDARRHLEYLKSLPSRQKKADEPDDISTVV  6424 1 1188 KKVSWPVAAMVHCSCVLFRKYGNFIDKLRLFTRGGSGGMGYPRL GGEGKGGDWVVAINRMTLKQLKDRYPRKEPVAGGANSKISA LKGSKGDWWVVAINRMTLKQLKDRYPRKEPVAGGANSKISA LKGSKGKDWBIPVPVGISVTDENGKIIGELNKENDRILVAQGGL VSHAKPAIADYAFTTLKPBLGKIMYSDFKQISVADLPGLIEGAH MNKGMSHKFLKHIERTRQLLFVVDISGFQLSSHTQVRTAPBTII LLTKBLBLYKEBLQTKPALLAVNKMDLPDAQDKFHBLMSQLQNP KDPLHLFERNNIPERTVBPQHIIPISAVTGEGIBELKNCIRSL DBQANQBNDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII LQGTIJVAVYAVATPFVPALRKVCLPFVPATMKQIENVVKNLR CRRGSLVDIGSGGGIPLETLKBESQSRHVLPASFEVNSLQKSNWGFILTG LVGGTIJVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKNLR CRRGSLVDIGSGGDGRIVIAAAKKGPTAVGYBLNPWLVWYSRYRA WRBGVBGSAKPYISDLMKVTFSQYSNVVIFGVPQMMLQLBKKLE RELEDDARVIACRFPPPHWTPDHVTGEGIDTVWAYDASTPRGRE KRPCTSMHFQLPIQA 6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHABEFAABRDWKOFPRILLLALVGEVGELABLFQWKTDGEPG PQGMSPRERAALQEBISDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTBLPHGAISEDQAVGPADIPCDSTGQT		ŀ		· ·
KNGI BFI DBHAFKGVABTLQTI LLSDNRI QSVHKNAFNNLKARA RIANNPWHCDCTLQQVIRSMASHBTAHNVI CKTSVI LDEHAGRP FINAANDADI CNLPKKTTDYAMLVTMPGWFTMVI SYVVYYVRQN QBDARRHLEYI KSI PSRQKKADBPDDI STVV  KKYSWPVAAMVHCSCVLFRKYGNFI DKIRLFTRGGSGGMYPRL GGBGGKGGDVWVVAHNRMTLKQLKDRYPRKRFVAGVGANSKI SA LKGSKGKDWBI PVPVGI SVTDENGKI IGELNKENDRI LVAQGGL GGKLLTNFI PLIKGQRRI IHLDLKLIADVGLVGFPNAGKSSLLSC VSHAKPAIADYAFTTLKPBLGKIMYSDFKQI SVADLPGLI BGAH MNKGMSHKPIKHI BRTRQLLFVVDI SGFQLSSHTQVRTAPBTI I LLTKBLELYKEBLQTKPALLAVNKMDLPDAQDKFHBLMSQLQNP KDPLHLFEKNMI PERTVEFQHI IPI SAVTGEGI BELKNCI RKSL DBQANQENDALHKKQLLINLWI SDITMSSTEPPSKHAVTTSKMDI I  6425  1850  1144  LAMBGGGGI PLETTLBESQSRHVLPASFEVNSLQKSNWGFILTG CRRGSLVDIGSGDGRI VI AAAKKGPTAVGYBLNPWLVWYSRYRA WRBGVHGSAKFYI SDLWKVTPSQYSNVVI FGVPQMMLQLEKKLE RELEDDARVIACRFPPPHWTPDHVTGEGI DTVWAYDASTPRGRE KRPCTSMHFQLIPIQA  6426  30  565  SRGAAVGGMSVAGGEI RGDTGGEDTAAPGRFSFSPEPTLEDI RR LHABFAABRDWBQFHQPRNI LLLALVGEVGELABLFQWKTDGEPG PQGMSPRERAALQBELSDVLI YILVALAARCRUDLPLAVLSKMDI NRRRYPAHLARSSSRKYTKLPHGAI SEDQAVGPADI PCDSTGQT ST	-		1222	
RIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRP FINAANDADLCNLPKKTTDYAMLVTMPGWFTMVISYVVYYVRQN QEDARRHLEYLKSLPSRQKKADEPDDISTVV  6424  1 1188 KKVSWPVAMVESCVLFRKYGNFIDKLRLFTRGGSGGMYPRL GGEGGKGGDWVVAHNRMTLKQDLKDRYPRRFVAGVGANSKISA LKGSKGKDWBIPVPVGISVTDENGKI IGELNKENDRILVAQGGL GGKLLTNFLPLKGQKRITHLDLKLIADVGLVGFPRAGKSSLLSC VSHARPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH MNKGMGHKPLKHIERTRQLLFVVDISGFQLSSHTQYRTAPETTI LLITKBLRLYRBELQTKPALLAVNKMDLPDAQDKFHRIMSQLQNP KDFLHLFEKNMIPERTVEFQHIIPISAVTGEGIBELKNCIRKSL DBQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII LAMBGGGGIPLETLKBESQSRHVLPASFEVNSLQKSNWGFILTG CRRGSLVDIGSGDGRIVIAAAKKGPTAVGYELNPWLVWYGRYRA WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPPPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA  6426  30 565 SRGARVGGMSVAGGETRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHABFAAERDWSQFHQPRNLLLALVGEVGGLAELFQWKTDGEPG PQGMSPRERRALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT	6423	614	1237	
FINAANDADLCNLPKKTTDYAMLVTMPGWFTMVISYVVYYVRQN QEDARRHLEYLKSLPSRQKKADEPDDISTVV  6424  1 1188 KKVSWPVAAMVHCSCVLFRKYGRFIDKLELFTRGGSGGMGYPRL LKGSKGKDWBIPVPVGISVTDENGKIIGELNKENDRILVAQGGL LKGSKGKDWBIPVPVGISVTDENGKIIGELNKENDRILVAQGGL GGKLLTNFLPLKGQKRITHLDLKLLADVGLVGFPRAGKSSLLSC VSHAKPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH MNKGMGHKPLKHIERTRQLLFVVDISGFQLSSHTQYRTAPETII LLITKELRYKEBLQTKPALLAVNKMDLPDAQDKFHRIMSQLQNP KDPLHLFEKNMIPERTVEFQHIIPISAVTGEGIBELKNCIRKSL DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII LAMEGGGIPLETLKEBSQSRHVLPASFEVNSLQKSNWGFLLTG LVGGTILVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA WRBGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA KRPCTSMHFQLPIQA LHABFAAERDMRQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGMSPRERAALQEBLSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT ST		1		I · · · · · · · · · · · · · · · · · · ·
QEDARRHLEYLKSLPSRQKKADEPDDISTVV  6424  1 1188 KKVSWPVAAMVHCSCVLFRKYCNPIDKLRLPTRGGSGCMGYPRL GGEGGKGGDWWVAHNRMTLKOLKDRYPRRRFVAGVGANSKISA LKGSKGWBIPVPVGISVTDENGKI IGELNKENDRILVAQCGL GGKLLTNFLPLKGQKRITHLDLKLLADVGLVGFPNAGKSSLLSC VSHARPAIADVAFTTLKPELGKIMYSDFRQISVRDPGLISGAH MNKGMGHKPLKHIERTRQLLFVVDISGFQLSSHTQYRTAPBTII LLTKBLRLYREBLQTKPALLAVNKMDLPDAQDKFHELMSQLQNP KDFLHLFERNNIPERTUFPQHITPISAVTGEGIBELKNCIKKSL DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII LAMEGGGGIPLETLKBESQSRHVLPASFEVNSLQKSNWGFILTG LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA WRBGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA KRPCTSMHFQLPIQA LHABFAABRNBQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGMSPRERAALQEBLSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT		ł		
6424  1 1188 KKVSWPVAAMVHCSCVLFRKYGNFIDKLRLFTRGGSGGMYPRL GGEGGKGGDVWVAHNRMTLKQLKDRYPRKPVAGVGANSKISA LKGSKGKDWRIPVPVGISVTDERGKI IGELINKRNDRILVAQGGL GGKLLTNFLPLKGQKRIHLDLKLLADVGLVGFPANGKSSLLSC VSHARPAIADAYAPTTLKPBLGKIMYSDFKQISVADLPGLIBGAH MNKGMGHKPLKHIERTRQLLFVVDISGFQLSSHTQYRTAFETII LLTKBLRLYRBBLQTKPALLAVNKMDLPDAQDKFHRIMSQLQNP KDFLHIFEKNNIPERTUSPQHITISAVTGEGIBELKNCIRKSL DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII LAMBGGGGIPLETLKBESQSRHVLPASFEVNSLQKSNWGFILTG LVGGTIJVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA WRBGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA 6426  30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHABFFAABRDWBQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGMSPRERBALQEBLSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT			I	· ·
GGEGGKGDVWVAHNRMTLKQLKDRYPRKRFVAGVGANSKISA LKGSKGKDWRIPVPVGISVTDENGKIIGELNKKNDRILVAQGGL GGKLLTNFLPLKGGKRITHLDLKLLADVGLUGFPNAGKSSLLSC VSHAKPAIADYAFTTLKPBLGKIMYSDFKQISVADLPGLIEGAH MNKGMSHKPLKHIERTRQLLFVVDISGFQLSSHTQYRTAFBTII LLTKBLRLYKEBLQTKPALLAVNKMDLPDAQDKFHBLMSQLQNP KDFLHLFEKNMIPERTVEPQHIIPISAVTGEGIBELKNCIRKSL DBQANQENDALHKKOLLNLWISDTMSSTEPPSKHAVTTSKMDII LAMEGGGIPLETLKEBSQSRHVLPASFEVNSLQKSNWGFLLTG LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGGGDGRIVIAAAKKGFTAVGYELNDWLVWYSRYRA WRBGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPPPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA 6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHABFAAERDWBQFHQPRILLLALVGEVGELABLFQWKTDGEPG PQGMSPRERAALQEELSDVLIYLVALAARCRUDLPLAVLSKMDI NRRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT	-	<u> </u>	1700	
LKGSKGKDWBIPVPUGISVTDENGKI IGELNKENDRILVAQGGL GGKLLTNFLPLKGQKRITHLDLKLIADVGLVGFPRAGKSSLLSG VSHAKPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH MNKGMGHKPLKHIERTRQLLFVVDISGFQLSSHTQYRTAPETTI LLITKBLRLYKBELQTKPALLAVNKMDLPDAQDKFHBIMSQLQNP KDFLHLFEKNMIPERTVEFQHIIPISAVTGEGIBELKNCIRKSL DBQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII LAMBGGGGIPLETLKBESQSRHULPASFEVNSLQKSNWGFILTG CRRGSLVDIGSGDGRIVLFAAKKGPTAVGYELNPWLVWYSRYRA WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPPPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA LHABFAAERDWSQFTQPRNLLLALVGEVGELABLFQWKTDGEPG PQGMSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT ST	6424	1 1	1100	The first of the f
GGKLLTNFLPLKGQKRIHLDLKLIADVGLVGFPNAGKSSLLSC VSHAKPAIADYAFTTLKPBLGKIMYSDFKQISVADLPGLIBGAH MNKGMSHKFLKHIBRTTQLLFVVDISGFQLSSHTQYRTAFBTII LLTKBLBLYKBELQTKPALLAVNKMDLPDAQDKFHBLMSQLQNP KDFLHLFEKNMIPERTVBPQHIIPISAVTGEGIBELKNCIRKSL DBQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII  6425 1850 1144 LAMBGGGGIPLETLKBESQSRHVLPASFEVNSLQKSNWGFILTG LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLBKKLE RELEDDARVIACRFPPPHWTPDHVTGEGIDTVWAYDASTPRGRE KRPCTSMHFQLPIQA KRPCTSMHFQLPIQA LHABERABROWRQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEBLSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST	Ì	1		
VSHAKPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH MNKGMGHKPLKHIERTRQLLFVVDISGFQLSSHTQYRTAPETII LLITKELKLYKRELQTKPALLAVNKMDLPDAQDKFHRIMSQLQNP KDPLHLFEKNMIPERTVEFQHIIPISAVTGEGIBELKNCIRKSL DEQANQENDALHKKQLLINLWISDTMSSTEPPSKHAVTTSKMDII  6425 1850 1144 LAMEGGGIPLETLKEBSQSRHVLPASFEVNSLQKSNWGFLLTG LVGGTILVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA WRBGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA KRPCTSMHFQLPIQA LHABFAARGNWAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHABFAARGNWRQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGMSPRERAALQEBLSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT ST	1	1	1	F .
MNKGMGHKPLKHIERTRQLLFVVDISGFQLSSHTQYRTAPBTII  LLTKBLRLYREBLQTKPALLAVNKMDLPDAQDKFHBLMSQLQNP  KDFLHLFERNNIPERTUEFQHIITISAVTGEGIBELKNCIIKKSL  DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII  LAMEGGGGIPLETLKEBSQSRHVLPASFEVNSLQKSNWGFILTG  LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR  CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA  WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE  RELEDDARVIACRFPPHWTPDHVTGEGIDTVWAYDASTFRGRE  KRPCTSMHFQLPIQA  6426  30  565  SRGAAVGGMSVAGGEIRGDTGGRDTAAPGRFSFSPEPTLEDIRR  LHABEFAARENBOFHQPRNLLLALVGEVGELABLFQWKTDGEPG  PQGMSPRERAALQEBLSDVLIYLVALAARCRVDLPLAVLSKMDI  NRRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT  ST		1	}	1 "
LLTKBLRLYRBBLQTKPALLAVNKMDLPDAQDKFHBLMSQLQNP KDFLHLFEKNMIPERTURFQHITPISAVTGEGIBBLKNCIRKSL DBQANQBNDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII 6425 1850 1144 LAMBGGGGIPLETLKEBSQSRHVLPASFEVNSLQKSNWGFLLTG LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA WRBGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPPPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA 6426 30 565 SRGAAVGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHABFAABRDWBQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGMSPRERAALQEBLSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT ST	1	[	1	
KDFLHLFEKNMIPERTVEFQHIIPISAVTGEGIBELKNCIRKSL DBQANQENDALHKKQLINLWISDTMSSTEPPSKHAVTTSKHDII  6425 1850 1144 LAMEGGGIPLETLKBESQSRHULPASFEVNSLQKSNWGFILITG LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGPTAVGYELNPWLVWYSRYRA WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPPPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA  6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHABFAAERDWSQFHQPRNLLLALVGEVGELAELFQWKTDGEPG PQGMSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST	1	i	1	
DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII  6425 1850 1144 LAMEGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGGGDGRIVIAAAKKGFTAVGYELNDWLVWYSRYRA WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPPPHWTPDHVTGEGIDTVWAYDASTPRGRE KRPCTSMHFQLPIQA  6426 30 565 SRGAAVGGWSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHABFAABRDWRQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT ST		1	1	
6425 1850 1144 LAMEGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFILTG LVGGTIJVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYEINPHLVWYSRYRA WREGYHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPPPHWTPDHVTGEGIDTVWAYDASTPRGRE KRPCTSMHFQLPIQA 6426 30 565 SRGAAVGGWVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHABFAABRDWRQFHQPRNLLLALVGEVGELAELFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST	1	1		
LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA WREGVEGSAKFYISDLÆKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA 6426 30 565 SRGAAVGGWVAGGEIRGDTGGRDTAAPGRFSFSPEPTLEDIRR LHABFAAERDWRQFHQPRNLLLALVGEVGELAELFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST	6425	1050	1244	- <del></del>
CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA WRBGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPPPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA 6426 30 565 SRGAAVGGMSVAGGEIRGDTGGRDTAAPGRFSFSPEPTLEDIRR LHAEFAARRDWRQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGMSPRERAALQEBLSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT ST	0425	7920	1144	
WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPPPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA 6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHABFAAERDWBQFHQPRNLLLALVGEVGELAELPQWKTDGEPG PQGMSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST	Ī	1		1
RELEDDARVIACREPPPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPCTSMHFQLPIQA  6426 30 565 SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRESESPEPTLEDIRR LHABFAABRDWEQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT ST	1	1		
KRPCTSMHFQLPIQA  6426 30 565 SRGAAVGGMSVAGGETRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHABFAABRDWEQFHQPRNLLLALVGEVGELABLFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT ST	[	1	]	
6426 30 565 SRGAAVGGMSVAGGETRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQNKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT ST	[	1	[	
LHAEFAAERDWEQFHQPRNLLLALVGEVGELAELFQNKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST	-	<del> </del>	<del> </del>	
PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTKLPHGAISEDQAVGPADIPCDSTGQT ST	6426	30	565	1
NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST		1		
ST		1	1	,
	l	1	1	
6427   145   959   AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK				
	6427	145	959	
NIREYVRHMMYWIVFALFMAAEIVTDIFISWFPFYYEIKMAFVL		<u> </u>	<u> </u>	NIREYVKMMMYWIVFALFMAAEIVTDIFISWEPFYYEIKMAEVE

			-
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
)	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
1			WLLSPYTKGASLLYRKFVHPSLSRHEKEIDAYIVQAKERSYETV
i		İ	LSFGKRGLNIAASAAVQAATKSQGALAGRLRSFSMQDLRSISDA
l			PAPAYHDPLYLEDQVSHRRPPIGYRAGGLQDSDTEDECWSDTEA
]		İ	VPRAPARPREKPLIRSQSLRVVKRKPPVREGTSRSLKVRTRKKT
L			VPSDVDS
6428	1982	444	SGSGGKMEDHQHVPIDIQTSKLLDWLVDRRHCSLKWQSLVLTIR
ł	Ĭ		EKINAAIQDMPESEBIAQLLSGSYIHYFHCLRILDLLKGTEAST
			KNIFGRYSSQRMKDWQEIIALYBKDNTYLVELSSLLVRNVNYEI
1			PSLKKQIAKCQQLQQBYSRKBBBCQAGAABMREQFYHSCKQYGI
1	1		TGENVRGELLALVKDLPSQLAEIGAAAQQSLGEAIDVYQASVGF
1	[		VCESPTEQVLPMLRFVQKRGNSTVYEWRTGTEPSVVERPHLEEL
			PEQVAEDAIDWGDFGVEAVSEGTDSGISAEAAGIDWGIFPESDS
			KDPGGDGIDWGDDAVALQITVLRAGTQAPEGVARGPDALTLLEY
			TETRNQFLDELMELBIFLAQRAVBLSEBADVLSVSQFQLAPAIL
ĺ			QGQTKRKMVTMVSVLEDLIGKLTSLQLQHLFMILASPRYVDRVT
ļ			BFLQQKLKQSQLLALKKKLMVQKQQEALREQAALEPKLDLLLEK
L			TKELQKLIEADISKRYSGRPVNLMGTSL
6429	3413	3442	EPSSWTAAPRGPLAAHPLEAAVQEDDRRALSFDSRIKVFANGTL
	1		VVKSVTDKDAGDYLCVARNKVGDDYVVLKVDVVMKPAKIEHKEE
l	ľ		NDHKVFYGGDLKVDCVATGLPNPEISNSLPDGSLVNSFMQSDDS
	ļ		GGRTKRYVVFNNGTLYFNEVGMREEGDYTCFAENQVGKDEMRVR
			VKVVTAPATIRNKTCLAVQVPYGDVVTVACBAKGEPMPKVTWLS
l			PTNKVIPTSSKKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGE
			DRKTVWIHVNVQPPKINGNPNPITTVREIAAGGSRKLIDCKAEG
)			IPTPRVLWAFPEGVVLPAPYYGNRITVHGNGSLDIRSLRKSDSV
			QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISBKITAMAGH
}			TISLNCSAAGTPTPSLVWVLPNGTDLQSGQQLQRFYHKADGMLH
ř			ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL
			VSIINGETLKLPCTPPGAGQGRFSWTLPNGMHLEGPQTLGRVSL
			LDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPR
			ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG
•			VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT
<u> </u>			TYIHVF
6430	1946	602	RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG
ŀ			AMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIKDFNKFCSFVLA
}			YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI
			QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM
			KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS
Ì			HPPRKKDRKNRKLGPGAGAGFGVLRRPRPTPGDGEKRSRIKKSK
			KRKLKKAERGDRLPPPGPPQAPPSDTDSEREREEEEERBEMA
	ļ.		TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE
			TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR
			PMIBCSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG
			GPPKSGEP
6431	3	605	WWNSSYNLPAYAPYLPCBACAMQDGRKGGAYAGKMEATTAGVGR
	1		LEEEALRRKERLKALREKTGRKOKEDGEPKTKHLREEEEEGEKH
			RELRLRNYVPEDBDLKKRRVPQAKPVAVBEKVKEQLBAAKPBPV
	[		IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER
	<u>.                                    </u>		LKGQEDSLASAVDAATEQKTCDSD
6432	56	1692	GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE
			DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR
	l		FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ
			WNELLETLHKLPIPDPGVSVHLSVHSYPTVPDTRELPSIPENRN
			LTEYFVAVDVNNMLHLYASMLYERRILIICSKLSTLTACIHGSA
			AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGIHLSLMEKVRN
			MALDDVVILNVDTNTLETPFDDLQSLPNDVISSLKNRLKKVSTT
	~~ <u>~~</u>		

		_	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
10	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l			
!	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	ì	\=possible nucleotide insertion)
			TGDGVARAFLKAQAAFFGSYRNALKIEPREPITFCERAFVSHYR
l		1	SGAMROFIONATOLOLFKOFIDGRLDLLNSGEGFSDVFEEEINM
ŀ		1	GBYAGSDKLYHQWLSTVRKGSGAILNTVKTKANPAMKTVYKFDI
<b>!</b>	1	1	AKNGCAPTPEROLPKTAPSPLVEAKDPKLREDRRPITVHFGQVR
[	1	1	PPRPHVVKRPKSNIAVEGRRTSVPSPBONTIATPATLHILOKSI
1	1	j.	
			THFAAKFPTRGWTSSSH
6433	1524	484	APVTKRKEVFAKDSKGSALDAGRDPKRPALPETLCESGWASNTA
	i	1	PTTPPQPGWCLCGKDFKSSCQTPGREKERRLATMHGSCSFLMLL
i			LPLLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDML
	ł	İ	HMRWDBELAAFAKAYARQCVWGHNKBRGRRGENLFAITDEGMDV
l		1	PLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCG
i	ł .	1	SHFCEKLOGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP
!	1	i	SGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMG
i			AEGPDKPSVVSGLNSGPGHVWGPLLGLLLLPPLVLAGIF
6476	<del> </del>	<del></del>	MPQLNFGMADPTQMGGLSMLLLAGEHALGTPBVFSGTCRPDVSE
6434	40	2002	
ł	Į.	l .	SPELRQKSPLFQFABISSSTSHSDASTKQCYTSALFQFABISSN
i		1	TSQLGGABPVKRCGKSALFQLAEMCLASEGMKMEESKLIKAKES
1			DGGRIKELEKGKEEKBIKMEKTDETRI-QKEABPEKSAKENLRDS
ļ			KELRNFEALQIDDIMAIKMEDPKEIRKEBLEEDHKCSHPPDFSY
ľ	ł	l	SASSKIIISDVPSRKDHMCHPHGIMIIBDPAALNKPEKLKKKKK
i		1	KSKMDRHGNDKSTPKKTCKKRQSSESDIBSVIYTIBAVAKGDWG
			IEKLGDTPRKKVRTS99GKGSILDAKPPKKKVKSREKKMSKEKS
i	i	Ī	SDTTKESRPPDFISISASKNISGETPEGIKAEPLTPMEDALPPS
ļ	1	! ·	LSGQAKPEDSDCHRKIETCGSRKSERSCKGALYKTLVSEGMLTS
	i	}	LRANVDRGKRSSGKGNSSDHEGCWNBESWTFSQSGTSGSKKPKK
] .			TKPKEDCLLGSAKLDEBFEKKFNSLPQYSPVTFDRKCVPVPRKK
I		1	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT
	ł	į .	MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ
ı	ì	ł	- '
			DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA
6435	2227	657	ALQRDAAAAYAHPEYEBRFLQEBTVSQQINSIBLLQTRPLALPB
	i		VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSKEENDIEE
l	Į.	1	QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA
l			VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD
l	i		PTRESVLQPSPQVPATTVAHTATQQPAAPAPPAVSPREALMRAM
1		}	HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEREDDTRNVI
ļ	1	1	GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY
		l	GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR
i	1	i	AFTRNIIKYDLKORYVAAWAMLHDVAYBEATPWRWQGHSDVDFA
	Į	1	VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG
1		1	LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR
l	1		
<u> </u>			LLFENBYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY
6436	1295	341	GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVM
l		1	YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL
	1	1	NVTATGAGPAHALYPACYEKLKKTLSDVIHPGGNSHIANGAAGC
1	1	1	VATLIHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG
Ì	1	!	AFYRSYTTQLTMNVPFQAIHFMTYEFLQBHFNPQRRYNPSSHVL
1	1		SGACAGAVAAAATTPLDVCKTLLNTQKSLALNSHITGHITGMAS
	}	1	AFRTVYOVGGVTAYFRGVOARVIYQIPSTAIAWSVYEFFKYLIT
l		1	KROKEWRACK
	1655		
6437	1828	360 .	PPAPAPPASPARHVTRTARGHLBGGSRAPPLLQAVPLQIKNMVK
		1	LIHTLADHGDDVNCCAFSFSLLATCSLDKTIRLYSLRDFTELPH
1	1	1	SPLKFHTYAVHCCCFSPSGHILASCSTDGTTVLWNTENGQMLAV
1		1	MEQPSGSPVRVCQFSPDSTCLASGAADGTVVLWNAQSYKLYRCG
Ī	1	1	SVKDGSLAACAFSPNGSFFVTGSSCGDLTVWDDKMRCLESEKAH
İ	[	I	DLGITCCDFSSQPVSDGRQGLQFFRLASCGQDCQVKIWIVSFTH
1	1	1	ILGFELKYKSTLSGHCAPVLACAPSHDGQMLVSGSVDKSVIVYD
L	<del></del>	L	

			ini na naka wa wata wa kasin iliofik
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ŀ			TNTENILHTLTQHTRYVTTCAFAPNTLLLATGSMDKTVNIWQFD
i	1		LETLCQARSTEHQLKQFTEDWSEEDVSTWLCAQDLKDLVGIFKM
1		ŀ	NNIDGKELLNITKESLADDLKIESLGLRSKVLRKIEELRTKVKS LSSGIPDEFICPITRELMKDPVIASDGYSYBEEAMKNWDPAKRN
İ			RTSPP
6438	109	901	EVQILRAKMPOTGGLIVPYGLLAOTMAOFGGLPVPLDOTLPLNV
0430	100	1	NPALPLSPTGLAGSLTNALSNGLLSGGLLGILENLPLLDILKPG
İ			GGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLRLGLVQSP
1		ĺ	DGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRD
l	i	1	KQERIHLVLGDCTHSPGSLQISLLDGLGPLPIQGLLDSLTGILN
1	1	ſ	KVLPELVQGNVCPLVNEVLRGLDITLVHDIVNMLIHGLQFVIKV
6439	23	412	SIQTASAITTEMASQSQGIQQLLQABKRAABKVADARKRKARRL
[	1	j	KQAKBEAQMEVEQYRREREHEFOSKQQAAMGSQGNLSAEVEQAT
		[	RRQVQGMQSSQQRNRERVLAQLLGMVCDVRPQVHPNYRISA
6440	3	517	RARWINSDMGDLPGLVRLS IALRIQPNDGPVFYKVDGQRFGQNRT
1	1		IKLLTGSSYKVEVKIKPSTLQVENISIGGVLVPLELKSKEPDGD
1		]	RVVYTGTYDTRGVTPTKSGKRQPIQITMPFTDIGTFETVWQVKP
		l	YNYHKRDHCQWGSPPSVIBYECKPNBTRSLMWVNKBSFL
6441	234	1373	KSGGLRRRQRPGRSAAVGEBELPPGMEKFKAAMLIGSVGDALGY
ļ	1		RNVCKBNSTVGMKIQBELQRSGGLDHLVLSPGEWPVSDNTIMHI
1			ATARALTIDYWCLDDLYREMVRCYVEIVEKLPERRPDPATIEGC
1	į.		AQLKPNNYLLAWHTPFNBKGSGFGAATKAMCIGLRYWKPERLET
ł		,	LIEVSVECGRMTHNHPTGFLGSLCTALFVSFAAQGKPLVQWGRD
1			MLRAVPLAEEYCRKTIRHTAEYQEHWFYFEAKWQFYLEERKISK DSENKAIFPDNYDAEEREKTYRKWSSEGRGGRRGHDAPMIAYDA
			LLAAGNSWTBLCHRAMFHGGESAATGTIAGCLFGLLYGLDLVPK
1			GLYQDLEDKEKLEDLGAALYRLSTEEK
6442	34	796	AEDPAGGLAGODTMFARGLKRKCVGHBEDVEGALAGLKTVSSYS
	i	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	LQRQSLLDMSLVKLQLCHMLVEPNLCRSVLIANTVRQIQERMTQ
ł			DGTWRTVAPQAAERAPLDRLVSTEILCRAANGQEGAHPASGLGD
ł			GHTQGPVSDLCPVTSAQAPRHLQSSAWKMDGPRENRGSFHKSLD
	'		QIFETLETKNPSCMEELFSDVDSPYYDLDTVLTGMMGGARPGPC
			EGLEGLAPATPGPSSSCKSDLGELDHVVRILVET
6443	2	555	MASPAASSVRPPRPKKBPQTLVIPKNAABEQKLKLERIMKNPDK
			avpipekmsemaprpppefvrdvmgssagagsgefhvyrhi.rrr
			KYORODYMDAMAKKOKLDAEFOKRLEKNKIAAEKOTAKRRKKRO
ł	ļ		KLKBKKLLAKKMKLEQKKQEGPGQPKEQGSSSSAEASGTEEKEE
			VPSFTMGR .
6444	390	899	GSTPRGKMRAPIPBPKPGDLIBIPRPFYRHWAIYVGDGYVVHLA
			PPSEVAGAGAASVMSALTDKAIVKKELLYDVAGSDKYQVNNKHD
1		Ī	DKYSPLPCSKI I QRAEBLVGQBVLYKLTSENCEHFVNBLRYGVA
5055	<u> </u>		RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ
6445	2	753	AGAAGAAGAARSPRPQAHTKGVRGLPSRRRSPDCGRMELAAGSF
	ł		SEEQFWEACARLQQPALAGADWQLLVETSGISIYRLLDKKTGLY
			EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQYVKELYEQECNGE
		•	TVVYWEVKYPPPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM PQLGBRSGVIRVKQYKQSLAIESDGKKGSKVFMYYFDNPGGOIP
			PQLOBROGYTRVRQYKQSLATESDGRRGSKYFMYYFDMPGGQIP   SWLINWAARNGVPNFLKDMARACQNYLKKT
6446	1	1651	RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENERDLPELS
5220	1	1021	DSGDBAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEBTFSHCKS
			EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV
		•	PWEKERYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS
			VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT
			CSSSTSVIADLOEDEDGVYFSSYGHYGIHEMLKDKIRTESYRD
			FIYONPHIFKDKVVLDVGCGTGILSMFAAKAGAKKVLGVDQSEI
	<u> </u>		Transport

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ı	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
I	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	† · · · · · · · · · · · · · · · · · · ·		LYQAMDIIRLNKLEDTITLIKGKIERVHLPVEKVDVIISKWMGY
	İ	ĺ	FLLFESMLDSVLYAKNKYLAKGGSVYPDICTISLVAVSDVNKHA
	<b>\</b>	l	DRIAFWDDVYGPKMSCMKKAVIPEAVVEVLDPKTLISEPCGIKH
	}		IDCHTTSISDLEFSSDFTLKITRTSMCTAIAGYFDIYFEKNCHN
ļ		i	RVVFSTGPQSTKTHWKQTVFLLEKPFSVKAGEALKGKVTVHKNK
l		1	KDPRSLTVTLTLNNSTQTYGLQ
6447	1554	1068	RLGPAEWHLSGPCHATLGAANRGRALGVRAAWRGAPLCORVMMP
· ·	<u>}</u>		SRTNLATGIPSSKVKYSRLSSTDDGYIDLQPKKTPPKIPYKAIA
1			LATVLFLIGAFLIIIGSLLLSGYISKGGADRAVPVLIIGILVFL
}	1	<b>[</b>	PGFYHLRIAYYASKGYRGYSYDDIPDFDD
6448	74	559	GQVLSHCYHYRSSRWRRGGLSRGRGAGVMALVPYEETTEFGLOK
1	1	ŀ	FHKPLATFSFANHTIQIRQDWRHLGVAAVVWDAAIVLSTYLEMG
1	ĺ		AVELRGRSAVELGAGTGLVGIVAALLACRIRYERDNNFLAMLER
1	1	1	QPIVRKVHYDPEKDVHIYEAQKRNQKEDL
6449	597	1876	EYGVCENLEKLEITGVSCEDVYAKLLHEYRHILGLWOPDIGPYG
l .	ł		GLLNVVVDGLFIIGWMYLPPHDPHVDDPMRFKPLFRIHLMERKA
1	ì		ATVECMYGHKGPHHGHIQIVKKDEPSTKCNQTDHHRMSGGRQKE
		1	FRTWLREEWGRTLEDIFHEHMQELILMKFIYTSQYDNCLTYRRI
1			YLPPSRPDDLIKPGLFKGTYGSHGLEIVMLSFHGRRARGTKITG
1			DPNIPAGQQTVKIDLRHRIQLPDLENORNFNBLSRIVLEVRERV
1		l	RQEQQEGGHEAGEGRGRQGPRESQPSPAQPRABAPSKGPDGTPG
,			BDGGEPGDAVAAAEQPAQCGQGQPFVLPVGVSSRNEDYPRTCRM
1			CFYGTGLIAGHGFTSPERTPGVFILFDEDRFGFVWLELKSFSLY
<b>(</b>		[	SRVQATFRNADAPSPQAFDEMLKNIQSLTS
6450	848	269	FVPAPRTVSGKRSLPGEWEERGEGEORTGREFSGNGGRAVEAAR
Į.	1		MRLLCGLWLWLSLLKVLQAQTPTPLPLPPPPMQSFQGNQFQGENF
1			VLGLAGNSPRPEHRALLNAFTATFELSDDGRFBVWNAMTRGQHC
P	l		DTWSYVLTPAAQPGQFTVDHRVWTHEQAGRPQDQPAGQELVAAS
l .			RDAGPVHLPGQSSGPLG
6451	232	939	HSPTPPTSPRASTMEDVKLEFPSLPQCKEDABEWTYPMRREMOE
ŀ	1		ILPGLFLGPYSSAMKSKLPVLQKHGITHIICIRQNIBANFIKPN
			FQQLFRYLVLDIADNPVENTIRFFPMTKEFIDGSLOMGGKVLVH
ł			GNAGISRSAAFVIAYIMETFGMKYRDAFAYVQERRFCINPNAGF
1			VHQLQEYBAIYLAKLTIQMMSPLQIERSLSVHSGTTGSLKRTHE
1			BEDDFGTMQVATAQNG
6452	1	652	RTRGESSNMEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQ
l		Ī	LKFLKPKINSFYAFEVKDAKGRTVSLEKYKGKVSLVVNVASDCQ
			LTDRNYLGLKELHKEPGPSHFSVLAFPCNQFGESEPRPSKEVES
	i		PARKNYGVTFPIFHKIKILGSEGBPAFRFLVDSSKKEPRWNFWK
1			YLVNPEGQVVKFWRPEEPIEVIRPDIAALVRQVIIKKKEDL
6453	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC
			RDKKNCKVVFSQQELRKRLTPLQYHVTQKKGTESAFEGEYTHHK
			DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSRAITFTDD
			FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT
1			PADSSGTAEGGSGVASPAQADKAEL
6454	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAOSGSC
1 1		•	RDKKNCKVVFSQQELRKRLTPLQYHVTQEKGTESAFEGEYTHHK
1			DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD
			FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSPT
1	·		PADSSGTARGGSGVASPAQADKARL
6455	1042	173	RVHLATVSASAAWDALGLPVRSHMQGSTRRMGVMTDVHRRFLQL
		. +	LMTHGVLEENDVKRLOTHCYKVHDRNATVDKLEDFINNINSVLE
1			SLYIBIKRGVTEDDGRPIYALVNLATTSISKMATDFAENELDLF
] .			RKALELIIDSETGFASSTNILNLVDQLKGKKMRKKEAEQVLQKF
<b></b>			VQNKWLIEKEGEFTLHGRAILEMEQYIRETYPDAVKICNICHSL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ľ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
			LIQGQSCETCGIRMHLPCVAKYFQSNAEPRCPHCNDYWPHEIPK
ł			VFDPEKERESGVLKSNKKSLRSRQH
6456	2	555	RPQSRSISMWRNSLLQVSSGLRWLRVCAMVDILGERHLVTCKGA
			TVBAEAALQNKVVALYFAAARCAPSRDFTPLLCDFYTALVAEAR
ŧ			RPAPFEVVFVSADGSSQEMLDFMRKLHGAWLALPFHDPYRHELR
ł	}		KRYNVTAIPKLVIVKQNGEVITNKGRKQIRERGLACFQDWVEAA
1		l	DIFQNFSV
6457	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
		j	KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
l		[	IILGKQYSLNIILSVFAIILGAFIAAGSDLAPNLEGYIFVFLND
l			IFTAANGVYTKQKMDPKBLGKYGVLFYNACFMIIPTLIISVSTG
		j	DLQQATBFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
f	į .	l	TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
		İ	SPLTLSSQLKPKPVGEENICLDLKS
6458	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
1 3.55			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
i	İ		IILGKOYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
i		ł	IPTAANGVYTKOKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
	ļ	j	DLQQATBFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
			SFLTLSSOLKPKPVGBENICLDLKS
6459	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
0.55	""		KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
1	ì		IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
		}	IPTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
		,	DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
1			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
	1		SFLTLSSQLKPKPVGEENICLDLKS
6460	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
ł		•	IFTAANGVYTKQKMDPKRLGKYGVLFYNACFMIIPTLIISVSTG
ł		1	DLQQATBPNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
1		1	TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
			SPLTLSSQLKPKPVGRENICLDLKS
6461	1653	360	LQQRTLRITAVGQTHPIAWMAWEPSLGAFYGPASFITFVNCMYF
			LSIPIQLKRHPERKYELKEPTEEQQRLAANENGEINHQDSMSLS
!	1		LISTSALENEHTPHSQLLGASLTLLLYVALWMFGALAVSLYYPL
			DLVFSFVFGATSLSFSAFFVVHHCVNREDVRLAWIMTCCPGRSS
1	1		YSVQVNVQPPNSNGTNGEAPKCPNSSAESSCTNKSASSFKNSSQ
	ŀ	1	GCKLTNLQAAAAQCHANSLPLNSTPQLDNSLTEHSMDNDIKMHV
1	1		APLEVQFRINVHSSRHHKNRSKGHRASRLTVLREYAYDVPTSVE
1	1		GSVQNGLPKSRLGNNEGHSRSRRAYLAYRERQYNPPQQDSSDAC
			STLPKSSRNFEKPVSTTSKKDALRKPAVVBLENQQKSYGLNLAI
1			QNGPIKSNGQEGPLLGTDSTGNVRTGLWKHETTV
6462	3	773	SERLDREKKLKEDSPRKTPNKESGVPSLPVSLTSIKEEPKKAKH
	1		PDSQSMEBSKLKNDDRKTPVNWKDSRGTRVAVSSPMSQHQSYIQ
]	1		YLHAYPYPQMYDPSHPAYRAVSPVLMHSYPGAYLSPGFHYPVYG
			KMSGREKTEKVNTSPSVNTKTTTESKALDLLQQHANQYRSKSPA
1	}	İ	PVEKATAERERRAERERDRHSPFGQRHLHTHHHTHVGMGYPLIP
1		1	GQYDPFQGLTSAALVASQQVAAQASASGMFPGQRRE
6463	2	350	VILCILGGWIFKNADRSMEKKKGEPRTRAEARPWVDEDLKDSSD
0 403	1 *	330	LHQABBDADEWQESEENVEHIPFSHNHYPEKEMVKRSQEFYBLL
			NKRRSVRFISNEQVPMEVIDNVIRTAGL
6464	12	1154	GILROKEREBRNRIHKKEILFLEHLLUVPSEMSSLSGKVQTVLG
0204	1 12	1	ATMMINISTRATIONAL TIMESTON SOUTH A LEGISLA CONTRACTOR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	corresponding to first	to first	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
)	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Doguesion	\=possible mucleotide insertion)
	bequess	<u> </u>	LVEPSKLGRTLTHEHLAMTFDCCYCPPPPCQEAISKEPIVMKNL
	[	į	YWIQKNAYSHKENLQLNQETBAIKEELLYFKANGGGALVENTTT
	}	1	GISRDTQTLKRLAKETGVHIISGAGFYVDATHSSETRAMSVEQL
ŀ	}	1	TDVLMNRILHGADGTSIKCGIIGEIGCSWPLTESERKVLQATAH
]	J		AQAQLGCPVIIHPGRSSRAPFQIIRILQBAGADISKTVMSHLDR
	ļ		TILDKKELLEFAQLGCYLEYDLFGTELLHYQLGPDIDMPDDNKR
		1	IRRVRLLVEEGCEDRILVAHDIHTKTRLMKYGGHGYSHILTNVV
			PKMLLRGITENVLDKILIENPKQWLTFK
6465	126	1396	KMTVFFKTLRNHWKKTTAGLCLLTWGGHWLYGKHCDNLLRRAAC
	ļ		QRAQVFGNQLIPPNAQVXKATVFLNPAACKGKARTLFEKNAAPI
İ			LHLSGMDVTIVKTDYEGQAKKLLRLMENTDVIIVAGGDGTLQEV
1	1		VTGVLRRTDEATFSKIPIGFIPLGETSSLSHTLFAESGNKVQHI
1			TDATLAIVKGETVPLDVLQIKGEKEQPVFAMTGLRWGSPRDAGV
	l		KVSKYWYLBPLKIKAAHFFSTLKEWPQTHQASISYTGPTERPPN BPEETPVQRPSLYRRILRRLASYWAQPQDALSQBVSPBVWKDVQ
i	1	ł	LSTIELSITTENNOLDPTSKEDFLNICIEPDTISKGDFITIGSR
}		ŀ	KVRNPKLHVEGTECLQASQCTLLIPEGAGGSFSIDSEBYEAMPV
(			EVKLLPRKLQFFCDPRKREQMLTSPTQ
6466	1134	828	VARGTELSQLEKAHPPADMGRRKSKRKPPPKKKMTGTLETQFTC
0400	11.3*	020	PFCNHEKSCDVKMDRARNTGVISCTVCLREFQTPITYLSBPVDV
Ì			YSDWIDACRAANQ
6467	301	2571	GRIRVLALAHGBLACHAVLTASLISIRSRIMDSDMDYBRPNVET
,	,		IKCVVVGDNAVGKTRLICARACNATLTQYQLLATHVPTVWAIDQ
1	1		YRVCQEVLERSRDVVDDVSVSLRLWDTFGDHHKDRRFAYGRSDV
			VVLCFSIANDMSLHHVKTMWYPEIKHFCPRAPVILVGCQLDLRY
	i	ł	ADLEAVNRARRPLARPIKPNEILPPEKGREVAKELGIPYYETSV
	1		VAQFGIKDVFDNAIRAALISRRHLQFWKSHLRNVQRPLLQAPFL
ļ		1	PPKPPPPIIVVPDPPSSSECPAHLLEDPLCADVILVLQERVRI
1 .	ļ ·	Į.	FAHKIYLSTSSSKFYDLFLMDLSEGELGGPSEPGGTHPEDHQGH
{	Ì	ļ.	SDQHHHHHHHHHGRDFLLRAASFDVCESVDRAGGSGPAGLRAST
		ł	SDGILRGNGTGYLPGRGRVLSSWSRAFVSIQEEMAEDPLTYKSR LMVVVKMDSSIQPGPFRAVLKYLYTGELDRNERDLMHIAHIAEL
1 .	ì	ļ	LEVFOLRMMVANILINNEAFMNORITKAFHVRRTNRVKECLAKGT
-	}	ļ	FSDVTFILDDGTISAHKPLLISSCDWMAAMPGGPFVESSTREVV
1	Į.	ì	FPYTSKSCMRAVLEYLYTGMFTSSPDLDDMKLIILANRLCLPHL
1			VALTEQYTYTGLMEATQMMVDIDGDVLVFLELAQFHCAYQLADW
			CLIHICTNYNNVCRKFPRDMKAMSPENQEYFEKHRWPPVWYLKE
	1	1	EDHYQRARKEREKEDYLHLKRQPKRRWLFWNSPSSPSSSAASSS
1	1		SPSSSSAVV
6468	3	1374	DAWAGTMMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLABPG
	_		LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNRPED
			KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
1			SRSEVRVKSPPEAGTQLPKIIPSRDEKVLGQSQEPNVNPASAGN
		J	QTQKTQDGGKSKRSTVDSKAMGRKSFSVHNNGGAVSFQFFFNIS
1			TDDQEGLYSLYFHKCLGKBLPSDKFTFSLDIEITEKNPDSYLSA
	1		GBIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWLMAAL
1			PFTKSLSLVFHAIDYHYISSQGFPIBGNAVVYYITHLLKGALLF
1	Į	1	ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES
ļ			TREGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD
	1	L	GKGKPSRAHFVLLSLL
6469	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLARPG
1	ļ		LGRVHHLALKDDVRHKVHLMTFGFFKDGYMVVNVSSLSLMEPED
}		1	KDVTIGFSLDRTKNDGFSSYLDRDVNYCILKKQSVSVTLLILDI
		1	SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN
1		1	QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS
L		<u> </u>	TDDQEGLYSLYFHKCLGKELPSDKPTFSLDIEITEKNPDSYLSA

Desiming moteotide   location   corresponding to first   mino acid amino ac	SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
NO: nucleotide corresponding to first amino acid amino acid residue of amino acid residue of amino acid sequence corresponding to first amino acid residue of amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first corresponding to first corresponding to first corresponding to first corresponding to the corresponding to the corresponding to the corresponding to first corresponding to			1	(A=A)anine C-Creteine D-Assartic Acid R
corresponding to first amino acid amino acid residue of amino acid amino acid aresidue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acid sequence				Glutamic Acid. F=Phenylalanine, G-Clucine
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence acid sequence aci	1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid and acid sequence amino acid sequence (2001, 1-possible mucleotide deletion, 1-possible mucleotide delet			to first	L=Leucine, M=Methionine, N=Asparagine,
### residue of amino acid residue of amino acid amino acid sequence amino acid sequence (amin	ł			P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence  Codon, /-possible mucleotide deletion,				S=Serine, T=Threonine, V=Valine,
Sequence   A-possible nucleotide insertion	,			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
GEIPLPKLYTSHAPFFFLSGTTWIHITERRERDVFKTHMENDA PPTKSLSLVFHATDVHYTSSQGFPTESGNAVVYTTHLIKSALL ITTALIGTGMAP IKHILSDUKKI FMVTD FREVLANVAYTIE TEGGTTETGEMKDSSPLVDLLCCGALIPFVVWSTEHLQRASAT GEKEPTATETGEMKDSSPLVDLLCCGALIPFVVWSTEHLQRASAT GEKEPTATETGEMKDSSPLVDLLCCGALIPFVVWSTEHLQRASAT GEKEPTATETGEMKDSSPLVDLLCCGALIPFVVWSTEHLQRASAT GEKEPTATETGEMKDSSPLVDLLCCGALIPFVVWSTEHLQRASAT GENEPRATETULAGEDASAGNARFSTERVFGSREHFSAFR GEPAPETOLOAQLQMPRAQMRFELAPGVSSS.NERPECRABR GURSSGGCCGCTESSPSSAAGRASMBEAREDCHSDTVRADDD ENESPARTDLQAQLQMPRAQMRFELAPGVSSS.NERPECRABR SLQKTSADDTGGGCGCATESSPSSAAGRASMBEAREDCHSDTVRANDD ENESPARTDLQAQLQMPRAQMRFELAPGVSSSTLENEPCRARR SLQKTSADDTGGGCASTESSPSSAAGRASMBEAREDCHSDTVRANDD ENESPARTDTGGCGCASTESSPSSAAGRASMBEAREDCHSDTVRANDD ENESPARTDTGGCGCASTESSPSSAAGRASMBEAREDCHSDTVRANDD ENESPARTDTGGCGCASTESSPSSAAGRASMBEAREDCHSDTVRANDD ENESPARTDTGGCASTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT		B .	sequence .	
PPTKSISIVYHAIDHYISSOGPIERSMAVYYTTHILKSAIL  ITTALIGINGRAPIKHILISDIKKII MIVTPREVLANNAYITIE  TEEGTEEVGLWRIDSLI-LVOLLCCGAILPPVVWSIRHLQBASAT  GKGKPSRAHFVLLISLI  6470  2726  1437  AASSGVSSRADAPVLAGSPASAGNORPSTFRVPGSRRHPSARR  CPLPREDGCETPGPQLLIPLGALLARPILLSSARTERSRHDV  QHPSGGGGKOSPSSSAAGPRAMMAREBECHISDIVRADDI  RWSPARTDLQAQLOWFRAGMPERLAGGVSSSNLENRPCRARR  SLQKTSADTIGKOGANAKEKAREL-LVANEGRALTYER HTV  RRAMQLVPDIBPKITTTRSPDGDGVCNSYIEDHDDDSKWADLLS  RRAMQLVPDIBPKITTTRSPDGDGVCNSYIEDHDDDSKWADLLS  RRAMQLVPDIBPKITTTRSPDGDGVCNSYIEDHDDDSKWADLLS  SDLARSLEGLSLIVCRGFYLTCARPDERWIRLACLKYMGRGCILLD  YPQOQLITQESVIKLCQPBLESSQIHISVLIPMEVINIYIRWVW  SDLDLRSLEGLSLVCKGFYLTCARPDERWIRLACLKYMGRGCILLD  PTTSNRDMPLERPRVRPGGVYLSKTTYIRQGGGSLOGPYRAMH  YPTSNRDMPLERPRVRPGGVYLSKTTYIRQGGGSLOGPYRAMH  YPTSNRDMPLERPRVRPGGVYLSKTTYIRQGGGSLOGPYRAMH  SVYNYXIRPPGCHVMHRTLAGEPTGLAGENGERTSVDDALRRERI  GAPINKAGGNRHLAGPRIGLEVOQPHEPVILAGERTGGLLSSELP  BKLFPVUTGSKEKGLFKKRTKVQKKSLLLKKPLRVDLILBNTSI  VPAPKOVLAHQUVNAKLLRKGQLWRRLAKQGELPRRVRRAQA  LINPSATRAKPGPQDTVERRPPTDLMAGDREPHOVQGDEPTGL  AAHBVELQRGKREARLGROCALPATEGAATSNPSPEDGUTLL  AAHBVELQRGKREARLGROCALPATEGAATSNPSPEDGUTLL  AAHBVELQRGKREARLGROCALPATEGAATSNPSPEDGUTLL  AAHBVELQRGKREARLGROLAFRIGLKYQAPDIDUQISSKIJTBLIRTIKKDE  GARRABADAKPRIGLIKYQAPDIDUQISSKIJTBLIRTIKKDE  RAMRUSHLRTVONNNEVI TEOFFARHGHEPPLOVGGOBPFIL  LINGSSARPAGNGALIGFILKYGKGLVULDERPARRERIOTIL  FRAVILOQQIINTIIDELGKASAKAGNISAPITSASRAGRRIIVY  ILKDSSARPAGNGALIGFILKYGYKGLVULDERPARRERIOTIL  DYTHLESVQRHGHGRGLFOYMIQKKRVEHOLIATDRPSKILKR  LIKKIYNLETTVONNNEVI TEOFFARHGHEPPLEARTHHERAR  AUDTPPAAPARLEPRRAGGILKYYSSGRPSKELKROPKILKTRIPQPA  AUDTPAAPARLEPRRAGGILKYSSGRPSKELKROPKILKTRIPQPA  AUDTPAAPARLEPRRAGGILKYSSGRPSKELKROPKILKTRIPQPA  BAPTEGSTGOAPHPPPESSSGLAGPHIGPTULIGTSPKASLEL  KSSIIGKKRPAAAKGIGAKKGLAGKVSSGSPSEERGAGAVAR  KLREGOAPAAKKGAGSSMARRILAVGEDILIGTPRASTELIGNEMMPC  LIKKGPUTARSARLARAFERGETABENTITSTAKSRGDMSMPC  LOGROGHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGGOGS  KVTKQBTYRRSARLISARCAPPEPPEPRRTSAKKERGAKISGA  KKREKCAGAGKEGTAPSENGETKABERIISKSTANKTSTROTP  PSTLSVKGGIETVRVKGTEN  462  LOGROGHPAA		sequence		
11TALIGTGMAP IKHILSDROKKITMIVIPERVLANVAYITER TERGTTER GERKINSIGLPUDLICGALIPPVWISTRILGRASAT GKGKESRAHFVILSIL  AAAGGVESRAHFVILSIL  AAAGGVESRAHFVILSIL  GPIPREGGCTFGPQLIPFLGALIRPPVILSBARTGERSHEPD QHPSGGCCTGGTESPSBAAGRPASMAEREEDCHSDTVRADDD EMESPARTIQAQIQUMPRAGMINFILAGOSKINENPCCARAS SQRTSADTIGKORGAKSEKARELLIKAVERSONDALIVALIVA REMAGLVPD IBFKITYTESPDGGVGKSYTJEDNDDGSMADILA YFQQQLTFQESVLKLQOPELESSQIHTSVLPMEVIJMITPHWV SDLDLRSLEQLSLVCRGFYLCARDPEIMPLACTKWGRSCIKIN PYTSMRDHPLERPRVPETGVYISKTTYIKGGSQSLDGFTRANIT VSYTRYIRPPDGHVMMITTPEBEPQSIVERLETS GPRINKGSKEGITKURVKYKOKSLILKAVERGSULGFTSAVIPE EKLFPUTGSGSVGGKUSSSSSDSGFGLERFSVUDALERREN GPRINKGSWERLANGPFJCLEVQOPHEDVILGERTSGGLISPAP EKLFPUTGSGSVGGKUSSSSSSGBDSGFGLERFSVUDALERREN GPRINKGSWERLANGPFJCLEVQOPHEDVILGERTSGGLISPAP EKLFPUTGSKKGGITKURVKYKOKSLILKAVERLANDILLENTSI VAPAFDULANGVANAKLERKSQLMERLANGGELPRVKRAQA LLINPSATRARPOPOTVERRPTYCUMASDHELVANGGELSPAP EKLFPUTGSKKKGITKNETKVKOKSLILKAVERLANDILLENTSI VAPAFDULANGVANAKLERKSQLMERLANGGELPRVKRAQA LLINPSATRARPOPOTVERRPTYCUMASDHELVANGGERISPAP EKLFPUTGSKKKGITKNETKVOKSLILKAVERLANDILLENTSI VAPAFDULANGVANAKLERKSQLMERLANGGERISPAP CYTKKGVKRORARLANDOPTOLMASDHAVERLANDIN CYTKKGGVKRORARLANDOPTOLMASDHAVERLANDIN CYTKKGVKRORARLANDOPTOLMASDHAVERLANDOPTOLMASDHAVERLANDOPTOLMASDHAVERLANDIN COTKKGGVKRORARLANDOPTOLMASDHAVERLANDIN ESDGGESPOGGSGPEAGDARVCPTRALLATTEKTERQORREKK VERRVQQAALBARALBHOELFRIQADFORTTTISSLITCLINGE ESDGGESPOGGSGPEAGDARVCPTRALLATTEKTERGORREKK VERRVQQAALBARALBHOELFRIQADFORTTITSSLITCLINGE ESDGGESPOGGSGPEAGDARVCPTRALLATTEKTERGERGSRITCH TARVOLQQUIMTIDELGKASAKAONISAPITSASROGRRITVY LIKOSAAPPARGAATOPTETTOLTERTILLEDIATICHTEKT LANGSARPARGAATOPTETTOLTERTILLEDIATICHTEKT LANGSARPARGAATOPTUTCHTOLTERIATICHTER ARVOLQQUIMTIDELGKASAKAONISAPITSASROGRRITVY LIKOSAAPPARGAATOPTUTCHTOLTERIATICHTEKTARATICHTA ANDDTPAAPARKLEPPERARGOLKERAPHVEVPLOCI DPYHLESVQRICHGRAGASSIGNABARNISAPITSASROGRRITMSARA NDSHASITYOVANOTY I FERTIFICATION TOLTERIATICHTER LANGSATARATOPTUTCHTOLTERIATICHTER LANGSATARATORATORATORATORATORATORATORATORATOR		1		
TERGTTETGLIMIUSLI-LOCGAILPPVWSIRHLQRASAT GKKYPSRAPFVLLSLI.  6470 2726 1437 AAASGVSSRADAFVLAQEDASAGNGRPSTPRVFGSRRHPSAFRE GPLPREDOCRTYGPQLLPLOCALLREVITLLSSAAGNGRSRESSRHPD GPRESGGGGGGGTESSSSAGRAPASHABREBGGGSTPVFADDD GHPSSGGGCGGTESSSSAGRAPASHABREBGGGSTPVFADDD EMESPABTDLQAQLQHFRAQAMFELARGYSSNLEMPCRAARA SLQKTSADTNGKGGDAKEKRAELPLKAVAKBEQNGALVRALEF RRAMQLVPDIEFRITYTSPDGDGVCNSYIEDDDSWADLL YPQOLTFOSSVLKLOPDSLUSSVIHISVLPMEVINYIPRWVV SDLDLRSLEQLSILVCRGFYICARDPSIMELACLKVNGRSCIKL PTTSNREMEFLERREVNEFDGVISKTYIRQGGSGLDFYRAMF SDLDLRSLEQLSILVCRGFYICARDPSIMELACLKVNGRSCIKL PTTSNREMEFLERREVNEFDGVISKTYIRQGGSGLDFYRAMF SDLDLRSLEQLSILVCRGFYICARDPSIMELACLKVNGRSCIKL PTTSNREMEFLERREVNEFDGVISKTYIRQGGSGLDFYRAMF SDLDLRSLEQLSILVCRGFYICARDPSIMELACLKVNGRSCIKL PTTSNREMEFLERREVNEFDGVISKTYIRQGGSGLDFYRAMF SPENDARGGGGGGGSSKSDADSGFIGLRPTSVUDPALRERRE GPRINKRGMKRIAGBELGEVODFILDEDGFTAGLRPTSVUDPALRERRE GRANKRELARDLEVODFILDEDGFTSGLLSERAP EKLFPVUTGSKERGGIFKKRTKVOKKSLLLKKPLEVULLLENTSI VPAPKOULLAGUPARAKKLRREGLAWENTAGGESTFGCLGGGGG GPRINKRGMKRIAGBELGVODFILDEDGTSGGLISERAP EKLFPVUTGSKERGGIFKKRTKVOKKSLLLKKPLEVULLLENTSI VPAPKOULLAGUPARAKKLRREGLAWENTAGGSTFGCLCGGGLS GENGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1			
GKKESBAHFVILISIL  AAASGYSSRADAPIJAGSBASAGNGRESTERVPGSRRHESAFR GPLPREDOCRTPGPQLLPLEGALLRERTILSSAABTGRSRHED GRESSGGRCRGGTSSSSAAGRASABAEREDGISTVRADDIS RESSGRCRGGTSSSSAAGRASABAEREDGISTVRADDIS RESSBATDLJAQLQUFFRISTPSPDGGGCKREGTSSPSSAAGRASABEREDGISTVRADDIS RESSBATDLJAQLQUFFRISTPSPDGGGCKREGTSSPSSAAGRASABEREDGISTVRADDIS SQKTSADTKSKOBOAKEKARELFILKAVERBONGGALVRA KEY RRAMGILVPDI FERITTTISPDGGGCKREGTSEDDDDGSKANDLL YPQQQLTPQSSVILKLQPBLESSQIHISVLPMEVIMYIPRWVV SDLDIRSLEGISIVCKGYYICARDPEIMELACKKWRGSCIKG PYTSNRUPHEERRYRVERDSVISKTTYTROGGGSLGGFYRAHH VEYTHYIRPPDGHVMMLTTERPGSIVERETR FYFDKMAGGGGGGGGSKSKSDADSGFUFTSVERPTWOPALRERR GPRINKRGWRRLAQBEIGLEVDQFLEDVELQBETSGGLISEAP BKLFPUTGSKEKSLTKKRTKVOKKSLLIKKPLEVDLILIBNTSI VPAPKDVLJARQVBRAKKLERREGLMELARGGSLIPREVWRAQA LLINPSATRARPGGPOTVERPPYDLMASDNPLDREVRQOBEPFLI QTKKKGWRRARHIRTPGAPAVEVAPASTPSFERDGTLLS AAHRVELQRGKRABKLERQLALPATRQAATGBSTFGELGGGLIS ESDGGGGFGGGGGFGAGDAVEVTPARTTEKKTEOGRERKK VERLEVQOAALRAARLRIGGLFATRGAATGBSTFGELGGGLIS ESDGGGGFGGGGGFGAGDAVEVTPARTTEKKTEOGRERKK VERLEVQOAALRAARLRIGGLFATRGAATGBSTFGELGGGRE ESDGGGGFGGGGGFGAGDAVEVTPARTTEKKTEOGRERKE VERLEVQOAALRAARLRIGGLFATRGAATGABTLETLLTLER GARRABAADKPRLGTLKYQAPDIDVQLISKTPARREGTITEKTTECORRERK VERLEVQOAALRAARLRIGGLFATRGAATGAATARSAFRGGTITEKTTEKTEORRERK VERLEVQOAALRAARLRIGGLFATRGAATGAATARSAFRGGTITEKTTECORRERK VERLEVQOAALRAARLRIGGLFATRGAATGAATARGAATGAATARGAAT	1			
6470 2726 1437 AAASGVSSRADAPULAQSPASAGNGRSTERVFGSRRHPSAER GPLPREDGCTPGPQLLPLEGALLRERTILLSSARFRERSHEND GPSLSGGCRGGTESSSAGRPASHARBERGGRHED GPSLSGGCRGGTESSSAGRPASHARBERGGRHED GRESSPABTDLQAQLQMFRAQMMFELARGYSSNIKBPCCAARR SLQXTASATNIKGKQBAKEKRALPLIKAVBERGOMALVSALKE RRAMQLVPDLEFKITYTESPDGDGVCNSYLEDNDDDSKMADLL YFQQQLTFQESVLKLQQFELESSGHISVLBWEKDMALVSALKE SDLDLRSLEQLSLVCRGFYLCARDPSHALACLKVWGRSCIKL PYTSNREMFLERPRVKFDGVYLSKTYTIRQGBGSLDGYRAWH VSTYRYLRFPDGHVMUTTEERPGSLDGYRAWH VSTYRYLRFPDGHVMUTTEERPGSLDGYRAWH GFRNKRGWRRLAGGEGVGKESSKSDADSGFYGLRFTSVDPALRRREI GPRNKRGWRRLAGGEGVGKESSKSDADSGFYGLRFTSVDPALRRREI GPRNKRGWRRLAGGEGLWGKESSKSCDADSGFYGLRFTSVDPALRRREI GPRNKRGWRRLAGGEGLWGKESSKSCDADSGFYGLRFTSVDPALRRREI GPRNKRGWRRLAGGEGLWGKESSKSCDADSGFYGLRFTSVDPALRRREI LIMPSATRARVGGCDTVERPFYDLWASDLLKRPLKVDLLLBETSS VARPRUVLANGUPMAKKLRREGGLWKLAKGGELDGFPURDFLOGDEFFHI OTIKKGVKRPARLHTKPSQAPAWVAPAGASYMPSFBDHQTLL AAHEUGLGGKERBKLERQLALPATQAATQBSTFQELCEGLLI ESDGEGEPGGSGPGGBGBGABCCFTPARLATTBKKTEQGRREKK VERLRVQQAALRARARLRIQGLIFFLIRGIKAQVALRLEALBARQGR RQARREBABAKPRHLGRUKYQADDIUGLSSKLTDGLETTLKDE KOARREBABAKPRHLGRUKYQADDIUGLSSKLTDGLETTLKDE ROARBEABAKPRHLGRUKYQADDIUGLSSKLTDGLETTLKDE NILBRRYKSPORRMITERRERAKYKWKULVEKRAFEETOL DFYTHESVGRUMEFFFENDALPFPERTYLDQLIRFPARRFFTTL LIKMSARPARGSFORMEFFFENDALPFPERTYLDQLIRFPARRFFTTL LIKMSARPARGSFORMEFFFENDALPFPERTYLDQLIRFPARRFFTTL LIKMSHABATTAVUTLGDLGSVGRIGHTPARPSREJKLAVVEDPWPLM RAPRRATTPAHPPPRSSLICHSPRAFGHRYBASHLKVAVEDPWPLM RAPRRATTPAHPPPRSSLICHSPRAFGHRYBASHLKAVEDPWPLM RAPREATTPAHPPPRSSLICHSPRAFGHRYBASHLKAVEDPWPLM RAPRESGTQQPASTESSGLAQPHGPNTDLLGTSPRASLEL LKSG1GKKRFARARTSLAKRANGLGAKKGLGRKVSSQFFSEIREQAQVAR LKGCAADAKKGLGARAKGLGAKKGLGRKVSSQFFSEIREQAQVAR KKRSCLGGGGRGTAPSRGGTKASREPHARKTSRAKREPGAKTSRGA KKKEKGERGFRAGGRGTATSRGGFKTASRTSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  462 LCGRGGBPAABAVVVRCFFFCFTDIVIMPKRKSPENTEGGGGS KVTKQBFTRRSARLSAKRAPPKPERFRYTSAKKBPGAKTSRGA KKKEKGRAGRAGGTATSSGGTKARBERTHISSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQYKGTMARKLISKGRWELSSTVULTDMKARGRALDHEER	1			
GPLPREDGCTTPGGGLIPLGCALLREPTLLSSAARTGERRHLD'  QRBSGGGRGGTESPSSAARTASAREDCTSDTYTRADDD  RNESPAETDLQAQLQMFRAQMMFELAPGVSSSNLENRPCRAPR  SLQKTSADTKGKGGAKEKARELPLKAVBERGMGALYBAIKEY-  RRAMGLUPDLEFRITTTESPDGGTCURGLUBNDDDSKAPDLL-  YFQQQLTFGGSVLKLCQPELESSGIHISVLFMEVLMYIPRWVV  SDLDLRSLGGLSLVCAGFFYLCARDPEILEDNDDSKAPDLL-  YFQQQLTFGGSVLKLCQPELESSGIHISVLFMEVLMYIPRWVV  SDLDLRSLGGLSLVCAGFFYLCARDPEILEDNDDSKAPDLL-  YFQDGLTFGGSVLKLCQPELESSGIHISVLFMEVLMYIPRWVV  SYPRYIRFPPDGHVUNLCLFRYSIGTHTGGGSLLGVPRAWH  VEYYRYIRFPPDGHVUNLTTEREPQSIVFRLRTR  GPRIKKRGWRRLAGGBLGLEVDQFLEDURLGETTSGGLLSPAPH  EKLFFVUNTGSKERGIJFKKRTVKVKSKLLHFTSVUPPALRRRRI  GPRIKKRGWRRLAGGBLGLEVDQFLEDURLGETTSGGLLSPAPH  EKLFFVUNTGSKERGIJFKKRTVKVKSKLHKPLRVDLLLENTSI  VPAPRDVLANGVUNDAKKLRREGGLMEKLAKGGRLPRFWURAGAN  LILMPSATRAKPGPQDTVERPPYDUMAGDINFLDRFLOKGLLSPAPH  GTKKKGVKRRARLHTKFDQAPAVEVAPARIASYMPSFEDBQTLLG  BEGGGEGFGGGGGPGAGDAVCTPARATTEKKTRQORRERKV  VIRILKVQQAALRARLRINGGLIFILGTIKGGVAALLELBRPQGR  ROARREABANDKPRLIGHLKYQAPDIDUGSKITJDELRTLLCDE  MILRORPKSPORRMITEPRERETRYLQGHLERPRAGTTIVLDGHLERPARGFTTYL  GARVELQQQINTI IDBIGKASARAQHLSSITJDELRTLLCDE  NILRORPKSPORRMITEPRERETRYLVDGHLERPARRFRFFTTYL  LIKUSSARPAGKGALTGFIKVGYKKLFVLDDREARHEVEPLCGIL  DEYYHLESVQHRHIGRELDKYABALTYSSLENREVIKVAVEDPWPLM  LIKUSSARPAGKGALTGFIKVGYKKLFVLDDREARHEVEPLCGIL  LIKUSHABALTYVEVLCIDCSGVIRSLGWHISTSTBLDSINMWFG  LIKUNGVGGNANATAFFRGHGCTANDANTKYNSRAAQMYRBELIKG  LIKUSQAALARKTOLLENTSAAVENSAAVENLAVQEDOPTHENTQPDGAR  AVDPTPAAPARKTDILLENSSAVENSPERKODOPTPEHTQPPA  DAPATEPSGTQQPAPSTESSGLAQPHRIPPRTDLLGTSPKASLLL  KSSIIGKKRENGARKGLGAKKGLGAKKGLGAQKVSSQFSSETERQAQVAR  KLRSQQABANAKGALSSAVASMELAVQELODR  GARAFRATTEVRICTERVKSTRN  DAPATEPSGTQQPAPSTESSGLAQPHRIPPRTDLLGTSPKASLLL  KSSIIGKKERKORADAKVGLESKARBERTHISRSTVNVSTSRGTP  PSTLISVKGQIETVRVKSTRN  CARREST DAPATTSSTVNVSTSRGTP  PSTLISVKGQIETVRVKGTRN  AVADEPTRRSARISAKPAPPREPERPRENTSTAKKBPGAKISRGA  KUKKERKGRAGRAGTCATSSRGBTKARBIHISRSTVNVSTSRGTP  PSTLISVKGQIETVRVKGTRN  ARAMAQYKGTMERBRAHLLLKKRRGREGMEVLKGRUKARGRALDHERET  GATOR PARATTERANDANARGLESSTVULUTIDAMKARGRALDHERE	6470	2726	1437	
GHPSGGGRCGGTESPSSAAGRPASMARAREDCHSDTVRADDD ENESPAETDLQAQLQMFRQGWFELAPGVSSSNLENRPCRAARE SIQKTSADTKGKGRGKEKARELPLKAVEBERGNGALYEATKF RRAMQLVPDISFKITTYTESPDEDGVGSSYIEDRDDDSKMADLLA YPQQOLTTOPSBVLKLQCPBLESGJINSJMENDERDDDSKMADLLA YPQQOLTTOPSBVLKLQCPBLESGJINSJMENDERDDDSKMADLLA PTSSMEMFLERPRVRFDGVYISKTYIRGGEGSLDGFYRAWH VEYYRYTRPPDGVYISKTYIRGGEGSLDGFYRAWH VEYYRYTRPPDGVYISKTYIRGGEGSLDGFYRAWH VEYYRYTRPPDGVIVMILTTEBEPQSIVVPRLERTR GPRIKKGGWRELAGBFIGLEVOPJENGGEGERDFYRAWH VEYRYTIRPPDGGVIKMINTTEBEPQSIVVPRLERTR GPRIKKGGWRELAGRIGGEPGGLGLEVOPJENGLGEGLIS GPRIKKGGWRELAGRIGGEVGKESKSSDADSGFIGLRPTSVUPALRERRR EKLFPUJIGSKEKGLITKJRTKVOKKSLLLKKPLRAVDLILLENTSI VPAPKOVLAHQVPNAKKLRKEGLUMEKLARGGELPREVRRAQAI LIMPSATRAKFGEQDTVRRPPVDLWASEDNFLDRFLVGGDEFFLI GYKKKGVKRIPARLHTIKPSQAPAVEVAPAGASYMPSFEDHQTILL AAHBVELQGRKEARKLERQLAPPATGATTSKKTFQORREKS VERLEVQOAALRAARLERQLAPPATGATTSKKTFQORREKS VERLEVQOAALRAARLERQLAPTGVAAGTSSTFOELCGGLIS ESDGSGEGGGGGGGGGGGAGDAAVCVPTARLATTSKKTFQORREKS VERLEVQOAALRAARLERQLAPTGVAATGSKTTLATGLECGILA ESDGSGEGGGGGFAGDABVCPTARLATTSKKTFQORREKS VERLEVQOAALRAARLERQUALPRERGTITT AAVDLQQQIMTIIDBIJGKASAKAGNLSAPTTSSSIMQSNRIIVVY LILKDSSAPPAGKGAITOFI KVGYKKLFVLDDREAHNEVEPLCII DPYHESVQRHGHGRRELGYQAHDUGLSPPARRFGTTT AAVDLQQQIMTIIDBIJGKASAKAGNLSAPTTSSSIMQSNRIIVY LILKDSSAPPAGKGAITOFI KVGYKKLFVLDDREAHNEVEPLCII DPYHESVQRHGHGRRELGYYMLQKERVEPHQLAIDRPSQKLLKR LAKHYNLETTVPQVNNFVI FSGFFAHGHRPPASILRATRHSRAA AVDTPTPAAPARLLPPRARGDI KPYSSSIDBERILKVAVEXPPPILN RAPRRATTPAHPPPRSSSIGNPERGGLRPFVP RAPPRATTPPAHPPPRSSSIGNPERGGLRPFVP RAPPRATTPPAHPPPRSSSIGNPERGGLRPFVP RAPPRATTPPAHPPPRSSSIGLAPBHTGFTTSTLDSNMMPC LACMQVGGNANATAFFRGGGCTAMDANTKYNSRAQMYREKIRK KSSIGKKERQAAGKGGALGAKKGLGAKKGLGAKKGLGGAKGGAGAGGAGAGAGA				
BRIESPARTDLAGAGOMPRAGMIFELAPGVSSSNLENRPCRAARS SLQKTSADTKGKQEQAKEKARELPLKAVBEEQINGALYEAIRF RRAMGLVPDISPKITYTESPEDGDGVGSSYIEDMEDDSKMADLLS YPQQQLTTQESSULKLCQPELESSQIHISULPMEYLMYIIFRWV SDLDLIRSLEGGISLVCKGFYTCARPEWIMYLTGKWVX SDLDLIRSLEGGISLVCKGFYTCARPEWIMYLTGKWVX SDLDLIRSLEGGISLVCKGFYTCARPEWIMYLTGKWVX SDLDLIRSLEGGISLVCKGFYTCARPEWIMYLTGKWVX VEYYRYRPPPDGIVMALTTEBEPQSYISKTTYIRQGEQSLOGFYRAWH VEYYRYRRPPDGIVMALTTEBEPQSYVPKIERTR  6471 1750 299 FFFDRMAAGGSGVGGKESSKSDADSGFGGLRPTSVUPALRRRR GPRIKKRGWRILAGBFLGLEVQDFLEDWILQBETTSGGLISPAPH BIKLFPVDIGSKEKGLIKKTKYGVGSELLKKPLRVDLLILENTSI VPAPKDVLAHQVUNAKKLRKEQLWEKLAKQGELPREVRRAQAI LLINPSATRAKBGPQDTVRRPFYDLMASDNILDEPLVGQDBFFLI LLINPSATRAKBGPQDTVRRPFYDLMASDNILDEPLVGQDBFFLI GPRIKKGVRRPARLIFTKFSQAPAVEVAPAGASYMPSFEDHOVILLS AAHEVSLQRGKRASKLERQLADPATQAATORSTFOFELCEGLIS, AAHEVSLQRGKRASKLERQLADPATQAATORSTFOFELCEGISLX ESDGEGFQGGEGPQGEGPAGDABVCTPTARLATTEKKTEQORRREKK VERLRVQQAALRAARLERGLEFYLKGIKKAVALITEKKTEQORRREKK VERLRVQQAALRAARLERGLEFYLKGIKKAVALITEKKTEQORRREKK VERLRVQQAALRAARLERGLEFYLKGIKKAVALITEKKTEQORRREKK VERLRVQQAALRAARLERGLEFYLKGIKKAVALITEKKTEQORRREKK VERLRVQQAALRAARLERGLEFYLKGIKKAVALITEKKTEQORRREKK VERLRVQQAALRAARLERGLEFYLKVALVEDPARRREFTTOT ARVDLQQQINTI IDELGKASAKAQNISAPITTSSIMQSNRILVI LLKGSSARPAGKGALIGFIKGYKKVIKULVEKARPEITOL DFYIHESVQRKGHGKRILFYNKVIKLVEKARPEITOL DFYIHESVQRKGHGKRILFYNKVIKULVEKARPEITOL DFYIHESVQRKGHGKRILFYNKVIKULVEKARPEITOL LKKHNILETTVPQVINNYVI YFEGFFAHGRRPPAPSLRATRISRAA AVDPTPAAPARKLPPVRSSISLGNPERGFLRYDVIKACFPOGGAK NSWASTTYGUFULDCSGVIRSLGVVILGPIRSTELDSINMBWRG LKKHNLETTVPQVINNYTYFTSFALDSINMBWRG LKKHNLETTVPQVINNYTYSFARGAPTSTELDSINMBWRG LKKHNLETVPQVINNATAFFRERAPTSTELDSINMBWRG LKKHNLETVPQVINNATAFFRERAPTSTELDSINMBWRG LKKHNLETVRGVINNATAFFRERAPTSTELDSINMBWRG LKKHNLETVRGVINNATAFFRERAPTSTELDSINMBWRG LKKHNLETVRGVINNATAFFRERAPTSTALLSTELDSINMBWRG LKKHNLETVRGVINNATAFFRERAPTSTELDSINGSTKAEPGAKISRGA KKREQQAADAKKGABESSWYASMELAYQBLOIDR KKREGQAADAKKGAERSWASARPLAYGETOTVINFKKKEPENTEGKOES KVTKQBPTRSSALLSAKAPPFKPEPRKTSAKKEPGAKISRGA KKREGQAADARKOGAETVRVKGTEN  462 LQRQCHPAAAPAVPVRCPTFCFTDIVINPK	į l			
SLOKTSADTKSKOROAKERKARELELKAVERBONGALYEA ITER RRAMQLVPD1BFRITYTRSPDGDGVONSY IEDNODDSKMADLL YFQQQLTFQESVLKLCQPBLESSQTHISVLFMSVIMY1FRWVV SDLDLRSLEQLSLVCRGFYLCARDPEIWRLACLKVWGRSCIKL PTYSNREWPLERPPRVPTGVYISKTYTGGGSGLDGYFRAWH VSYYRYIRPFPDGIVMMLTTPERPQSIVPRLETR  6471 1750 299 FFFDKMAAGGSVGGKRSKSDADSGFIGLPTSVDPALRRRRI GPRIKKRGWRELAGBELGLEVQPHEDVRLQERTSSGLISEAP BKLFPVDJGSKEKGLTKKRTKVQKKSLLLKKPLRVDLLILBRIST VPAPKDVLAHGVPURAKKLRKRSQUMALKAGGELPPEVRAQAY LINDSATRAKBGPQDTVERPPYDLWAGDNFLORPLVOQDEPFLI QTKKKGVKRPARLHTKPSQAPAVEVAPAGATSTPSFEHDQTLL AAHBVELQRGKEARKLERQLALPATAGAATQBSTCBELCEGILL BSDGEGEGGGGGEAGDABVCPTFARLATTEKKTFQORREKK VIRLBVQQAALRAARLHGULFIRLAKOVALIKLEALRARQR RQARREABAUKPRILGRLKYQAPDIDVQLSSKLTDSLETLLXDE ROARREABAUKPRILGRLKYQAPDIDVQLSSKLTDSLETLLXDE ROARREABAUKPRILGRLKYQAPDIDVQLSSKLTDSLETLLXDE ROARREABAUKPRILGRIKYQAPDIDVQLSSKLTDSLETLLXDE ROARREABAUKPRILGRIKYQAPDIDVQLSSKLTDSLETLLXDE ROARREABAUKPRILGRIKYGAPDIDVGLSSKLTDSLETLLXDE ROARREABAUKPRILGRIKYGAPDIDVGLSSKLTDSLETLLXDE ROARREATGRAFFORWAGNEAPTTSASRMQSNRIUVY LIKUSSARPAGKGAL 1GFI KVGYKKLEVLDDRRAINRWEPLCTI DPYTHESVQRHGHGRELPQVMLQKERVEPHQLAIDRPSQKLLKE LNKHYNLETTVPQVNNFVI IFBGFFAHGHRPPASIGRATRHISRAA AVDETPAAPARKLEPFRRABGI IKVYSSSDRETIKVAVENEPHDL RAPRRATTPAHPPPRSSSLGNPERGFLRPVDV RAPRRATTPAHPPPRSSSLGNPERGFLRPVDV RAPRRATTPAHPPPRSSSLGNPERGFLRPVDV RAPRRATTPAHPPPRSSSLGNPERGFLRPVDV RAPRRATTPAHPPPRSSSLGNPERGFLRPVDV RAPRRATTPHTPPPRSSSLGNPERGFLRPVDV RAPRRATTPHTPPPRSSSLGNAPRSTROTHROPPAM DAPATEPSGTQQPAPSTBSSGLAQPBIGPNTILLGTSKASLEDING KKENEPGGARGTAPSRNOGTKAREHILSRSTVNVSTSRGTP PSTLSVKGQIETVEKGTRN  462 LQRQGUPAAAPAVPVRCPTFCFTDIVIMPKRKSDENTEGKDGS KVTKQBFTRRSARLSAKPAPPKDERFKTSAKKEPGAKISRGA KKKERQGARGGTAPSSNOGTKAREHILSRSTVNVSTSRGTP PSTLSVKGQIETVEKGTRN  6474 3 462 LQRQGUPAAAPAVPVRCPTFCFTDIVIMPKRKSDENTEGKDGS KVTKQBFTRRSARLSAKPAPPKPERFKTSAKKEPGAKISRGA KKKERQGARGGTAPSSNOGTKAREHILSRSTVNVSTSRGTP PSTLSVKGQIETVEKGTRN  6475 3 462 LQRQGUPAAAPAVPVRCPTFCFTDIVIMPKRKSDENTEGKDGS KVTKQBFTRRSARLSAKPAPPKPERFKTSAKKEPGAKISRGA KKERGCRGARGGTAPSSNOGTKAREHILSRSTVNVSTSRGTP PSTLSVKGQIETVEKGTRN				
RRAMQLVPDIBEKTITYTSPDGIOGVCNSYLEDNDDDSKMADLL YPQQQLTFQESVLKLCQPBLESQITISVLPMEVIMYIFRWVY SDLDLRSLEQUSLVCRGFYLCARDPEIMILACLKVWGRSCIKL) PYTSMREMFLERPRVRPPGVYISKTTYIRQGGSLDGYTRAWH VEYTRYTRPPDGVYISKTTYIRQGGSLDGYTRAWH VEYTRYTIRPPDGVYISKTTYIRQGGSLDGYTRAWH VEYTRYTRPPDGVISKTTYIRQGGSLDGFTGRPTSVDPALRRRRI GPRIKKRGWRRILAGEFLGLKVDQFLEDVJGERTSGGLLSAPE BKLFFVJYTGSKEKGLTKKRTKVOKKSLLLKKPLIGETLGGLLSAPE BKLFFVJYTGSKEKGLTKKRTKVOKKSLLLKKPLIGETLGGLLSAPE BKLFFVJYTGSKEKGLTKKRTKVOKKSLLLKKPLIGETLGGLASAPE GRINKRGWRRILAGEFLGLKVOKKSLLLKKPLIGETSGGLISAPE BKLFFVJYTGSKEKGLTKKRTKVOKKSLLLKKPLIGETSGGLISAPE BKLFFVJYTGSKEKGLTKKRTKVOKKSLLLKKPLIGETSGGLISAPE BKLFFVJYTGSKEKGLTKKRTKVOKKSLLLKKPLIGETSGDEFLGG GFRIKKGVRRPARLHTKPGQAPAGASYNPSFEHDYOLLER LLMAGSTRANGPOTVVERPFYDLWAGADNPLORPFLIGGLESALS AMEWELQRQKEABKLERQLALPATSQAAATGSTTGBELCGGLIS ESIGGEPGQGSGPEAGGARVCFTPARLATTEKKTEOGRRPKK VERLEVQOAALRAARLERGGLAPATGCAAATGSTTGBELCGGLIS ESIGGEPGQGSGPEAGGARVCFTPARLATTEKKTEOGRRPKK VERLEVQOAALRAARLERGGLAPATGCAAATGSTTGBELCGGLIS ESIGGEPGQGSGPEAGGARVCFTPARLATTEKKTEOGRRPKK VERLEVQOAALRAARLERGGLAPKVOADLIGETPARAGTTTLKPK KURLOQGARMETPFDUVALAFPERTTYLDGULRPPARAGTTTLY ROARREASPARAGTARGALFFRCHGCTANIASPTTASSARMQSNRIVIVY LIKDSSARPAGKGAILGFIKVGYKKLFVLDDRRAHNEVEPLCTI DPYTHESVQRIKHGRELFGYMLQRRRYSEPHOLATDRPSOKLLKR LKKHVILATTVQVONNVIYEFFFFANGHEPPAPSKARMGSNRIVIVY ANDPTPAAPARKLEPPKRAGGIKPYRSGSRRIKLKVAVEPPWPILM RAPRRATTPPAHPPRSSSLGNSPRRGPLRPVPV  6473 22 912 SSAVEFVWEGKRMAAEPNTETGTLFFKELRAVPTNKACFPCGGR NSSMASITYGVPLCIDCSGYHRSLGYHLSFRITTELDSNINNWG LGGAALARHGTDLWIDMSKAYSGNSSFIRENGAVYNKKIRG LGGAALARHGTDLWIDMSKAYSGNSGFIRENGAVYNKKIRG KKREGGAALGARGGIARKGGAKKGGAKKGGAKKGGAKKGGAKKGGAKKG				
SDLDLRSLEGULSLVCRGFYTICARDPELWRLACLKVWGRSCIKLI PYTSWREMFLERPRVRFDGVYISKTTYRQGBGSLDGFYRAWH VSYYRYIRFPFDGHVMMLTTPEEPGSIVPRLETT  6471 1750 299 FFFDKWAAGGSCVGGKRSSKSDADSGFLGLRFTSVDPALRRRR GPRIKKRGWRRLAGBFLGLRVDGEBVRLQBETSGGLLSEAPT GPRIKKRGWRRLAGBFLGLRVDGEBVRLQBETSGGLLSEAPT EKLFPVIJTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLJLERTSS VPAPKUVLAHQVPRAKKLRRGGLWEKLAKQGELPRBVRRQAB LINPSATRRKPGDQCDTVBRPDYDLMASDMPLDRPLVGGDEFFLI OTKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSPEDHQTTLL AAHEVELQRQKEABKLERQLALPATEQATQBETFQLLCGGLLS ESGGEBEGQGSGPEAGDABVCPTPARLATTEKKTEQQRREKK VERLRVQQAALRAARLERQGLFRLIGKKVQAVALRLAELARQBR RQARRARAADKPRHLGRLKVQAVALRLAELARQBR RQARRARAADKPRHLGRLKVQAVALRLAELARQBR RQARRARAADKPRHLGRLKVQAVALRLAELARQBR RQARRARAADKPRHLGRLKVQAVALRLAELARQBT NILRDFKSFQRRMMIRPRERAKFKKVKVKLVEKRAFREIQL LIKDSSARPAGKGALIGPIKVGYKKLFVLDDRBAINBVEDLCIL DFYIHESVQRHGHGRELFQVMLQKERVEPHQLAIDRPSQKLLKR LIKHYNLETTVPQVNNVI JEEGFANGHRPPAPSLRATRHISRAA AVDDTYPAAPARKLPPKRARGGIKPYSSSGRBFLKVAVEPPWPLN RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP SSAVEFVWEGEKMAAEPNRTRIQTLFKRLRAVPTNKACFDCGAR NPSWASITYGVFLCIDCSGVHRSLGVHLSFTRSTELDSNMWRC LICHWYGGNAMATAFPRGHGCTANDANTKYNSRAAGVYRKKING LIGSAALARHGTDLWIDMNSSAVPNISPERKNGDFFTEHTOPPAM DAPATEPSGTQQPAPSTESSGLAQPHGPNTDLIGTSPKASILL KSSI IGKKKRAAARKKGIGAKKGIGAKVSSGFSEIRRQAQVAS KKSSI IGKKKRAAARKKGIGAKKGIGAKKGEBFRVDSTFFTEHTOPPAM DAPATEPSGTQQPAPSTESSGLAQPHRFSTERSTENDSSKRGF KVTKQBPTRRSARLSAKRAPPKPERFRKTSAKKEPGAKISRGA KGKRERQPAGKEGTAPSRNGETKREFHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKSTSRN  6476 106 1090 ARAMAQVKGTWREAGRAPHLLKKREQEVELKSTRAVVSTSRGTP PSTLSVKGQIETVRVKSTSRN  6476 106 1090 ARAMAQVKGTWREAGRAPHLLKKRRGARVINGSTURCST				RRAMQLVPDIBFKITYTRSPDGDGVGNSYIEDNDDDSKMADLLS
6471 1750 299 FFFDKWARGSGSGVGGKESSKSDADSGFIGLRPTSVDPALRERE 6471 1750 299 FFFDKWARGSGVGGKESSKSDADSGFIGLRPTSVDPALRERE GPRNKERGWRILAGBIGLBVDQFLEDURLQERTSGGLLSEAP BKLFPVDTGSKEKGLFKKRTKVQKKSLLLKKPLRVDLILENTSI UVAPKDVLABQVPNAKKLRKSCJWEKLAKGSELPREVRRAQA LLNPSATTRAKPGPQDTVERPPYDLWASDNPLDRFLVGQDEFFLL OTKKKSVKRPBALHTKPSQDAVBVAPAGASYNPSPBEDHQTLL AAHEVELQRQKEABKLERQLALPATEQAATQBSTFQELCSGLLS ESDGSGEPGQGSGPERGBAUCPTPARKJENGKRGVALRLAELARRQR RQARREABADKPRIJGRFRLKYQAPDIDVQLSSKLTDSLRTLKDEK VURLKRVQQAALBARAKIRGLGFRLKGJAAPATQBSTFQELCSGLLS ESDGSGEPGQGSGPERGBAUCPTPARKJENGKAGVALRLAELARRQR RQARREABADKPRIJGRLKYQAPDIDVQLSSKLTDSLRTLKDEK NILRDFKSFQRRMMIEPRERAKKVKLVUKKRKFREIQL ESDGSGEPGQGSGPERGBAUCPTPARKKVKLVUKKRFREIQL ILKDSSARPAGKGALIGFIKKGVALPUKLRALBRARRGR RQARREABADKPRIJGRKKYVALPUKLRARRGR RQARREABADKPRIJGRKKYVALPUKLARRERE ILKKHYNLSTTVPQVNNFYLLDGREAHNEVEPLCTI LKSSARPAGKGALIGFIKKGVKLPVLDDREAHNEVEPLCTI LKSSARPAGKGALIGFIKKGVKLPVLDDREAHNEVEPLCTI LKSCHRHYNLSTTVPQVNNFYLFSGFFAHORPPAPSILRATRISRAA AVDPTPAAPARKLPPKRAGI KPYSSGDREVLKVAVEPDWPLM RAPRRATPPAHPPPRSSSLGNSPERGGIRPFVP  6473 22 912 SSAVEFVWEGSKMAAEPSKTEIQTIFKRLRAVPTNKACPDCGAK NSMASITYGVPLCLDCSGVRSLGVHLSPTLSTBLDSNNNWFQ LRCMQVGGNANATAFFYRGHCCTANDANTKYNSRAAQMYRKKIRG LGSAALARKTDLWILMNSSAVPHISEKKOSDFTTEHTQPPARA PAPAPEPSGTQDAPAFSTSSLLAGPERGPTETDLLGTSFKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSPSEIERQAQVAB KLREQQAALBKGTLAKKGLGAAKKGLGAQKVSSQSPSEIERQAQVAB KLREQQAALAKKQABESHVASMELAYGLGIDTR  6474 3 462 LQRQRQHBAAAPAVVRCPTEPTDIVIMKRKSPENTEGKDGS KVTKQBPTRRSARLSAKRAPPKPEPRFKTSAKKEPGAKISRGGF PSTLSVKQQISTVZVKGTEN  6475 3 462 LQRQRQHBAAAPAVVRCPTFFFTDIVIMKRKSPENTEGKDGS KVTKQBPTRRSARLSAKRAPPKPRKYTSAKKEPGAKISRGGF PSTLSVKQQISTVZVKGTEN KKKEEKQEAGKEGTAPSKNGETKAERIHISRSTVMVSTSRGTP PSTLSVKQQISTVZVKGTEN  6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHVDAVVRGFER	l i			YFQQQLTFQESVLKLCQPBLESSQIHISVLPMEVLMYIPRWVVS
6471 1750 299 FFFDMAAGGSVGGKRSKSDADSGFIGLRFTSVDPALRRRRI GPRINKRGWRRIAGBEIGLEVOPFLEDURLGERTSGELLSEAP EKLFPUITGSKEKGLYKKRTKVOKKSLLIKKPLRVDLILERTSI VPAPKDVLAHQVPINAKKLRKEQLWEKLAKGELPREVRRAQAI LIMPSATRAKPOPQDTVERPPYDLMAGNIPLDRELVGGDEFFLI OTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSPEBOHQTILL AAHEVELQRGKEAPEKLERQLALPATEQAATQBSTGELCSGLILK ESGGEGEQGGGGPEAGDABVCPTPARLATTEKKTEQORRREK VIRLRVQQAALRAARLRHGELFRLAGVALRIATEKKTLEQORRREK VIRLRVQQAALRAARLRHGELFRLAGVALRIATELARQRE RQARREABADKPRRLGTLKYQAPDIDVQISSKLTDSLRTLKPBC NILRDRFKSFQRRNMIEPRERAKKKKKVKVKLVEKRAFREIQL ARVDLQQQIMTIIDBLGKASAKQNLSAPITSASRMQSNRHVYY LIKDSSARPAGKGALIGFIKVGYKLLFVLDGHLRPPARFPGTTTE ARVDLQQQIMTIIDBLGKASAKQNLSAPITSASRMQSNRHVYY LIKDSSARPAGKGALIGFIKVGYKLLFVLDGHLRPPARFPGTTTE ARVDLQQQIMTIIDBLGKASAKQNLSAPITSASRMQSNRHVYX LIKDSSARPAGKGALIGFIKVGYKLLFVLDGHLRPPARFPGTTTE ARVDLQQQIMTIIDBLGKASAKQNLSAPITSASRMQSNRHVYX LIKDSSARPAGKGALIGFIKVGYKLLFVLDGHLRPPARFPGTTTE ARVDLQQQIMTIIDBLGKASAKQNLSAPITSASRMQSNRHVYX LIKDSSARPAGKGALIGFIKVGYKLLFVLDGHRAPHSVERLC LIKHMLBTTVPOVNNFVIFEGFFAHQHPPADSILRATRHSRAA AVDPTPAAPARKLPFKRAEGDIKFYSSDIRKFVLKVAVEPPWPLN RAPRRATTPPAHPPRESSIGINSPRRGIPFPVD RAPPRATTPAHPPRESSIGINSPRRGIPFPVD RAPPRATTPAHPPRESSIGINSPRRGIPFFVD LIKCMQVGGRANATAFFRGHGCTANDANTKYNSRAAQMYRKIKG LIKCMQVGGRANATAFFRGHGCTANDANTKYNSRAAQMYRKIKG LIKCMQVGGRANATAFFRGHGCTANDANTKYNSRAAQMYRKIKG KKREGQAADAKKQASESMVABALYQGELQIB LKRSIIGKKKPAAAKKGLGAQKVSQSFSEIERQAQVAK KKRSQADAKKGLARQASESMVABALYQGELQIB KYKQBPTRRSARLSAKPAPPKPERFRKTSAKKEPGAKISRGA KYKQBPTRRSARLSAKPAPPKPERFRKTSAKKEPGAKISRGA KYKKGEPTRRSARLSAKPAPPKPERFRYSAKKEPGAKISRGA KYKKGEPTRRSARLSAKPAPPKPERFRYSAKKEPGAKISRGA KYKKGEPTRRSARLSAKPAPPKPERFRYSAKKEPGAKISRGA KYKKEEKQGAAGKECTAPSKWGETKAERIHLSRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEEFIL KSQVDKRFSAHYDAVVAREEL	1 1			SDLDLRSLEQLSLVCRGFYICARDPEIWRLACLKVWGRSCIKLV
6471 1750 299 FFFDKWARGGSGVGGKRSKSDADSGFIGLRPTSVDPALRRRRI GPRNKKRØWRLAGBEIGLEVDQFIEDDRLQERTSGGLISEAPI BKLFPUDTISKKRGWRLAGBEIGLEVDQFIEDDRLQERTSGGLISEAPI BKLFPUDTISKKRGJIKKRYGVKRSLLIKKPLRVDLILENTSI VPAPKDVLAHQVPNAKKLRKEQLWEKLAKQGELPREVRRAQAI LINPSATRAKPGPQDTVERPFYDLWASDNPLDRELVGQDEFFIL AAHEVELQRQKEAHKLERQLALPATEQAATQBSTFQELCEGLIL ESDGEGEPGQGSGPERGDABVCPTPARIATTEKKTEQORREKK VERLKRVQOAALBARAKIRGELAKGKATATEKKTEQORREKK VERLKRVQOAALBARAKIRGELAKGKATATEKKTEQORREKK ROARREABADKPRIJGRLKYQAPDIDVQLSSKLTDSLRTLKPEC NILRROFFSFGRRINHIBPRERRAKFRKYKVKLVEKRAFREIQL ESDSDAGWAMBFPFDVDALPPERTVLDQULREPPARPEGTTF ARVDLQQIMTIIDBLGKASAKAQNLSAPITSASRMGSNRHVVY LIKDSSARPAGKGATJGFIKVGYKKLPVJDDREAHINKVEPLCII DFYIHESVQRIKHGRELFQYMLQKERVSPHOLAIDRPSOKLLKE LIKHYNLETTVPQVNNFVIFGGFFAHGHRPPASSLRATRHSRAA AVDTPPAAPARKLPPKRARGDIKPYSSBREFILKVAVEPDWPLN RAPRRATPPAHPPPRSSLGNIPFRSBREFILKVAVEPDWPLN RAPRRATPPAHPPPRSSLGNIPFRSBREFILKVAVEPDWPLN LIKGSAALARHGTULWIDANSSAVPHISFEKKOSDFFTEHTQPPAN DAPATEPSGTQQPAPSTESSGLAQPRISPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSPSEIERQAQVAB KLRBQQAADAKKQAESSWJASMRLAYQBLQIDR 6474 3 462 LQRORQHBAAPADVDVCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKRJGAKKGLGARKSPCAAKKBCBAKKSRGAK KEKKERKQEAGKEGTAPSRIGATKABEHISRSTVNVSTSRGTP PSTLSVKGQIFTVRVKGTEN 6475 3 462 LQRORQHBAAPADVPCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKRAPPRPEPRPRKTSAKKEPGAKISRGA KGKKEKKQEAGKEGTAPSRIGGTKABEHISRSTVNVSTSRGTP PSTLSVKGQIFTVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMVLKQRIAEEFTIL KSQVDKRESAHYDAVRBERKSSTVGLVTILMDMKARQEALVRERE				
GPRINKERGINELAGBPIGLEVDGPLEDVRLQRETSGGLLSEAP  BKLFPUJTGSKEKGLITKKPTKVOKKSLLLKKPLEVDLILLENTSS  BEKLFPUJTGSKEKGLITKKPTKVOKKSLLLKKPLEVDLILLENTSS  VPAPKOVLANGVDVARKLRKEQLMEKLAKQGBLPREVRRAQAI  LINPSATRAKPGPQDTVERPFYDLMASDNPLDRPLVOGDSFFIL  QTKKKGVKRPARLHTKPGQAPAVEVAPAGASYMPSPEDHOTILL  AAHEVSLIQRGKEABKLLERQLADPATEQAATQBSTPGSEGLLS  ESDGEGEPQGBGPEAGDASVCPTPARLATTBKKTEQORREKK  VUERLRVQQAALRAARLEHQELFRILRGKAQVALRLASTLARRQPS  ROARREAGADKPERLGRUKYQADPIDVOLSSKITTDELRTLKDEC  NILRDRFKSFQRRNMIRPRERAKFKRKYKVKLVEKRAFREIQL  FORSTROARDARDARDFRETTVILDGHLAPPARRFGTTTT  ARVDLQQQIMTI IDBIGKAASARAQNISAPTASASRMQSNRHVVY  ILKDSSARPAGKGALIGFIKVGYKKLFVULDDREAHNEVSPLCII  DPYIHESVQRHGHIGRELFQYMLQKERVEPHQLAIDRPSOKLLKE  LAKHYNLETTVPQVNNFVI LEGPFAHOHRPAPSSIRATRHSRAA  AVDPTPAAPARKLPPKRARGDIKPYSSSDREFIKVAVEPPWPIN  RAPRRATPPAHPPPRSSSLGNSPREGFLKVAVEPPWPIN  RAPRRATPPAHPPPRSSSLGNSPREGFLKVAVEPPWPIN  RAPRRATPPAHPPPRSSSLGNSPREGFLKVAVEPPWPIN  RAPRRATDLWINDRSAVENHSPEKKDSDPFTEHTOPPAM  LECMQVGGRANATAFFRGGCTANDANTKYNGRAAQMYREKIEG  LGSAALARKTOLWINDRSAVENHSPEKKDSDPFTEHTOPPAM  DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASLEL  KSSIIGKKKPAAAKKGLGAKKGLGAKKGLGAKKOLGAKVSSGSPSBIERQAQVAB  KLREQQAADAKKQAESSMVASMRLAYGBLQIDR  6474  3 462 LQRQRQHPAAAPAVPVRCPTFCFTDLVIMPKRKSPENTBSKDGS  KVTKQBPTRRSARLSAKPAPPKPEPRFRKTSAKKBPGAKISGGA  KKKKEEKQEAGKGTAPSENGETKABEHHISRSTVMVSTSRGTP  PSTLSVKGQIETVRVKGTEN  6475  106  1090 ARAMAQYKGTMRRAGRAMHLLKKRRQREQMEVLKQRIAEETIL  KSQVDKRSTMRRAGRAMHLLKKRRQREQMEVLKQRIAEETIL  KSQVDKRSANHDAVEAGLKSSTVGLVTLINDMKARQRALJVERE	- CA71	1770		
EKLFPUJTGSKEKGLITKKRTKVQKKSLLIKKPLRVDIJLENTSI VPÄPKDVLÄHQVPNÄKKLRKEGLÜBERLÄRGGELPRIVRRAQAH LLINPSATRAKPGEQDTVERPTYDLMASDIPLÖPLÜGDEFFLI OTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSPEDHQTLLS AAHEVSLQRQKRABKLERQLÄLPÄTEQÄATQASTFORLGEGLIJA ESGGEGEGGEGGEGAGABAVCPTPARLATTEKKTEGORGREKK VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRQRI RQARREBADKPRRLGRLKYQAPDIDVQLSSKI.TDSLRTLKPEK ROARREBADKPRRLGRLKYQAPDIDVQLSSKI.TDSLRTLKPEK ROARREBADKPRRLGRLKYQAPDIDVQLSSKI.TDSLRTLKPEK ROARREBADKPRRLGRLKYQAPDIDVQLSSKI.TDSLRTLKPEK ROARREBADKPRRLGRLKYQAPDIDVQLSSKI.TDSLRTLKPEK ROARREBADKPRRLGRLKYQAVELUVALUERPPARREGTTIP ARVDLQQQIMTII IDBIGKASAKAQNI.SAPITSASRMQSNRHVYV LIKDSSARPAGKGAI IOFIKVGYKLFVLDDHERPARREGTTIP ARVDLQQQIMTII IDBIGKASAKAQNI.SAPITSASRMQSNRHVYV LIKDSSARPAGKGAI IOFIKVGYKLFVLDDHERPARREGDILLK DPYIHESVQRHCHGRELFQYMLQKERVEHPQLAIDRPSOKILLKE LANHVALETTVPQVINNFVI PEGFFAHQHRPPAPSIRATRHSRAA AVDPTPAAPARKLPPKRARGDI KYYSSSDREFYLKVAVEPPWPIN RAPRRATPPAHPPPRSSSLANSPERGPLRPFVP  6473 22 912 SSAVEFVWEGERMAAEPNETEIQTLPKRLRAVPTINKACPDCGAK NESWASITYGVFLCI DCSCVHRSILGVHLSFIRSTELDSMINNINFO LIRCMYGGHANATAFFRQHGCTANDANTKUNSRAAQMYRKI KR LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPFAN DAPATEPSGTQQPAPSTESSGLAQPRHGPNTDILLGTSPKRSLEL KSSITGKKKPAAAKKGLGAGKVSSQSFSBIERQAQVAB KLREQQAADAKKQAESSWVASMRLAYQBLQIDR  6474 3 462 LQRQRQHPAAAPAVVPCCFTFCFTDLVIMPKRKSPENTESKOGS KUTKQBPTRSARLSAKAPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKBEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6475 3 462 LQRQRQHPAAAPAVVPCCFTFCFTDLVIMPKRKSPENTESKOGS KUTKQBPTRSARLSAKAPAPPKPEPKPRTSAKKEPGAKISRGA KGKKBEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQYKGTMREAGRAWHLLKKRERQREQMEVLKQRIABEFTIL KSQVUKRTSAHYDAVABELKSSTVGLVTINDMKARQBALJVRERE	] 04/1	1.120	299	
VPAPKOVLAHQVPNAKKLRKEQLMEKLAKQGELPREVRRAQAI  LIMPSATRARPGPQDTVBRPPYDLDREUNGQDBFFLI  OTKKKGVKRPARLHTKPSQAPAVEWAPAGASYNPSPEDHOTLLE  AAHEVELQRQKEABKLERQLALPATEQAATQBSTFQELCSGILLE ESGGEGEPGGGSGPEAGDABVCPTPARLATTBKKTEQORREKK VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRQRE RQARRBABAKPRRLGRLKYQAPDIDVQLSSKILTDSLRTIK,PER RQARRBABAKPRRLGRLKYQAPDIDVQLSSKILTDSLRTIK,PER RQARRBABAKPRRLGRLKYQAPDIDVQLSSKILTDSLRTIK,PER RQARRBABAKPRRLGRLKYQAPDIDVQLSSKILTDSLRTIK,PER RQARRBABAKPRRLGRLKYQAPDIDVQLSSKILTDSLRTIK,PER RQARRBABAKPRRLGRLKYQAPDIDVQLSSKILTDSLRTIK,PER RQARRBABAKPRRLGRLKYQAPDIDVQLSSKILTDSLRTIK,PER RQARRBABAKPFDVDALFPERTTVLDQHLRPFARREGITTE ARVDLQQQIMTI IDBLGKASAKAQNLSAPITSARRAQSNRHVVY LLKDSSARPAGKGAI IGFI KVGYKKLFVLDDREAHNEVEPLCII DFYIHESVQRHGHGRELFQYMLQKBRVSEPHOLAIDPSOKLLKE LNKHYNLRTIVPQVNNFVI FEGFFAHQHRPPAPSLRATRHSRAA AVDPTPAAPARKLPPKRRBGDI KPYSSSDRBFLKVAVKEPPWPL RAPRRATPPAHPPPRSSSLGNSPREGPLRPFVP  6473 22 912 SSAVEFVWESKMABEPNETEIQTLPKRLRAVPTNKACFDCGAK NSSMASITYGVFLCIDCGGVRRSLGVHLSFTRSTELDSMMNNFC LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYRBKLRQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYRBKLRQ LAGGALARKGTDLWIDNNSSAVPHISPEKKDSDFFTEHTQPPAN KSSITGKKRPAAAKKGLGAKKGLARKGVSSGSFSEIERQAQVAB KSSITGKKRPAAAKKGLGAKKGLARKGVSSGSFSEIERQAQVAB KSSITGKKRPAAARVDVRCPTFCFTDIVIMFRKSPENTEGKDGS KVFKQBPTRRSALSAKPAPPKPEPPRRKSPENTEGKDGS KVFKQBPTRRSARLSAKPAPPKPEPPRRKSFENTEGKDGS KVKKBEKQEAGKEGTAPSRNGETKABEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTBN  6475 3 462 LQRQRQHPAAAPAVPVRCPTFCFTDIVIMFKRKSPENTEGKDGS KVTKQBPTRRSARLSARAPPPKPBPRPRFTSAKKBPGAKISRGA KGKKEKQEAGKEGTAPSRNGETKABEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTBN  KYKKGEKQEAGKEGTAPSRNGETKABEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTBN  6476 1090 ARAMAQVKGTMREAGRAMHLLKKRERQREQMEVLKQRIABETIL KSQVDKRFSAHYDAVSABELKSSTYGLVTLMDMKARQRALUVRERE KSQVDKRFSAHYDAVSABELKSSTYGLVTLMDMKARQRALUVRERE				
LIMPSATRAKEGPQDTVERPPYDLMASDNPLDRPLVGQDEFFILI QTKKKGVKRPARLHTKFSQAPAVEVAPAGASTNPSFEDHOTILL AAHEVEILQRQKEABKLERQLAIPATEQAATQBSTFGEDLCGGLIK ESDGEGEPQGSGPEAGDABVCPTPARLATTEKKTEQORREKK VUHLKRVQQAALRAARLERQELFRLKGIKAQVALRIABELARRQRE ROARREABANKPRILGRIKQAVALRIABELARRQRE ROARREABANKPRILGRIKQAVALRIABELARRQRE NILRDFKSFQRRMMIEPPERAKFERKYKVKLVEKPAFREIQL NILRDFKSFQRRMMIEPPERTVLDQHLRPPARRFGTTTE ARVDLQQQIMTIIDBLGKASAKAQNLSAPITSASRMQSNRHVVY LIKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVBPLCII DFYIHESVQRHGHGRELFQYMLQKERVEPHQLAIDRPSQKLLKE LAKHYNLETTVPQVNNRVIFSGSSREFLKVAVVEPPWPLN RAPRRATPPAHPPPRSSSLGNSPERGPLRPVP  6473 22 912 SSAVEFVWEGERMAAEPNETEIQTLFKRIRAVPTNKACFDCGAK NPSWASITYGVPLCIDCSGVHRSLGVHLSFIRSTBLDSNNNWPQ LRCMQVGGRANATAFPRQHGCTANDANTKYNSRAAQMYREKIRG LAGSAALARHSTDLWIDNNSSAVPHISPEKKDSDFFTEHTQPPAM DAPATEPSGTQQPAPSTESSCLAQPEHGPNTDLLGTSPKASLEL KSSIIGKKPAAAKKGLGAKKGLGAQKVSSGSFSEIERQAQVAB KLRBQQAADAKKQAESMVASMPLAYQELQIDR  6474 3 462 LQRQRHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTESKDGS KVTKQBPTRRSALSALGAPPPKPPEPRPKTSAKKEPGAKISRGA KURKGPAAPAPVVRCPTFCFTDIVIMPKRKSPENTESKDGS KVTKQBPTRRSALSARAPPPKPBPRPKTSAKKEPGAKISRGA KGKKEEKQEAGKGGTAPSRNGETKAERHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKSTBN  6475 3 462 LQRQRQHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSALSARAPPPKPBPRPKTSAKKEPGAKISRGA KGKKEEKQEAGKGGTAPSRNGETKAERHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKSTBN  6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVSAELKSSTYGLVTLMDMKARQRALUVRERE	l i			
GTKKKGVKRPARLHTKPSQAPAVEVAPARASYNPSPEDHQTLLA AAHEVELQRQKEABKLERQLALPATEQAATQBSTTGELGGIJLA ESDGEGEPGQGSGPEBGDABVCPTPARLATTEKKTEQQRRREKK VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRQRE RQARREABADKPRRLGRLKYQAPDIDVQLSSKIJTDSLRTLKPE ROARREABADKPRRLGRLKYQAPDIDVQLSSKIJTDSLRTLKPE ROARREABADKPRRLGRLKYQAPDIDVQLSSKIJTDSLRTLKPE NILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFREIQL 6472  3 897 SCGSDERQWAMEFPEDVDALFPERITVILDGHLRPPARRESTTTE ARVDLQQQIMTIIDBLGKASAKAQNLSAPITSASRMQSNRHVVY ILKDSSARPAGKGALIGFIKVGYKKLPVLDDRRAINBVEPLCII DPYTHESVQRHGHGRELFQYMLQKERVSPHPLAIDRPSORLLKT LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATHHSRAA AVDPTPAAPARKLPPKRAEGIIKPYSSSDRRPLKVAVEPPWPLN RAPRRATPPAHPPPRSSSLGINSPERGPLRPFVP 6473  22 912 SSAVEFVWEGEKMAABEPNTEIQTLFKRLRAVPTNKACCFDCGAK NPSMASITYGVPLCIDCSGVHRSLGVHLSPIRSTBLDSNNNHFQ LRCMQVGGNANATAFPRQHGCTANDANTKUNSRAAQMYREKIRQ LGGAALARHGTDLWIDMSSAVPNHSPEKKDSDFFTEHTQPPAN KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSKIERQAQVAB KLREQQAADAKKGLGAKKGLGAKKGLGAQKVSSQSFSKIERQAQVAB KLREQQAADAKKQAESSWVASRAVQSLQDIDR 6474  3 462 LQRQRQHPAAAPAVPVRCPTFPCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KSKKBEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6475  3 462 LQRQRQHPAAPAVPVVRCFTFPCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPERKPRKTSAKKEPGAKISRGA KSKKEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476  1090 ARAMAQYKGTMREAGRAHLLKKRRRQREQMEVLKQRIABETIL KSQVDKRFSAHYDAVBAELKSSTVGLUTLMDMKARQRALURERE	l l			
AAHBVBLQRQKRABKLERQLALPATBQAATQBSTFQELCEGLIA ESDGEGEPGGGBPEAGDABVCPTPARLATTEKKTEQORREKK VERLRVQQAALRAARLRHOBLFRIRG IKAQVALRIABLARRQRE ROARREABADKPRRLGRLKYQAPDIDVQLSSKLTDSLRTLKPEC ROARREABADKPRRLGRLKYQAPDIDVQLSSKLTDSLRTLKPEC NILRDRFKSFQRRNMIEPPERAKFKRYKVKULVEKRAFREIQL  6472 3 897 SCGSDRAQWAMEFPFDVDALFPERTTVLDQHLRPPARRPGTTTE ARVDLQQQIMTIIDBLGKASAKAQNISAPTTSASRMQSRRHVVY ILKDSSARPAGKGALIGFIKVGYKKLFVLDDREAHNEVEPLCII DPYIHESVQRHGHGRELFQYMLQKERVEPFDLAIDRFSOKLLKE LANKHYNLETTVPQVMNFVIFEGFFAHORRPPAPSILATRHSRAA AVDPTPAAPARKLPPKRAEGDIKPYSSSDREFLKVAVEPPWPLN RAPRRATPPAHPPPRSSSLGNSPERGFLRPVP  6473 22 912 SSAVEFVWEGKKMAAEPNETBIQTLPKRLRAVFINKACFDCGAK NESMASITYCYPLCIDCSCVHRSLGVHLSFIRSTBLDGSNMWFQ LACMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ NESMASITYCYPLCIDCSCVHRSLGVHLSFIRSTBLDGSNMWFG LACMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ DAPATEPSGTQQPAPSTBSGLAQPRGPMTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIEDQAQVAB KLRBQQAADAKKQLAESSWASMRLAYQBLQIDR  6474 3 462 LQRQRQHFAAAPAVPVRCFFFFCFTDIVIMPKRKSPENTEGKDGS KUTKQBPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISKGA KGKKBEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6475 3 462 LQRQRQHPAAPAVPVRCFFFFFFFTDIVIMPKRKSPENTEGKDGS KUTKQBPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISKGA KGKKEEKQEAGKRGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQYKGTMREAGRAHLLKKRRQREQMEVLKQRIABETIL KSQVDKRFSAHYDAVBAELKSSTVGLVTLMDMKARQRALVRERE	1	•		OTKKKGVKRPARI-HTKPSOAPAVKVAPAGASVNPSPRDHOTT.I.S
ESDGEGEPGGGEPEAGDAEVCPTPARLATTEKKTEQQRREKK VHRLRVQQAALRAARILEHQLFRLIGILKQQVALILAELARRQRE RQARREAADKPRILGELKYQAPDIDVQLSSKI.TDSLRTLKPEK NILRDRFKSPQRRNMIBPERAKFKRKYKVKLVEKRAFREIQL NILRDRFKSPQRRNMIBPERAKFKRKYKVKLVEKRAFREIQL SCSSDRAQMAMEPPFDVDALPPERITVLDQHLRPPARRPSTTTE ARVDLQQQIMTIIDBIGKASAKQANLSPITSASRMQSRRHVVY ILKBSSARPAGKSALIGPIKVGYKKLPVLDDREAHNEVEPLCII DPYIHESVQRHGHRELFQYMLQKERVEHQLAIDRPSQKLLKE LAKHYNLETTVPQVNNFVI FEGFFAHQHRPPAPSLRATRHSRAA AVDPTPAAPARKLPPKRABGDIKPYSSSDREFLKVAVKEPPWPLN RAPRRATTPAHPPPRSSILGNSPERGPLRPFVP SSAVEFVWEGERMAAEPNETRIQTLFKRLRAVPTNKACFDCGAK NPSWASITYGVPLCIDCSGVHRSLGVHLSFIRSTBLDSNMNWFQ LCGCANATAFPRGHCTANDANTKYNSRAAQMYREKIRG LGSAALARHGTDLWINMSSAVPNHSPEKKDSDFFTEHTQPPAM DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSBIERQAQVAB KLREQQAADAKKQAESMVASMRLAYQBLQIDR KLREQQAADAKKQAESMVASMRLAYQBLQIDR KUREQQAADAKKQAESMVASMRLAYQBLQIDR KUREQQAADAKKQAESMVASMRLAYQBLQIDR KUREQQAADAKKQAESMVASMRLAYQBLQIDR KUREQQAADAKKQAESMVASMRLAYQBLQIDR KUREQQAADAKKQAESMVASMRLAYQBLQIDR KUREQQAADAKKQAESMVASMRLAYQBLQIDR KUREQQAADAKKQAESMVASMRLAYQBLQIDR KUREQQAADAKKQAESMVASMRLAYQBLQIDR KUREQQAGKGGTAPASRMGETKABEHIISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTBN  6474 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKOGS KVTKQEPTRRSARLSAKPAPPKPEPKPKTSAKKEPGAKISRGA KGKKBEKQEAGKGGTAPSRMGETKABEHIISRSTVNVSTSRGTP PSTLSVKGGIETVRVKGTBN  6475 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKOGS KVTKQEPTRRSARLSAKPAPPKPEPKPKTSAKKEPGAKISRGA KGKKBEKQEAGKGGTAPSRMGETKABEHIISRSTVNVSTSRGTP PSTLSVKGGIETVRVKGTEN  6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIABETII, KSQVVBKFSAHYDAVVBAEKKSSTYGLVTLNDMKARQBALVRERE	!!			
VIRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRQRE RQARRBABADKPRILGRIKYQAPDIDVQLSSKITDSLITILKPER NILBGFKSFQRRMMEPPERAKFKRKYKVKLVEKRAFREIQL 6472 3 897 SCGSDRAQWAMEPPEDVDALFPERITVLDQHLRPPARRPGTTTE ARVDLQQQINTIIDBLGKASAKAQNLSAPITSASRMQSNRHVVY ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPLCII DFYIHESVQRIKHIGERLFQYMLQKERVEPHQLAIDRPSQKLLKEF LAKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHSRAA AVDPTPAAPARKLPPKRAEGDIKPYSSSDREPLKVAVEPPWPLN RAPRRATTPPAHPPPRSSSIGNSPERGFLRPFVP 6473 22 912 SSAVEFVWGEKMAAEPNETEIQTLPKRLRAVPTNKACFDCGAK NSWASITYGVPLCIDCSGVHRSLGVHLSPIRSTELDSNNNNFG LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDMNSAVPNHSPEKKDSDFFTEHTQPPAM DAPATEPSGTQQPAPSTESSGLAQPERGPNTDILIGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIEPQAQVAE KLREQQAADAKKQAESSMVASRFLAVGELQIR 6474 3 462 LQRQRQHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPRPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSRNGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVVVKGTEN 6475 3 462 LQRQRQHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPRRFKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSKNGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVVVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVSBELKSSTVGLUTLBDMKARQGEALVKERE				
NILRDRFKSFQRRNMIBPRERAKFKRKYKUKLVEKRAFREIQL   6472   3   897   SCGSDRAQWAMEFPEDVDALFPERTTVLDQUILRPPARREGTTTE   ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRRQSRRHVVY   ILKDSSARPAGKGATIGFIKVGYKKLFVLDDREAHNEVEPLCII   DPYIHESVQRHGHGRELFQYMLQKERVEPHQLAIDRPSQKLLKR   LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHSRAF   AVDPTPAAPARKLPPKRAEGDIKPYSSSDREFLKVAVEPPWPIN   RAPRRATPPAPPPRSSSLGNSPERGPLRPFVP     6473   22   912   SSAVEFVWEGERMAAEPNETREIQTLFKRLRAVPTNKACFDCGAK   NPSWASITYGVFLCIDCSGVHRSLGVHLSPIRSTEILDSNMNHFQ   LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ   LGSAALARHGTDLWIDNMSSAVPNHSPEKKOSDFFTEHTQPPAN   DAPATEPSGTQAPASTESSGLAQPKHGPNTDLLGTSPKASLEL   KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE   KLREQQAADAKKQAEESMVASMRLAYQELQIDR     6474   3   462   LQRQQHBAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS   KUTKQBPTRRSARLSAKPAPPKPBRPRRTSAKKEPGAKISRGA   KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP   PSTLSVKGQIETVRVKGTEN     6475   3   462   LQRQQHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS   KVTKQBPTRRSARLSAKPAPPKPBRPRRTSAKKEPGAKISRGA   KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP   PSTLSVKGQIETVRVKGTEN     6476   106   1090   ARAMAQYKGTMRRAGRAHHLLKKRERQREQMEVLKQRIAEETIL   KSQVDKRFSAHYDAVEAELKSSTVGUTINDMKRQCALVRERE	[ [	[		VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRQRR
6472 3 897 SCGSDRAQWAMEFPFDVDALFPERITVLDQHLRPPARRFGTTTE ARVDLQQQIMTI IDELGKASAKAQNI.SAPITSASRMQSNRHVVY ILKDSSARPAGKGAI.GFI KVGYKKIPVLDDREAHNSVEPLCII DPYIHESVQRHGHGRELFQYMLQKERVEPHQLAIDRPSQKLLKE LIKHYNLETTVPQVNNFVI FEGFFAHQHRPPAPSLRATRHSRAA AVDPTPAAPARKLPPKRAEGDI KPYSSSDREFLKVAVVEPPWPILN RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP  6473 22 912 SSAVEFVWEGERMAAEPNRTEIQTLFKRLRAVPTNKACFDCGAK NPSWASITYGVPLCIDCSGVHRSLGVHLSFIRSTELDSNMNHFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAM DAPATEPSGTQQPAPSTESSGLAQPRHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSKIERQAQVAB KLRBQQAADAKKQAEESMVASMRLAYQRIQIDR  6474 3 462 LQRQRQHPAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPERKTSAKKEPGAKISRGA KGKKBEKQEAGKGTTAPSSRIGETKABEHHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6475 3 462 LQRQRQHPAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPBKPRKTSAKKEPGAKISRGA KGKKEKQEAGKGTAPSENGETKAEEHHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQYKGTMRRAGRAHHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGUTINDMKARQRALVRERE	i l	,		ROARREABADKPRRLGRLKYQAPDIDVQLSSKLTDSLRTLKPEG
ARVDLQQQINTI IDEIGKASAKAQNISAPITSASRMQSNRHVYY ILKDSSARPAGKGAI IGFI KVGYKKLFVLDDREAHNEVEPLCII DFYIHESVQRHGHGREIFQYMLQKERVEPHQLAI DRPSQKLLKE LNKHYNLETTVPQVNNFVI FEGFFAHQHRPPAPSIRATRHSRAA AVDPTPAAPARKLPPKRAEGD IKPYSSSDREFILKVAVKEPPWPLN RAPRRATPPAHPPPRSSSIGNSPERGPLRPFVP  6473 22 912 SSAVEFVWEGEKMAAEPNETEIQTLFKRLRAVPTNKACFDCGAK NPSWASITTGVPLCI DCSGVHRSLGVHLSPIRSTBLDSNMNNFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRG LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAN DAPATEPSGTQQPAPSTESSGLAQPEHGFNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE KLREQQAADAKKQAESSMVASMRLAYQBLQIDR  6474 3 462 LQRQRQHPAAAPAVVPCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPREPRFRKTSAKKEPGAKISRGA KGKKEEKQGAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6475 3 462 LQRQRQHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPREPRFRKTSAKKEPGAKISRGA KGKKEEKQGAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQVKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLUTINDMKARQRALURERE	I-2000 I			
ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDRRAHNEVEPLCII DPYTHESVQRHGHGREIFQYMLQRERVEPHQLAIDRPSQKLLKE LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHSRAA AVDPTPAAPARKLPPKRAEGDIKPYSSDREFLKVAVEPPWPIN RAPPRATPPAHPPPRSSSLGNSPERGPLRPFVP  6473 22 912 SSAVEFVWEGEKMAAEPNETEIQTLFKRLRAVPTNKACFDCGAK NPSWASITTGVPLCIDCSGVHESLGVHLSFIRSTBLDSNMNWFQ LRCMQVGGNANATFFRQHGCTANDANTKYNSRAAQMYREKIRG LASAALARFDLWIDNMSSAVPHSPEKKDSDFFTEHTQPPAW DAFATEPSGTQQPAPSTESSGLAQPEHGFNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE KLREQQAADAKKQAESMVASMRLAYQELQIDR  6474 3 462 LQRQRQHPAAAPAVVPCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPEPRPKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6475 3 462 LQRQRQHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPBPKPKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQVKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTINDMKARQRALURERE	64/2	3	897	
DFYTHESVQRIGHGRBLFQYMLQKERVBPHQLAIDRPSQKLLKE LNKHYNLBTTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHSRAA AVDPTPAAPARKLPPKRABGDIKPYSSSDREFILKVAVEDPWPLN RAPRRATPPAHPPPRSSSLGNSPBRGPLRPFVP  6473  22  912  SSAVEFVWEGEKMAAEPNRTETQTLFKKLRAVPTNKACFDCGAK NPSWASITYGVPLCIDCSGVHRSLGVHLSFIRSTBLDSNUNWFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAN DAPATEPSTQPAPSTESSGLAQPRHGPNTDLLGTSPKASILBL KSSIIGKKRPAAAKKGLGAKKGLGAQKVSSQSPSBIERQAQVAB KLREQQAADAKKQAEESMVASMRLAYQBLQIDR  6474  3  462  LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPEPRFKTSAKKBPGAKISRGA KGKKEEKQEAGKEGTAPSRNGETKARBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTRN  6475  3  462  LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQRPTRRSARLSAKPAPPKPBPRFKTSAKKBPGAKISRGA KGKKEEKQEAGKEGTAPSKNGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476  106  1090  ARAMAQVKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVBAELKSSTVGLUTINDMKARQRALURERE	{ ]			
LINKHYNLETTVPQVNNFVIFEGFFAHOHRPPAPSLRATRHSRAM AVDPTPAAPARKLPPKRABGDIKPYSSSDREFLKVAVEPPWPIN RAPRRATPPAHPPPRSSSIGNSPERGPLRPFVP  6473  22  912  SSAVEFVWEGEKMAAEPNETEIQTLFKRLRAVPTNKACFDCGAK NPSWASITYGVPLCIDCSGVHRSIGVHLSPIRSTBLDSNWNNFG LRCMQVGGMANATAFFRQHGCTANDANTKYNSRAAQMYRBKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAM DAPATEPSGTQQPAPSTESSGLAQPKHGPNTDILGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSQSFSBIERQAQVAB KLREQQAADAKKQAEESMVASMRLAYQBLQIDR  6474  3  462  LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPEPKPKKTSAKKEPGAKISRGA KGKKBEKQEAGKEGTAPSRNGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTRN  6475  3  462  LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEKQEAGKEGTAPSRNGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476  106  1090  ARAMAQYKGTMRRSAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLUTINDMKARQRALURERE	1 1			
AVDPTPAAPARKLPPKRABGDIKPYSSSDREFI,KVAVEPPWPIM RAPRRATPPAHPPPRSSIGNSPERGPLRPFVP  6473  22  912  SSAVEFVWEGEKMAAEPNETEIQTLFKRILRAVPTNKACFDCGAK NPSWASITYGVPLCIDCSGVHRSLGVHLSFIRSTBLDSNUNWFG LIRCMQVGGMANATAFFROHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAN DAPATEPSGTQQPAPSTESSGLAQPRHGPNTDILGTSPKASLEL KSSIIGKKRPAAAKKGLGAKKGLGAQKVSSQSFSBIERQAQVAB KLRBQQAADAKKQAEESMVASMRLAYQBLQIDR KLRBQQAADAKQAEESMVASMRLAYQBLQIDR KVTKQBPTRRSARLSAKPAPPKPEPKPKTSAKKEPGAKISRGA KGKKEKQEAGKEGTAPSRNGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6475  3  462  LQRQRQHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSRNGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476  106  1090  ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELXSSTVGLVTLNDMKARQRALJRERE				
RAPRRATPPAHPPRSSSLGNSPERGPLRPFVP  6473  22  912  SSAVEFVIRESEKMAAEPNRTEIQTLPKRLRAVPTNKACPDCGAK NPSWASITYGVPLGDCSGVHRSLGVHLSFIRSTELDSNMNNFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIJ LGSAALARKTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAN DAPATEPSGTQQPAPSTESSGLAQPRHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSKIERQAQVAE KLREQQAADAKKQAEESMVASRRLAYQELQIDR  6474  3  462  LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPRPKTSAKKEPGAKISRGA KGKKBEKQEAGKEGTAPSRNGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6475  3  462  LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPKTSAKKEPGAKISRGA KGKKBEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476  106  1090  ARAMAQVKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTINDMKARQRALVRERE	i 1			
NPSWASITYGVPLCIDCSGVHRSLGVHLSPIRSTBLDSNWNWFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYRBKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAN DAPATEPSGTQQPAPSTESSGLAQPKHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFGSEIERQAQVAB KLREQQAADAKKQAESSMVASMRLAYQBLQIDR 6474 3 462 LQRQRQHPAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPEPKPKKTSAKKEPGAKISRGA KGKKBEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6475 3 462 LQRQRQHPAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPERKTSAKKEPGAKISRGA KGKKBEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMRBAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQRALVRERE		1		
NPSWASITYGVPLCIDCSGVHRSLGVHLSPIRSTBLDSNWNWFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYRBKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAM DAPATEPSSGLAQPRHGPNTDLLGTSPKASLEL KSSIIGKKPAAAKKGLGAKKGLGAQKVSSQSPSBIERQAQVAB KLREQQAADAKKQAESSMVASMRLAYQBLQIDR 6474 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTBGKDGS KVTKQBPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KKSEKQEKQEAGKEGTAPSRNGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTRN 6475 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPEPKPKTSAKKBPGAKISRGA KGKKEEKQEAGKEGTAPSKNGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQVKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVBAELKSSTVGLVTLNDMKARQRALVRERE	6473	22	912	SSAVEFVWEGERMAAEPNRTRIQTLPKRLRAVPTNKACFDCGAK
IRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYRBKIRG IGSAALARKSTDLWIDNMSSAVPNHSPEKKDSDFFTBHTQPPAN DAPATEPSGTQQPAPSTESSGLAQPBHGPNTDLIGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSBIERQAQVAB KLRBQQAADAKKQAESSMVASMRLAYQBLQIDR 6474 3 462 LQRQRQHPAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPEPRPKKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIBTVRVKGTEN 6475 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQRALVRERE		1		NPSWASITYGVPLCIDCSGVHRSLGVHLSFIRSTBLDSNWNWFQ
DAPATEPSGTQQPAPSTESSGLAQPRHGPNTDILIGTSPKASLELL KSSIIGKKRPAAAKKGLGAKKGLGAQKVSSQSPSBIERQAQVAB KLRBQQAADAKKGLAGKKGLGAQKVSSQSPSBIERQAQVAB KLRBQQAADAKKQAEESMVASMRLAYQBLQIDR  6474 3 462 LQRQRQHPAAAPAVPVRCPTPCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPEPKPKTSAKKEPGAKISRGA KGKKBEKQEAGKEGTAPSRNGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6475 3 462 LQRQRQHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKBEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELXSSTVGLVTINDMKARQRALVRERE	}	Ì		LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYRBKIRQ
KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE KLREQQAADAKKQAESMVASRRLAYQELQIDR  6474 3 462 LQRQRQHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPEPKPKTSAKKEPGAKISRGA KGKKBEKQEAGKEGTAPSRNGETKABEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6475 3 462 LQRQRQHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPBPKPRKTSAKKEPGAKISRGA KGKKBEKQEAGKECTAPSKNGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQVKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTINDMKARQRALVRERE		ļ		LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAW
KLREQQAADAKKQAEESMVASMRLAYQBLQIDR  6474 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPKKTSAKKEPGAKLSRGA KGKKEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6475 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGETAPSKNGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQRALVRERE	1	{		
6474 3 462 LQRQRQHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKBEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIBTVRVKGTEN  6475 3 462 LQRQRQHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPBPKPRKTSAKKEPGAKISRGA KGKKEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEBTIL KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE				
KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKREPGAKISRGA KGKKBEKQEAGKEGTAPSRNGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6475 3 462 LQRQRQHPAAAPAVPVRCPTFCPTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKBPGAKISRGA KGKKBEKQEAGKEGTAPSRNGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQYKGTMREAGRAWHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELXSSTVGLVTLNDMKARQRALVRERE	6474		463	
KGKKEEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6475 3 462 LQRQRQHPAAAPAVVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSAPLSAKPAPPKPPKPRKTSAKKBPGAKLSRGA KGKKEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE	U 7 / 12	3	402	
PSTLSVKGQIETVRVKGTRN  6475 3 462 LQRQRQHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBPTRRSARISAKPAPPKPBRPRKTSAKKBPGAKISRGA KGKKEEKQEAGEGTAPSKUGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETII, KSQVDKRFSAHYDAVEAELXSSTVGLVTINDMKARQRALVRERE	İ			
6475 3 462 LQRQRQHPAAAPAVPVRCPTFCPTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPBPKPRKTSAKKBPGAKISRGA KGKKBEKQEAGKEGTAPSKNGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE	}	Ì		
KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEKQEAGKRGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE	6475	<del>3</del>	462	
KGKKBEKQEAGKEGTAPSKNGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQRALVRERE		- 1		
PSTLSVKGQIETVRVKGTEN  6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVIKQRIAEETII KSQVDKRFSAHYDAVEAELKSSTVGLVTINDMKARQEALVRERE		ļ		
6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVIKQRIAEETII KSQVDKRFSAHYDAVEAELKSSTVGLVTINDMKARQEALVRERE		1		
KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE	6476	106	1090	
ROLAKROHLBEORLOOERORROEORRERKEKISCI.SFALIDILDI		1		
	1			RQLAKROHLEEQRLQQERQREQEQRRERKRKISCLSFALDDLDD
	1		Ì	QADAAEARRAGNI.GKNPDVDTSFLPDRDREEEENRLREELRQEW
	1		1	EAQREKVKDEEMEVTFSYWDGSGHRRTVRVRKGNTVQQFLKKAL
QGLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK	j	· ]	j	QGLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK
SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF			{	SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF
PASRWEAYDPEKKWDKYTIR	1			PASRWBAYDPEKKWDKYTIR

F 070	1 500 33 44 3	No. 37 mend and	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ı	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6477	227	915	LQGHLMGIMAASRPLSRFWEWGKNIVCVGRNYADHVREMRSAVL
1	ì		SEPVLFLKPSTAYAPEGSPILMPAYTRNLHHBLELGVVMGKRCR
			AVPEAAAMDYVGGYALCIDMTARDVQDECKKKGLPWTLAKSFTA
			SCPVSAFVPKEKIPDPHKLKLWLKVNGELRQEGETSSMIF51PY
1			IISYVSKIITLEEGDIILTGTPKGVGPVKKNDEIEAGIHGLVSM
i			TFKVEKPRY
6478	2	1495	FVSSRILPESLASSRASTLEAMGRKEEDDCSSWKKQTTNIRKTF
1			IFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRDSSLEN
1			RIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGRLFDRILE
	ĺ		RGVYTKKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPE
J			Enskimitopglskmeqngimstacgtpgyvapevlaqkpyska
1	ł	i	VDCWSIGVITYILLCGYPPFYEBTESKLFEKIKEGYYRFESPFW
1			DDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDI
1	ļ		YPSVSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNLHSPGVRP
1			EVENRPPETQASETSRPSSPEITITEAPVLDHSVALPALTQLPC
1			QHGRRPTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGCC
ì			SSCLNIGSKGKSSYCSBPTLLKKANKKQNPKSEVMVPVKASGSS
	i '	ĺ	HCRAGQTGVCLIM
6479	3	949	SCRCPGWHPAGGQAGAMELLSALSLGELALSPSRVPLFPVFDLS
			YFIVSILYLKYEPGAVELSRRHPIASWLCAMLHCFG9YILADLL
1			LGBPLIDYFSNNSSILLASAVWYLIFFCPLDLFYKCVCFLPVKL
			IFVAMKEVVRVRKIAVGIHHAHHHYHHGNFVMIATGWVKGSGVA
1	i '		LMSNFEQLLRGVWKPETNEILHMSFPTKASLYGAILFTLQQTRW
1	[		LPVSKASLIFIFTLFMVSCKVFLTATHSHSSPFDALEGYICPVL
i .	ĺ		FGSACGGDHHHDNHGGSHSGGGPGAQHSAMPAKSKKELSEGSRK
}		*	KKAKKAD
6480	192	514	DFMSIYPPIHCPDYLRSAKMTEVMMNTQPMEEIGLSPRKDGLSY
1 .			QIFPDPSDFDRCCKLKDRLPSIVVEPTEGEVESGELRWPPEEFL
ł	!		VQEDEQDNCEETAKENKEQ
64B1	110	1131	KSRMDLDVVNMFVIAGGTLAIPILAFVASFLLWPSALIRIYYWY
	1		WRRTLGMQVRYVHHEDYQFCYSFRGRPGHKPSILMLHGFSAHKD
			MWLSVVKFLPKNLHLVCVDMPGHRGTTRSSLDDLSIDGQVKRIH
			QFVECLKLNKKPFHLVGTSMGGQVAGVYAAYYPSDVSSLWLVCP
1			AGLQYSTDNQFVQRLKELQGSAAVEKIPLIPSTPEEMSEMLQLC
1.			SYVRFKVPQQILQGLVDVRIPHNNFYRKLFLBIVSBKSRYSLHQ
ì			NMDKIKVPTQIIWGKQDQVLDVSGADMLAKSIANCQVELLENCG
	L		HSVVMERPRKTAKLI I DFLASVHNTONNKKLD
6482	2517	568	BPVSKVSQSRRKAGVPTANIBESQAVRAAMANVPWABVCBKFQA
ļ			ALALSRVELHKNPEKRPYKSKYSARALLEEVKALLGPAPEDEDE
1			RPEAEDGPGAGDHALGLPAEVVEPEGPVAQRAVRLAVIEFHLGV
			NHIDTEELSAGEEHLVKCLRLLRRYRLSHDCISLCIQAQNNLGI
1	j		LWSEREBIETAQAYLESSEALYNQYMKEVGSPPLDPTERFLPEE
1			BKLTEQBRSKRFSKVYTHNLYYLAQVYQHLEMFSKAAHYCHSTL
			KRQLBHNAYHPIBWAINAATLSQFYINKLCPMEARHCLSAANVI
1	Į		PGQTGKISATEDTPBAEGBVPBI.YHQRKGEIARCWIKYCLTLMQ
1	1		naqlsmodnigeldldkoselralrkkeldebesirkkavofgt
	]	•	GELCDAISAVEEKVSYLRPLDFERARELFLLGQHYVFRAKEFFQ
1	1		IDGYVTDHIEVVQDHSALFKGLAFFETDMERRCKMHKRRIAMLE
i	[		PLTVDLNPQYYLLVNRQIQFEIAHAYYDMMDLKVAYADRLRDPD
		1	SHIVKKINNLNKSALKYYOLFLDSLRDPNKVFPEHIGEDVLRPA
1	}		MLAKFRVARLYGKIITADPKKELENLATSLEHYKFIVDYCEKHP
			BAAQBIEVELBLSKEMVSLLPTKMERFRTKMALT
6483	3	623	NSHLLCGLRARAPLSANGREARAMBORLABFRAARKRAGLAAOP
			PAASQGAQTPGEKAEAAATLKAAPGWLKRFLVWKPRPASARAQP
			GLVQEAAQPQGSTSETPWNTAIPLPSCWDQSFLTNITFLKVLLW
1			LVLLGLFVBLEFGLAYFVLSLFYWMYVGTRGFBEKKEGEKSAYS
	L		TARREST AND AND AND AND AND AND AND AND AND AND

			The first of the second of the second of the second of the second of the second of the second of the second of
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
I	amino acid	sequence	Codon, /-possible nucleotide deletion,
i	sequence	L	\=possible nucleotide insertion)
			VFNPGCRAIQGTLTAEQLERELQLRPLAGR
6484	201	965	QLAVKTKMSGLRPGTQVDPEIELFVKAGSDGESIGNCPFCQRLF
ı			MILWLKGVKFNVTTVDMTRKPRELKDLAPGTNPPPLVYNKELKT
		1	DFIKIEBFLEGTLAPPRYPHLSPKYKESFDVGCNLFAKFSAYIK NTOKEANKNFEKSLLKEFKRLDDYLNTPLLDEIDPDSAEEPPVS
İ			RRLFLDGDQLTLADCSLLPKLNIIKVAAKKYRDFDIPAEFSGVW
		ļ	RYLHNAYAREEFTHTCPEDKEIENTYANVAKQKS
			FYDLVRAVEFLPCPDSQKLEKECQSSEESMGSNSMRSILBEDEE
6485	6	1091	DEEPPRVLLYHEPRSFEVGMLVWHKHKKYPFWPAVVKSVRQRDK
]			KASVLYIEGHMPEMKGFTVSLKSLKHPDCKEKQTLLNQAREDF
1	1	1	NQDIGWCVSLITDYRVRLGCGSFAGSFLRYYAADISYPVRKSIQ
Į.	1		ODVLGTKLPQLSKGSPEEPVVGCPLGQRQPCRKMLPDRSRAARD
1	1	1	RANOKLVEYIGKAKGAESHLRAILKSRKPSRWLQTFLSSSQYVT
1		<u> </u>	CVETYLEDEGQLDLVVKYLQGVYQEVGAKVLQRTNGDRIRFILD
ł	Į.		VLLPEATICAISAGDEVDYKTAREKYIKGPSLSYREKEIFDNQL
1	j	]	LEERNRRR
6486	10	581	LVLQAGGAHLSPSRVTQGIYYMLAFSKMPKPPDYSBLSDSLTLA
0 300	1		GGTGRFSGPLHRAWRMMNFRQRMGWIGVGLYLLASAAAFYYVFB
1			ISETYNRLALEHIQQHPEEPLEGTTWTHSLKAQLLSLPFWVWTV
Ĺ			IPLVPYLQMFLFLYSCTRADPKTVGYCIIPICLAVICNRHQAFV
1	'		KASNQISRLQLIDT
6487	352	863	SPLKPLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN
1			YYNGCIFHRNIKGFMVQTGDPTGTGRGGNSIWGKKFRDEYSEYL
-			KHNVRGVVSMANNGPNTNGSQFFITYGKQPHLDMKYTVFGKVID
			GLETLDELEKLPVNEKTYRPLNDVHIKDITIHANPFAQ
6488	878	241	TALQEFGTSGPPLSLRFALPSGTGRFKPLPGARGPSWPPSPRVP
1			MEPPNLYPVKLYVYDLSKGLARRLSPIMLGKQLEGIWHTSIVVH
1	· ·	[	KDRFFFGSGGISSCPPGGTLLGPPDSVVDVGSTEVTERIFLEYL
			SSLGESLFRGEAYNLFRHNCNTFSNEVAQFLTGRKIPSYITDLP
			SEVISTPFGQALRPLIDSIQIQFPGGSSVGRPNGQS
6489	1457	375	KVAKMATALSERELDNEDYYSLLNVRREASSEBLKAAYRRLCML
ì	ł		YHPDKHRDPELKSQABRLFNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRRTPABIREEFERLQREREERRLQQRTNPKGT
1		1 .	ISVGVDATDLFDRYDEBYEDVSGSSFPQIEINKMHISQSIEAPL
1	1	1	TATOTAILSGSISTQNGNGGGSINFALRRVTSAKGWGELEFGAG
1	1	1	DLOGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR
1			NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP
1		1	TWDAKCSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR
1		1	SKRRTGGG
6490	3	1183	HEAGCEVWLGYGPRAAAAAATVLFGGAGPTBTMFVARSIAADH
1 6490	,	1103	KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT
1	1	1	HSGSVWRVTWAHPEFGOVLASCSFDRTAAVWEBIVGESNDKLRG
1	1	1	QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE
	į.		APDVMNLSQWSLQHBISCKLSCSCISWNPSSSRAHSPMIAVGSD
1		1	DSSPNAMAKVQIPEYNENTRKYAKAETLMTVTDPVHDIAFAPNL
1	1	1	GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD
		1	NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL
	1	1	KENGSPVNGSSQQGTENPSLGSNIPSLQNSLNGSSAGRKHS
6491	3	1183	HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH
1 3372	1	1	KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT
			HSGSVMRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG
	1		QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE
	1	1	APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD
1	1		DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL
Ĭ			GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFRIHIVAQFD
İ	1	}	NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCIGIL
<u></u>			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
100	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion.
1	sequence	111	\=possible nucleotide insertion)
<b> </b>	<del>                                     </del>		KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS
6492	34	2573	1PFLKSCCCCCLFDFPPPPLDQVQEEECEVRRVTEHGTPKPFRK
			FDSVAFGRSQSEDEQFENDLETDPPNWQQLVSREVLLGLKPCEI
			KRQEVINELFYTERAHVRTLKVLDQVFYQRVSREGILSPSELRK
1			IFSNLEDILQLHIGLNEOMKAVRKRNETSVIDQIGEDLLTNFSG
ĺ	1		PGEEKLKHAAATPCSNQPFALEMIKSRQKKDSRPQTFVQDABSN
			PLCRRLQLKDIIPTOMORLTKYPLLLDNIATYTEWPTEREXVKK
L	Ì		AADHCRQILNYVNQAVKEAENKQRLEDYQRRLDTSSLKLSEYPN
ľ	1		VERLENLIDLTKRKMIHEGPLVWKVNRDKTIDLYTLLEDILVLL
1			QKQDDRLVLRCHSKILASTADSKHTFSPVIKLSTVLVRQVATDN
1	<b>,</b>		KALFVISMSDNGAQIYELVAQTVSEKTVWQDLICRMAASVKBOS
	1		TKPIPLPQSTPGEGDNDEEDPSKLKEEQHGISVTGLQSPDRDLG
1			LESTLISSKPOSHSLSTSGKSEVRDLFVAEROFAKEOHTDGTLK
			EVGEDYQIAIPDSHLPVSEERWALDALRNLGLLKQLLVQQLGLT
1			BKSVQEDWQHFPRYRTASQGPQTDSVIQNSENIKAYHSGEGHMP
ł			FRIGIGDIATCYSPRISTESFAPRDSVGLAPODSOASNILVMDH
I			MIMTPEMPTMEPEGGLDDSGEHFFDAREAHSDENPSEGDGAVNK
I	}		EEKDVNLRISGNYLILDGYDPVQESSTDEEVASSLTLQPMTGIP
1	}	•	AVESTHOOOHSPONTHSDGAISPFTPEFLVOORWGAMEYSCFEI
l .			QSPSSCADSQSQIMBYTHKIBADLEHLKKVKESYTILCORLAGS
ł			ALTDKHSDKS
6493	557	1147	TPARMAYQGSSTSDCMSKTLDSASAHFAASAVVSAPVPSRSEVA
1			KEONTGHNNINGVVOPSGTSKTLYSTNMALSSSPGISAVOLVRT
1			VGHTTTN-ILIPALCTSSPQTLPMNNSCLTNAVHLNNVSVVSPVN
j			VHINTRTSAPSPTALKLATVAASMDRVPKVTPSSAISSIARENH
1			EPERLGLNGIAETTVAMEVT
6494	2425	1052	AVAGGARPCSTPSSPHRRCRRHRPRPLPRPPAAIMSASAVYVLD
1			LKGKVLICRNYRGDVDMSEVEHFMPILMEKEEEGMLSPILAHGG
ł			VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSBYFKEL
l	•		EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQRYITQEGHKL
ľ	·		BTGAPRPPATVTNAVSWRSEGIKYRKNEVPLDVIESVNLLVSAN
!			GNVLRSBIVGSIKMRVFLSGMPBLRLGLMDKVLFDMTGRGKSKS
			VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLMTHVK
i '		•	PLIWIESVIEKHSHSRIEYMIKAKSQFKRRSTANNVEIHIPVPN
i			DADSPKFKTTVGSVKNVPENSEIVWSIKSFPGGKEYLMRAHFGL
1			PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL
(4.55			PWVRYITQNGDYQLRTQ
6495	2425	1052	AVAGGARPCSTPSSPHRRCRRHRPRPLPRPPAAIMSASAVYVLD
			LKGKVLICRNYRGDVDMSEVEHFMPILMEKEEEGMLSPILAHGG
			VRFMWIKHNNLYLVATSKKNACVSLVPSFLYKVVQVFSEYFKEL
			BBESIRDNFVIIYBLLDELMDFGYPQTTDSKILQBYITQBGHKL
]			RTGAPRPPATVINAVSWRSEGIKYRKNEVFLDVIESVNLLVSAN
	İ	i	GNVLRSEIVGSIKMRVFLSGMPRLRLGLINDKVLFUNTGRGKSKS
			VELEDVKFHQCVRLSRFENDRTISFIPPDGEFBLMSYRLNTHVK
	Ì		PLIWIESVIEKHSHSRIEYMIKAKSQFKRRSTANNVEIHIPVPN
			DADSPKFKTTVGSVKWVPENSEIVWSIKSFPGGKEYLMRAHFGL
			PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIBKSGYQAL
7400			PWVRYITQNGDYQLRTQ
6496	247	559	LRAVSLLPLQLVLPRYSIHSLFCIMFLCAQEWLTLGLNVPLLFY
			HFWRYFHCPADSSELAYDPPVVMNADTLSYCQKEAWCKLAFYLL
<u> </u>			SFFYYLYCMIYTLVSS
6497	1053	352	ANTQICRLCPRRHLHPPCGAKMGNGTEEDYNFVFKVVLIGESGV
			GKTNLLSRFTRNEFSHDSRTTIGVEFSTRTVMLGTAAVKAQIWD
	i	ļ	TAGLERYRAITSAYYRGAVGALLVFDLTKHQTYAVVERWLKELY
	·	1	DHAEATIVVMLVGNKSDLSQAREVPTEEARMFAENNGLLFLETS
لـــــا			ALDSTNVBLAFETVLKBIFAKVSKQRQNSIRTNAITLGSAQAGQ

Predicted   Predicted   Predicted				
Incation   Corresponding   C	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
location   corresponding   to first   main acid   residue of   main acid   residue of   main acid   sequence	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
LeLeucine, M-Methionine, M-Asparagine, amino acid residue of residue of amino acid sequence   P-profile, Q-Golutamine, R-Arginine, Serine, n-threonine, V-Valine, amino acid sequence   P-profile, Q-Golutamine, R-Arginine, S-Serine, n-threonine, V-Valine, amino acid sequence   P-profile, Q-Golutamine, R-Arginine, S-Serine, n-threonine, V-Valine, amino acid sequence   P-profile, V-Prossine, V-Duknown, *-Stop Codon, /-possible nucleotide deletion, V-possible nucleotide insertion)   P-profile, V-Profile,	NO:			Glutamic Acid, F-Phenylalanine, G-Glycine,
to first amino acid residue of amino acid residue of amino acid amino acid sequence  8		location		H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence  Seserine, T-Threonine, V-Valine, amino acid sequence  Codon, /-possible nucleotide deletion, V-possible nucleotide		corresponding		L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence (Codon, *possible nuclectide deletion, *possible nuclectide deletion, *possible nuclectide deletion, *possible nuclectide insertion)  6498 2636 272		to first		P=Proline, Q=Glutamine, R=Arginine,
antno acid sequence  Codon, /-possible nucleotide deletion,		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Sequence		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
6498 2636 272 SELECPROTELEGYTMELSSLIALIARPALPLILISLSLIGGSIST.  LRYSHIGGREDPCVRAVERGGEPONDESRALLOSDEDFERY I VPYYDDRREPYKULARTRY LIGHLIGERRELIAVANTSRATISTI.  AVAVRITVABHEPBLLY PYGORGARAPAGNOVUSHGDER PAHL  SETLIRILAHTHFGALYDHOP FINADDITVOPARTALAHLAHLISTHOD  LYGRAREP I GREGORY LLGRGER CHOOCYT SEPLAKING BE REDSSAFILSARAVEDVS KETI MURIKRYPSALLER TANGEL TRIOL  QAQIRNITUTUT PEGEALISM VICLAP PITTERS YES IROL  QAQIRNITUTUT PEGEALISM VICLAP PITTERS YES IROL  QAQIRNITUTUT PEGEALISM VICLAP PITTERS YES IROL  QAQIRNITUTUT PEGEALISM VICLAP PITTERS YES IROL  QAQIRNITUTUT PEGEALISM VICLAP PITTERS YES IROL  QAQIRNITUTUT PEGEALISM VICLAP PITTERS YES IROL  QAQIRNITUTUT PEGEALISM VICLAP PITTERS YES IROL  QAQIRNITUTUT PEGEALISM VICLAP PITTERS YES IROL  QAQIRNITUTUT PEGEALISM VICLAP PITTERS YES IROL  QAQIRNITUTUT PEGEALISM VICLAP PITTERS YES IROL  QAQIRNITUTUT PEGEALISM VICLAP PITTERS YES IROL  QAQIRNITUTUT PEGEALISM VICLAP PITTERS YES IROL  QAQIRNITUTUT PEGEALISM VICLAP PITTERS YES IROL  QAQIRNITUTUT PEGEALISM VICLAP PITTERS YES IROL  QARINA PITTERS YES IROL PITTUTUT PER PEGEALISM PITTUT PITTERS YES IROL  QARINA PITTERS YES IROL PITTUT PITTERS YES IROL  QERRESSEL PEGEALISM VICLAP PITTERS YES IROL  GERRAP PEGEALISM VICLAP PITTERS YES IROL  GERRAP PEGEALISM VICLAP PITTERS YES IROL PITTUT PITTERS YES IROL  GERRAP PEGEALISM VICLAP PITTERS YES IROL PITTUT PITTERS YES IROL  GERRAP PEGEALISM VICLAP PITTERS YES IROL PITTUT PITTERS YES IROL  GERRAP PER PITTERS YES IROL PITTUT PIT		amino acid	sequence	Codon, /=possible nucleotide deletion,
6499 2636 272 SEECPORTHERSTITIRESSILALIERALPILICISLICSISISI LEVINIGEEDPEVERAVEREGIPONDESERALIOSDEDEREN VPYTYDENRYPYKULTERYLTYISLESERELILAVULTERATISTI AVAVERTVAHERPETTIALESERELILAVULTERATISTI AVAVERTVAHERPETTIALESERELILAVULTERATISTI AVAVERTVAHERPETTIALESERELILARUSHOODOVERSEEPELAKREDE EVESSAFICARAVULPVERGUNTVOAREALARISHINDI LYIGHABEPTGAGGOARYLGEGERALIAGHISINDI LYIGHABEPTGAGGOARYLGEGERALIAGHISINDI LYIGHABEPTGAGGOARYLGEGERALIAGHISINDI LYIGHABEPTGAGGOARYLGEGOARAVAGOVERGOEPERAKREDE EVESSAFICARAVULPVERGUNTVOAREALAGAGHISINDI QAQIINNITVILTEEGEAGISHVOLPAPPTTHEREPTUGBOVETE QUITESCAGARAVULPVERGUNTVOAREALAGHISINDI QAQIINNITVILTEEGEAGISHVOLPAPPTTHEREPTUGBOVETE QUITESCAGARAVULPVERGUNGARAVULPULTURERVERGUNGARAVULPVERGUNGARA		sequence	_	
LAVSNIGGEEDPCVBAVGERGEIPONDESBALLOSDEDFERST VPYYDDPRNYFYKLVAETRY LOTEKLESPRELIAVALUSBATLESTI AVAVARITVABHEPBLLY PYGGRGARAPASHOVVSHGDERPANI SETLIHLHITHFGADYDMPF PIMDDTVQARELALAGHIG INOD LYLGRABEP I GGRGGARY CHEODPGYLLSRGILLRUPHLDGCGG DILSARDBRUGRCLIDSIGGCVSGHGGGOPTEFELAKRISH IND LYLGRABEP I GGRGGARY CHEODPGYLLSRGILLRUPHLDGCGG DILSARDBRUGRCLIDSIGGCVSGHGGGOPTEFELAKRISH IND GAGIRNILVILTPEGERGISHWVGLPAPFTHERFEVLGBUFFEL GHEFSCADGAFACT (GGRARADMELHREPSALLERRYSE I EQU GAGIRNILVILTPEGERGISHWVGLPAPFTHERFEVLGBUFFEL GHEFSCADGAFACT (GGRARADMELHREPSALLERRYSE I EQU GAGIRNILVILTPEGERGISHWVGLPAPFTHERFEVLGBUFFEL GHEFSCADGAFACT (GGRARADMELHERVSALLERRYSE I EQU GAGIRNILVILTPEGERGISHWVGLPAPFTHERFEVLGBUFFEL GHEFSCADGAFACT (GGRARADMELHERVSALLER) LEPLEGRYEILDPHVTPATRATQUL LILLUZUGGRBERALARRYS GREINBERLLITLLLVS (GFREGGRAPDPFIGGRAAAALBERA AVALEPBERLLITLLVS (GFREGGRAPDPFIGGRAAAALBERA ELAGGEBERALLGGGGFUNDVFLRFSGLHLFRAVEFGLJQKFSLRD DPSPPGADPSRGAP I GGRPPORO RSEGCY PAND TULARARILAG ELAGGEBERALGGGGFUNDVFLRFSGLHLFRAVEFGLJQKFSLRD GERLSTERSGERFYGGGFPRORABEGCY FAND TULARARILAG ELAGGEBERALGGGGFUNDVFLRFSGLHLFRAVEFGLJQKFSLRD ADGIFLIRGCLESSLGGVILSTWEFFTUSPHFIFT ERGURATYALDA GRANGSPBELCEPYSRDPDGLPCGLKKPCNEPSGLEDOGOVITALAG ADGIFLIRGCLESSLGGVILSTWEFFTUSPHFIFT ERGURATYALDA GRANGSPBELCEPYSRDPDGLPCGLKKPCNEPSGLEDOGOVITAL ADGIFLIRGCLESSLGGVILSTWEFFTUSPHFIFT ERGURATYALDA GRANGSPBELCEPYSRDPDGLPCGLKKPCNEPSGLEDOGOVITAL LIADIELLCCCHFGSVRGGVYFMREKAGGTVALSLLTATHERE FWHISSLITERBABERLISGGVYLDFFHIFT ERGURATYALDA KTURTYALLSODHARTAGARACA LUVERRET LYSNYRMELGGVYLDFFHIFT INFORMALGLITAC LUKERGE TYSDAYBORTHALGGGVILSTWEFTH AND TAKVILKGGTBEADALL LIADIELLCCCHFGSVRGGVYFMREKAGGTVALSLLTATHERE RKFSSSGVWEFTYTMERISGRYCHTHOGURTHALGALTAGALTAC LUKERGETYSRDPGRAGATAGARACA LOTHER THE AND TAKVILKGGTBEADAGGGGLATE BWREBOLIKASSPGRAGAGATAGARACA  GEPTHASADARGURSTVERKERKGLIDVATKVILGGTBEADAGGGGLATE BWREBOLIKASSPGRAGAGATAGARACA  GSGREBABAGGGGGARACA AGREPAGATAGAGGGGARACA AGREPAGATAGAGGGAAAACA  GSGRESSSLAGRAGAGAGGGAAACA  GSGRESSSLAGRAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG				BPGPGBKRACCISL
LEVSNIGGEEDFCVBAVGERGEPONPDSSRALIGSDEDFERFY VPYTROPREYEKULERTHY LIGHTLESERELLIANTISPATLISTI AVAVBRIVAHIETPHICHLESERELLIANTISPATLISTI AVAVBRIVAHIETPHICHLESERELLIANTISPATLISTI AVAVBRIVAHIETPHICHLESERELLIANTISPATLISTI AVAVBRIVAHIETPHICHLESERELLIANTISPATLISTI DILISARDEBRICRCLIDSLGVGCVSONGOGOVESPELAKVROPBE REGISSAFILSARAVIEVSERTIMICHERPHALICERIYSE HSOL QAGIRNITUTUTEGERGLISHVGLEPAPFTEHSEFSULGBUPFRIGHT CHIFSCANGAPECT (GASRANDUGLETALISEL)RENDLGGERE CRORLINGVBEPPDEBROMSTILDLLECVTORGHERALISERUL LERLESEVELIAPPVTETATROQUELELLIANTADERGERE CRORLINGVBEPPDEBROMSTILDLLECVTORGHERALARAN NVLEPREBBALLITLLIVTGFREGGRAPDPFLGVKAAAALBERA AVALEPREBALLITLLIVTGFREGGRAPDPFLGVKAAAAELBAG ELMGGREERALBGLEVMDVFLRFSGLHLERAVBEPLTUTVBERG PETLAMILAVRABAS SOVELAUVS SKRIPUTUTLFVTERFC PETLAMILAVRABAS SOVELAUVS SKRIPUTUTLFVTERFC PETLAMILAVRABAS SOVELAUVS SKRIPUTUTLFVTERFC PETLAMILAVRABAS SOVELAUVS SKRIPUTUTLFVTERFC PETLAMILAVRABAS SOVELAUVS SKRIPUTUTLFVTERFC PETLAMILAVRABAS SOVELAUVS SKRIPUTUTLFVTTATROG CSRTUTTRSGOMBER IGEPPRORDS REGETYNADIOLARARILAG ELMGGREERALBGLEVMDVFLRFSGLHLERAVSPOLOVERSIGD DPSS PORGDSSRAPP IGGPRORDAS SECTYMADILARARILAG ELMGGREERALBGLEVMDVFLRFSGLHLERAVSPOLOVERSIGD OFFICE STREET SOVELAUVS SKRIPUTUTLFVTLAVBER PETLAMILANDA SECTION SECT	6498	2636	272	SLRLCPWGTHLAGPTTMRLSSLLALLRPALPLILGLSLGCSLSL
VPYTRDENFYKKULETRYIQTELGSREELIJVAVLTSERATIST  AVAVRIVABIEPPILJPYTGGKARAPAGKQVVSHGEBERARIM SETLEHLHTHPEADVIMPPI HODDTTVQAPRIJAGHLIS HOLGE LIVEGRAEPTIGGRGSDAYTCHGGPGYLLSRELLIKERPHLIGEGG DILBAREPBIGGRGSDAYTCHGGPGYLLSRELLIKERPHLIGEGG DILBAREPBIGGRGSDAYTCHGGPGYLLSRELLIKERPHLIGEGG DILBAREPBIGGRGTHLIKEPPAGHERERYSELEGUE REGSSAFLSAFAVHUVSEGTIJVAVLLIKEPPAGHERERSTSELEGUE GARINITVILTBEGAGLSWPUGLPAPPTHERFEVLGHOVPHER GIRTSCALGAFKCPLGASRATUGDALETALEGIANRYOPPHER GIRTSCALGAFKCPLGASRATUGDALETALEGIANRYOPPHER GIRTSCALGAFKCPLGASRATUGDALETALEGIANRYOPPHER GIRTSCALGAFKCPLGASRATUGDALETALEGIANRYOPPHER GIRTSCALGAFKCPLGASRATUGHALETALEGIANRYOPPHER GIRTSCALGAFKCPLGASRATUGHALETALEGIANRYOPPHER GIRTSCALGAFKCPLGASRATUGHALETALEGIANRYOPPHER GIRTSCALGAFKCPLGASRATUGHALETALEGIANRYOPPHER FORLIANITANABAPASQUALIDVUSKRIPVITLPFLITVAVREG FORLIANITANABAPASQUALIDVUSKRIPVITLPFLITVAVREG FORLIANITANABAPASQUALIDVUSKRIPVITLPFLITVAVREG FORLIANITANABAPASQUALIDVUSKRIPVITLPFLITVAVREG FORLIANITANABAPASQUALIDVUSKRIPVITLPFLITVAVREG FORLIANITANABAPASQUALIDVUSKRIPVITLPFLITVAVREG FORLIANITANABAPASQUALIDVUSKRIPVITLPFLITVAVREG FORLIANITANABAPASQUALIDVUSKRIPVITLPFLITVAVREG FORLIANITANABAPASQUALIDVUSKRIPVITLAPILARADGUALID GERGARAGAPASCUCHVITLAVITANABAPASAPATILARADGUALITANA GIRANCOPPALITANABAPASAPATILARADGUALITANABAPATILARADGUALITANA FORLIANITANABAPASAPATILARADGUANABAPATILARADGUALITANABAPATILARADGUALITANABAPATILARADGUALITANABAPATILARADGUANABAPATILARADGUALITANABAPATILARADGUANABAPATILARADGUALITANABAPATILARADGUANAB	0120			LRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLDQSDEDFKPRI
AVAVARITVAHHPPRILIPTYGGGGARAPAGNGVYSHEDBERPAMM SETIRHIHTTEGADYDMPF JUNDDTYVOAPRIALAGHIS INQU LYIGRABEPTGAGGARYCHGGFGYLLSRSLLIARIZAPHLGCRG DILSARPDEWLGRCLIDSLEVGCVGOTGGGOYDEPHANGEDER REGSSAFLSAFAVHEVSEGTLMYRLHKRYSALELERRYSBIRDIL OQAIRNITVLTPEGEAGLSWPVGLPAPPTHSERPEVLGBDYPTE GHTPSCAGGARVCPLQGASSANUGDALETALEQJARRYOPRIR GKORLLMSYREPDPARGMEYTLDLLLSCYTORGHRYRLARRYSL LRPLGRVBILDWYVTGATRUGDALETALEQJARRYOPRIR OKORLLMSYREPDPARGMEYTLDLLLSCYTORGHRYRLARRYSL LRPLGRVBILDWYVTGATRUGDALETALEGJARRYOPRIR PGTRIAMLAVRABASQVIRTMUVSKHRIPVILTPLITVMTEGG EBVLARCCHMALSGAGAFFFVHIGBEFFRALSCASPGPFGGFGAF DPSPPGADDSBAGATGGRFDRUASAGAFFRISAFAARABARAFLERRYS PGTRIAMLAVRABASGVURTMUVSKKHRIPVILTPLITVMTEGG EBVLARCCHMALSGAGAFFFVHIGBEFFRALSCASSPGPFGGFG PBVBRCHSBELTHLLLVVGPREGGGAABECTAMADVLARARLAG LLAGOSEREALBELEVMOVFLRFSGLIHFRAVEFGLVQKFSLRD CSPRLSBELTHRCHISJUBGLGARAGAFFTUSPLALGFETFQVACLA- GHPVPRQVSGGGAMPDPAHLFPFYGGSGRABGEFHALAGM ADGIFLLRQCHSELGGVYLGHDVAFRGHETBRQLAGFTYALAG GRAHCGPRELCEFYSRDPDGLECHLRRCGGTALAGLAGA ADGIFLLRQCHSELGGVYLGHDVAFRCHGTFFAQACLA CHRAPCHYNTKLISAGAGARYCTERFGTTAGURTKLAGAGA ADGIFLLRQCHSELGGVYLGHDVAFRCHGTFTAGLAGGFTYALAG GRAHCGPRELCEFYSRADGAGAGYCTRRKKGTUTALAGAGAFYCTUSPLALGFTYALAGA CKRACCHSSANASGAAAPTLDAHPSTLTHQRRIDTLARGGGTALTAG WHIISSLTRBASRKLYSGAQTOGKFILHRRKGGGTALTAGAT WHIISSLTRBASRKLYSGAQTOGKFILHRRKGGTATAGATY LLADIELGCGNEGSVRGAKYTERFTTATUQRRIDTLARGGGFLKK LLADIELGCGNEGSVRGAVYRRKKGTUVATKULGATBRADYL LVGKRRETLYSKNYAELHQVSMMKYLEERNFYHEDLAARNVLL VNRHYAKLSDFGISKALGADDSTYTKEPTTATUGRAGGGFLKK LVGKRRETLYSKNYAELHQVSMMKYLEERNFYHEDLAARNVLL VNRHYAKLSDFGISKALGADDSTYTKEPAGAGGGFLKKF LVGKRRETLYSKNYAELHQVSMMKYLEERNFYHERGGFTALAGAG KVGGPPGGTGKABACA  GSPTHASADANGGVRSVTRMCANVRONFCAALSCPGGANTAAVK TYTTHCCHARBFFSSENVVERSINGTTOMAMRKATAGAGAGHLKARAVK TYTTHCCHARBFFSSENVVERSINGTNAMMRKATAGATAK TYTTHCCHARBFFSSENVVERSINGTNAMMRKATAGAGAGHLKARAVK TYTTHCCHARBFFSSENVVERSINGTNAMMRKATAGAGAGHLKARAVK URGSGSFEFFYGGGAARGGGKROSLICHGRAMMHEHEHHIL NGHLVALSKCREHLQNDAFFTAGAGAGRUKACLBANAKE HERBLDIAASSKCRHAQNDAFMKGQPRATAGAGHLKRO TROMBEDLALAKSSTF  6502 213 1650 AGNRTAMAGGGSRATATVLPDVSVPHREDG				VPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTL
SETLEHLIHTIFEGADZUMPFIMODITYVOAFRIAALIAGHILSINOD LYLGRARBFIGAGBQARYCIGOGOYSIGSELAANIADDE KUGSSAFLSAFAVHDVSEGTIMYRHKRYSALELGERAYSEIROL OAGINNITULTPEGERALSWPVGLPAPFTHSRFEVLGHDYPTE GHTSCADGAPKCPLQGASRADVGDALETALEQINRRYQFBLRP GKGRLINGYREPPARGMETTLDLLISCYTORGIRRALARNSE LRPLSRVBILPMPYTTRATRVQLVIPLLVARAAAAPAFLERRY PGTELAMILAVVARAASASQVRIMUVSKRIPVVTLPFLITVMTEPG FEVLANICAWAA ISOQAPFPUTGGRAPPTHOSPFPALGABAA NVLEPREHALITLTLLVYCEPBEGGRAPDPTGVARAAAAELBARY PGTELAMILAVRARASSQVRIMUVSKRIPVVTLPFLITVMTEPG FEVLANICAWAA ISOQAPFPUTGGSFPALSSPFGPGGAGP DPSPPGADPSRGAPIGGFPDROASASGCYYMADYLAARALBAG ELAGGBEREALBGLEVUVPTLRPSGLHLPRAVEPGLVQKPSLRD CSCHLURTSGGADPTVGGRAAAGAFRTUSPILALGETPTOVACLP GENLSBELTHRRCINSLBSCLGGRAPDPAHALFARVEPGLVQKPSLRD CSCHLURTSGGADPTVGGRAAAGAFRTUSPILALGETPTOVACLP GENLSBELTHRRCINSLBSCLGGRAPDPAHALFPYGGSLSABABEBLKLAGAG ADGIFLLRQCLRSLGGVVLSLUHDVRTHHPP1ERQLAGTYLAAA ADGIFLLRQCLRSLGGVVLSLUHDVRTHHPP1ERQLAGTYLAGA GKANCOPBELGEFYSRDPOLICPLKKPKCHTSARABEBLKLAGAG ADGIFLLRQCLRSLGGVVLSLUHDVRTHHPP1ERQLAGTYLAGA CKANCOPBELGEFYSRDPOLICPLKKPKCHTSARABEBLKLAGAG KKANCOPBELGEFYSRDPOLICPLKKPKCHTSARABEBLKLAGAG KKANCOPBELGEFYSRDPOLICPLKKPKCHTSARABEBLKLAGAG KKANCOPBELGEFYSRDPOLICPLKKPKCHTSARABEBLKLAGAG KKURCOPBELGEFYSRDPOLICPLKKPKCHTSARABEBLKLAGAG KKURCOPBELGEFYSRDPOLICPLKKPKCHTSARABEBLKLAGAG KTYTYYLISQDKAGKYCTPERKFDTLWOLUNYKLKGADALIYC LKRRCCHNSASANASGAADTLPAHPSTTLTUPGUTATALGCKARAVIL LLADIELGCGREGSVGGVYRMRKQIUVYXLKKAGAGVTALBCHT EMPRENQLIMKGLOVOQARALHUHWBAGGGFLIKK LVKRRETIVSAVNASLALHQVSMMKYLLERBNVILBLARANVLL VNRHYAKISDGISKINGADDSYYTARASCRYRLLKATAPBECTHP RKFSSSDVMSYGVTYMRALSYGONYYKRMRGPEVMAFIKGTK WEGSSSFLKAVVALASDCGHTYKARAGPLANVLL VNRHYAKISDGISKINGADDSYYTARASCRYRLLKATAPBECTHP RKFSSSDVMSYGVTYMRALSYGONYYKRMRGPEVMAFIKGKR MECPPECPBELYALANDCHTYKARUGCARATATHRA KKRSSPLANGTARANACA THTHCHCKAREFSSENVSVESINIANIALMINGKAYKYATAK MECPSSSPLANGTARANIALANIALMIN PROCEPGGGGHTKTISCH RKFSSSPLANGTARANIALANIALANIA CHARANYAR THTHCHCKAREFSSENVSVESINIANIALANIANIANIA THERILLARAFTYNDLTPHANGARANIALANIA SIGNIKANIA THTHCHCKAREFSSENVSVESINIANIALANIANIANIANIA THTHCHCKAREFSSENVSVESINIAN				AVAVNRTVAHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLM
LYLGHAREPIGAGGANYCIGOGOVILISSILLIALIAPHICOCRO DILSARPDBHICCCIIIDIGLOVCYSOTICOGOVISPELANNOPDE REGISAPLSAPANHPUSEGTIMYRLHKRESALRICERAYSER ROL QAQIRINITULTPEGEAGLSWPUGLPAPTHENERYUGBOYPTE OHTPSCADGAPKCPIQGASRADVGDALETALEQIMRRYOPRIRE OKRILINGYREPDEAGCHSTLDILLICUTORGHRRIARRYSL LEPLERVEILIPMYTTERATULVILEUTORGHRRIARRYSL LEPLERVEILIPMYTTERATULVILEUTORGHRRIARRYSL LEPLERVEILIPMYTTERATULVILEUTORGHRRIARRYSL LEPLERVEILIPMYTTERATULVILEUTORGHRRIARRYSL LEPLERVEILIPMYTTERATULVILEUTORGHRRIARRYSL LEPLERVEILIPMYTTERATULVILEUTORGHRRIARRYSL LEPLERVEILIPMYTTERATULVILEUTORGHRRIARRYSL LEPLERVEILIPMYTTERATULVILEUTORGHRRIARRYSL LEPLERVEILIPMYTTERATULVILEUTORGHRRIARRYSL LEPLERVEILIPMYTTERATULVILEUTORGHRRIARRYSL POPTLAMILAVERABASQURTHOVILEUTORGHRAARAPAERAPELERRYA POPTLAMILAVERABASQURTHOVILEUTORGHRAARAPERAPELERRYA POPTLAMILAVERABASQURTHOVILEUTORGHRAARAPERAPELERRYA ADGIPLIPACICURISLIGAVILLIAUTORGHRAARAPERAPELAJAGBA ADGIPLIPACICURISLIGAVILLIAUTORDHRAARAPERAPENALAGHATAATAR ADGIPLIPACICURISLIGAVILLIAUTORDHRAARAPERAPENALAGHATAATAR CEAPHYROVAGGAGAMPOVAGRAAAAPARTOSGALAGTATAAGA GKAHCGPAELCEPYSROPDGLOCHINGTATAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA				SETLRHLHTHFGADYDWFFIMQDDTYVQAPRLAALAGHLSINQD
DILSARPDBBICRCLIDSLGVGCYGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				LYLGRAREFIGAGEOARYCHGGFGYLLSRSLLLRLRPHLDGCRG
KEGSSAFILSAPAHIPUSEGTIMYRLHKRPSALEKIRSATSHENJI QAQIRMITUTIPEBERGISBWUGLAPPTFHISPEPULGBUYFTE QHTFSCADGAPKCPLQGASRADUGDALETALEQIANRYQPELRP QKQRILLKYJRRFDBARGHYTLDLLLECVTQRGBRRALARRYSI, LRPLSRVSILDMYYTEATRQUIVEBLAVCHARAAAPATELBAPAA NULEPBEHALLTLLLVYCPBEGGRGAPDPTGGVRAAABLERRYSI, NULEPBEHALLTLLLVYCPBEGGRGAPDPTGGVRAAABLERRYSI, PGTRLAMILAWARBARSQUKHUJVUSKHEHVUTLFPTLTTVWTRPC PBULANCRWAALSGOAPFPVHRQBENDGASBECTYNADYLAARARLAG ELAGQEEBEALEGLEVMDVFLRPSGLHLBPAVEBGLUQKFSLRD DPSPPGADJBSGAPTGGGFDRQASBECCFYNADYLAARARLAG ELAGQEEBEALEGLEVMDVFLRPSGLHLBPAVEBGLUQKFSLRD GEHDVERQVSGGSGAMPTDRAAHLPFYGGLSRAAABRLAG GKAHCGPAELCEFYSBDPDGLACHKPCNRPSGLEBOANST AGALFLLRGCLRSLGSVYLSUMBVRFHHPF1ERQLMGTYALAG GKAHCGPAELCEFYSBDPDGLACHKPCNRPSGLEBOGNVFDC LRDAMWRDVVROTNKLEGERALGOATIGAKFLLEPRKEGGTYALGLYC KTYYHYLISQDKAGKYCI PEGTKFDTINQLVWSLLKARDOLLYC LKRACPNSSAANASGAADATLPHFSTLTHUQRRIDTTABERM PWYHISLTREBABRKLYSGAQTOKKFLLEPRKEGGTYALGLYC LKRACPNSSAANASGAADATLPHFSTLTHUQRRIDTTABERM PWYHISLTREBABRKLYSGAQTOKKFLLEPRKEGGTYALGLYC LKRACPNSSAANASGAADATLPHFSTLTHUQRRIDTTABERM PWYHISLTREBABRKLYSGAQTOKKFLLEPRKEGGTYALGLYC LKRACPNSSAANASGAADATLPHFSTLTHUQRRIDTTABERM PWYHISLDTREBABRAQHHGLUNDYTURLIGVCQABALMUJMEMAGGPFLUKF LVOKRREILPSANNASGAADATLGARTWARKAGGFRKATE EMPRRAQIHHGLUNDYTURLIGVCQABALMUJMEMAGGFPLUKF LVOKRREILPSANNASGAADATLGARTWARKAGGFRKATE EMPRRAQIHHGLUNDYTURLIGVCQABALMUJMEMAGGFPLUKF LVOKRREILPSANNASGAADATLGARTWARKAGGFRKATE RKFSSSDVMSYGYUTMBBALSYGOKPYKOMKGGFPUNGAANAC MECEPECCPPELIYALMSDCWITKTKMDDRDPDLTVERGRMRACYYSLA SKUSGPPGSTGKABAACA  6500 1773 726 SOPHASDDLAKTGGSSFTAUKFDGBPDFLTVERGRMRACYTSLA KUSGPPGSTGKABAACA  GEFTHASDANAFWAGSTFAUKFDUNGATHYTKSVGLISTARAYTYED VOKGCCSINAWATNGLTGHASSPYPYCLIKPKDVSLAHAAVK KYRQUYMWFFLARPTTFAILBHLYTLIKKDPSOPPYLGHTIKSG DLYVCMGCGSDMAVTNGLTGNSPYPYLGHAVAKRHALAWAK KRGUSGGFEFPVCGCBARGGGKKRDSLGTAGGAHKKILBRUHHKILBHLHL HISHLIDHRPVLQGBTYFYVKBFBEKGGGAHKKILBRUHHKILBHL HISHLIDHRPVLQGBTYFYVKBFBEKGGGAHKKILBRUHHKILBHLH HISHLIDHRPVLQGBTYFYVKBFBEKGGGAHKKILBRUHHKILBHLH HISHLIDHRPVLQGBTYFYVKBFBEKGGGAHKKILBRUHHKILBHLH HISHLIDHRPVLQGBTYFYTKBFBOFPBELTAMISLACRO YABH				DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPE
QAQIRMITVITPEGERGISMEVGLPAPFTEHSREVILGEDVETE QHTFSCADGAPKCPLQGASRADVIGALAETTALGOINRYOPELRP QKQRILASYRRFDPARGMEYTLDLLLECVTORGERRALARRYSI, LEPLSRUSILDMYYUTRATROQUIDFLILVBEADAAPAPILEAPAA NULEPREIBALITLLILVTQFREGGRGAPDPFIGGYRAAARAELERRY PGTRLAMILAVWARAEPSQVRIMDVUSKHEVUTTLEFILTTWITEPG PEWIJANICANNALSGNQAPFVHOGENPRALPGRESPOPPGPGFPG PEWIJANICANNALSGNQAPFVHOGENPRALPGRESPOPPGGPGGP PEWIJANICANNALSGNQAPFVHOGENPALPGRESPORPPGGPGGP PPSPPGADPSRGAPTGGRAPAGARAETHERITAMILAG LIAGGEEREALESLEVMDVFLRPSGLILFRAVEGLUQKFSIRD CSCHPUNEQUSGGGNAMPDPAHLPPYSGLAPBETQVACLEY GENPUNEQUSGGGNAMPDPAHLPPYSGLAPBETQVACLEY ADGI-PLIRQCIRSLIGGYVLSLVBHUVFHHPPIEQUINGTYALAG (KARLGPAELCEYYSRDDPAHLPPYSGLARDEGHERICLIAGM ADGI-PLIRQCIRSLIGGYVLSLVBHUVFHHPPIEQUINGTYALAG (KARLGPAELCEYYSRDDPAHLPPYSGLAPBCHEROWYDC LROAMVRDYVRQTYKLBGEALGOAITSQAPQUEKLIATTAHERM PWHISSLTREBARRILYSGAQTOSKFLIRPREGGYTALSLIYG KTYHYLLISQDKAGKCUT PEGTKRDTIMOQHVYLKLKAGGLIYC LKRACPINSSANASGAAPTLPAHPSTLATHQURIDTHASDGYT PEPARTTSPDKAPHMYVVRQTYKLIGVCQARAIMLURMAGAGGPLIKF LUKKRE ILVSNVASILLBIQVSMGMKYLLEEKNFURDLAARNULL VINHIYAKISDDFGISKAIGADDSYYTARSAGKQLKWYAFECINF RKFSSISDVMSGYTYMBALSTGKYV KAMEBCAGGESWMAFIEQKR MECPBECPPEILYALMSDCHIYKMEDRPDLITVEQRMBACYTSLA KWEGPPGSTOKARAACA MECPSSTIKKVMIGSIPCALITHGHIIIGHGSWMAFIEQKR MECPBECPPEILYALMSDCHIYKMEDRPDLITVEQRMBACYTSLA KWEGPGSTOKARAACA  6500 1773 726 TIGPTHASADAMGLVRSVTEWCANVRGNPCAAALSCPONVLDAGK MLSESSSFLKGVMIGSIPCALITHGHIIIGHGSPWAFIEQKE MECPBECPPEILYALMSDCHIYKMEDRSPYNFITISG OLEYVCMEGGIVLSVSSMRRIMSLINT PRKCCPGGGHIKKISED KYRGYMSTILARSTFT VARFORDFYTIGHTI ILSG DLEYVCMEGGIVLSVSSMRRIMSLINT PRKCCPGGGHIKKISED KURGYNEDILARSTFT VARFORDFYTIGHTI ILSG DLEYVCMEGGIVLSVSSMRRIMSLINT PRKCCPGGGHIKKISED KURGYPGGTARAYTHOPUNGHVMYGVYGLIKARTOFYTC  6501 1 570 LVMSGGGTETPVCCRAPGGGSKRRDSJJTAGSAHLITIDJGE KORNENDILARSTFT VARFORDFYTIGHTI ILSG MECHALARSTFT VARFORDFYTIGHTI ILSG MECHALARSTFT VARFORDFYTIGHTI ILSG MECHALARSTFT VARFORDFYTIGHTI ILSG MECHALARSTFT VARFORDFYTIGHTI ILSG MECHALARSTFT VARFORDFYTIGHTI ILSG MECHALARSTFT VARFORDFYTIGHTI ILSG MECHALARSTFT VARFORDFYTIGHTI ILSG MECHALARSTFT VAR				KEGSSAFLSAFAVHPVSEGTLMYRLHKRFSALELERAYSEIEQL
OHITESCADGAPKCPLQGASRADUGDALETTALEQLIRRYOPELRY OKORTLING VERFEDDARGETTALLILECTURGEBERALARRYOEL LRPLSRVEILPMPYTEATRYOLIVIELLVARAAAAPAPAFLEARRA NULBPREHALLITLILLVYGPREGGRGADDPFLGVKAAAAELERRY PEGTRLAMLAWARARSQVKLMDVVSKKHPUTLFPLITTVWTREG BPULMINCRWANAIGGAPFPVHRQERNPALSPCRSPGPGGGF DPFSPPGADDFSGRAPLGGFBRQASAGGFCFYNADYLAARAALLERRY PEGTRLAMLAWARARSQVKLMDVVSKHPUTLFPLITTVWTREG BPSURANCRWANAIGGAPFPVHRQERNPALSPCRSPGPGGAFG DPFSPPGADDFSGRAPLGGFBRQASAGGFCFYNADYLAARARLAG ELAGOGERERALBGLEVMDVFLRPSGLHLPRAVERGUKFSLRD CSPRLSEILVHRCHSINLEGLGGRQLAMAALFGCEDANST CSPRLSEILVHRCHSINLEGLGGRQLAMAALFGCEDANST ADDIFLIRGCLESLGGYVLIKUFUNFHHPFIRGLAGFBFFOVACLP GHPVWEQVSGGGAMFDPAAHLPFPYGSLGRARABEHLKLAGM ADDIFLIRGCLESLGGYVLIKUFUNFHHPFIRGLAGFBFFOVACLP GRANCGPBELCEFYSBDPGGLPCHLRPCNRPSGLEBOGGVFDC LRDAWMPDVVRQTNKLBGERALEGADISGNVRLKLKARDALTY GRANCGPBELCEFYSBDPDGLPCHLRPCNRPSGLEBOGGVFDC LRDAWMPDVVRQTNKLBGEALEGADISGNVRLKLKARDALTY KTVYHYLISQDKAGKCT PEGTREDTINGVKLKLKARDALTY KTVYHYLISQDKAGKCT PEGTREDTINGVKLKLKARDALTY KTVYHYLISQDKAGKCT PEGTREDTINGVKLKLKARDALTY LLDAIELGGGFGSVRQGGVYMBRKKQLDVALKVLKARDATELTY DEPARLTSSDCPRRMMDTSVVESPYSDPEELKDKKLFLKRDALTY LLDAIELGGGGFGSVRQGVYMBRKKQLDVALKVLKARDATELTY LVGRRBEILFSSNASGAADATTHADPSTVALGOVRRAPECINF RKPSSRSDVMSVTGTYMBRLSTGDVALKVLKKARDATELTY VNHHTAKISDFGISKALGADDSYYTARSAGKRRLKMYABECINF RKPSSRSDVMSVTGTYMBRLSTGVOVALKVLKARDATELTY NHHTAKISDFGISKALGADDSYYTARSAGKRRLKMYABECINF RKPSSRSDVMSVTGTYMBRLSTGVOVALKRAPTEROKR MECPERCPPELYALMSDCMIYKMCRPPDFLTVGQMRRACYYSLA KNEGPPGSTICKARAACA  GSPTHASADAMGUNESVTBWCANNTGNPCAAALSCPQAVLDAGK MECPERCPPELYALMSDCMIYKMGNPCAAALSCPQAVLDAGK MECPERCPPELYALMSDCMIYKMGNPCAAALSCPQAVLDAGK MECPERCPPELYALMSDCMIYKMGVYGNPCAAALSCPQAVLDAGK MECPERCPPELYALMSDCMIYKMGVYGNPCAAALSCPQAVLDAGK MECPERCPPELYALMSDCMIYKMGVYGNPCAAALSCPQAVLDAGK MECPERCPPELYALMSDCMIYKMGVYGNPCAAALSCPQAVLDAGK MECPERCPPELYALMSDCMIYKMGVYGNPCAAALSCPQAVLDAGK MECPERCPPELYALMSDCMIYKMGVYGNPCAAALSCPQAVLDAGK MECPERCPPELYALMSDCMIYKMGVYGNPCAAALSCPQAVLDAGK MECPERCPPELYALMSDCMIYKMGVYGNPCAAALSCPQAVLDAGK MECPERCPPELYALMSDCMIYKMGVAGATAGGGKKRATUKADLAMAVK VRHITAKTAGLSOP		1	1	OAOIRNLTVLTPEGEAGLSWPVGLPAPFTFHSRFEVLGWDYFTE
OKORILINGYREPDEAGMSYTILLILECVTOGREIRALARRASI LRPLSSVBILIMPYOTERATVOULUN-PLUVABAAAPAFILARPAA NVLEPREHALITLILLVYGPREGGRGA PDPPLGVKAAAABLERRYA NVLERREHALITLILLVYGPREGGRGA PDPPLGVKAAAABLERRYA PGTRILAMILAVRARAPSQVRIMWVSKKEPUTDTLFPLTTVWTRPG PERVLANCKRWAISGOGAPPVHIFGEFFRRAIS PGRSPFOGFGAGF DPPSPFGADPSRGAPLGGEFFRRASSPGRSPEOGPFGAGF DPSPFGADPSRGAPLGGEFFRRASSPGASECCYNADAULARARLAG ELAGORERERALGELEWDWVFLIPSGLIH.FRAVEPGLVOKFSLRD CSPRLSEBLYHRCRLERLEGLAGRAQLAMALFROEGANST CSPRLSEBLYHRCRLERAAGAFRTGSPLALGPETPQVACLP CHPVARPGQVSGGCAMPDVPALEAAAGAFRTGSPLALGPETPQVACLP CHPVARPGQVSGGCAMPDVPALEAAAGAFRTGSPLALGPETPQVACLP CHPVARPGQVSGGCAMPDVPALEAAAGAFRTGSPLALGPETPQVACLP CHPVARPGQVSGGCAMPDVPALEAAAGAFRTGSPLALGPETPQVACLP CHPVARPGQVSGGCAMPDVPALEAAAAGAFRTGSPLALGPETYALAGA ADGI-FLLRQCLRSLGSVGVUSLUPDVRFHHEP LERQLNGTYALAG GKAHCOPPACLCCYSTGATUSLUPDVRFHHEP LERQLNGTYALAG GKAHCOPPACLCCYSTGATUSLUPDVRFHHEP LERQLNGTYALAG GKAHCOPPACLCCYSTGATUSLUPDVRFHHEP LERQLNGTYALAG GKAHCOPPACLCCYSTGATUSLUPDVRFHHEP LERQLNGTYALAG HYNTYLISQDKAGKYCIPEGTKFDTLMQLVEYLKKAGDGVT LERGLADHOLDDPYTYSLSPDELLOKALILKAGDISCY LKRACPNSSASNASGAAAPTLEAHBSTLTHUQUVSTLKKAGTEKADTE EMMERAGINGTSVRGGVYRMRKQIDVAKUKGYTEKADTE EMMERAGINGTSVRGGVYRMRKQIDVAKUKGYTEKADTE EMMERAGINGTSVRGGVYRMRKQIDVAKUKGYTEKADTE EMMERAGINGTSVRGGVYRMRKQIDVAKUKGYTEKADTE EMMERAGINGTSVRGGVYRMRKQIDVAKUKGYTEKADTE EMMERAGINGTSVRGGVYRMRKQIDVAKUKGYTEKADTE EMMERAGINGTSVRGGVYRMRKQIDVAKUKGYTEKADTE EMMERAGINGTSVRGGVYRMRKQIDVAKUKGYTEKADTE EMMERAGINGTSVRGGVYRMRKQIDVAKUKGYTEKADT RKYSSKSDWEGGVTUMBALSYGDVILGKGANIGNTDAAALICKGATEKADTE LVGKRBEIPVSNVAELHQVSMGMIKYLEENNYLEGEKR MECPPECPPELYALMSDCWITTMGHTROLARDOLARDVALAGATA  6500  1773  726 TGPTHASADAMGUVSVTERGANVGGNPCAAALISCPQAULAGA KUKEPPEGFGTKARAACY  MLESSSSFLKGWUKESINGTDTAALSCOPAULAGA KUKEPPEGFGTKARAACY  MLESSSSFLKGWUKESINGTDTAALSCOPAULAGA  KUKEPPEGFGTKARAACY  GFTHASADAMGUVSVTERGANVGGNPCAALISCOPAULAGA KUKEPPEGFGTKARAACY  LVGMSGGGTETPVGCEAAPGGGSKRGDSLGTAGSAHLITKDIGB CHANCALVALKYAGVFARNAGATATUSDSOFTYTAASSVVKEKATYBN  OVVSGCGSTMAVTWRGLTROMGHTMATCYLLARMYCGOREGGRKKI HSDHLVALSKGGRIBLDFTGVVGHTMATCHAANAVACH				OHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRP
LEPLERVETLEMBYOTERATROLUTELUVERABAAPATEREPAA NVLEPREHALITILIUVGPREGGEGREPLGVRABABELERRY PGTRIAMILAVRAERAPSQVRIMUVVSKKHFUDTLPPLTTVWTRDG FEWLANCERMALGSMQAFFPUHTGEFRHEASPGREPOFPERGE DPPSPEGADE SERGP LIGERPERGASECTYNADTLARRALIAG ELAGGERERALEGLEWMDVFLIRPGLHIFRAVERPGLVQKFSLEN CSPRLSEBLYHRCZLESHEGLEWMDVFLIRPGLHIFRAVERPGLVQKFSLEN CSPRLSEBLYHRCZLESHEGLEWMDVFLIRPGLHIFRAVERPGLVQKFSLEN CSPRLSEBLYHRCZLESHEGGYALFOTERALAGAFRTGSPLALGPETPQVACLP CHEPVEPQVSGGGGAMPDVGLRAAAGAFRTGSPLALGPETPQVACLP CHEPVEPQVSGGGGAMPDVGLRAAAGAFRTGSPLALGPETPQVACLP CHEPVEPQVSGGGGAMPDPALALIPPYSGSISRABABEHLIKAGA ADGIFLIRGCLRSIGSGYVISLWEDWFHPPI ERQLNGTYALG GKAHCGPAELCEPYSRDPOGLECHLKPCNR PSELEPOFGVPDC LRDAMVRDYVRQTWKLEGBALEGALISJOAPQUKKLITTAHERM PWHISSLITEBBABRKLYSGAQTIGKFLLRPRKEQGTYALSLLYG KTVYHYLISQDKACKYCIPEGFKFDTIJMQLWETYLKKAGDGLIYC KERCPINSSAGNAGGAAAPTLPAHPSTLTHPQRR IDTIMSDCYT PEPARTTSPDKPRPMFMDTSVYESPYSDPEBLKKALFLKRDNI, LIADIELGCSNFGSVRGGVYNBRKAGDTAKVLKAGDGLIYC KERGPERSSAGNAGGAAAPTLPAHPSTLTHRQRR IDTIMSDCYT PEPARTTSPDKPRPMFMDTSVYESPYSDPEBLKKALFLKRDNI, VONENTAKLSDFGLSKALGADDSYYTARSAGKRQLKWYAPECINF RKYSSRSDWBSGYTMBALSTGOKPYKKMRGPEKAMTAPECINF RKYSSRSDWBSGYTMBALSTGOKPYKKMRGPEKAMTAPECINF RKYSSRSDWBSGYTMBALSTGOKPYKKMRGPEKAMTAPECINF RKYSSRSDWBSGYTMBALSTGOKPYKKMRGPEKAMTAPECINF RKYSSRSDWBSGYTMBALSTGOKPYKKMRGPEKAATYSEA WCGPPECPPBIYALMSDCWIYKWEDRPDFLINGDHARAVKE MECPPERCPPBIYALMSDCWIYKWEDRPDFLINGDHARAVKE TYTHCDKABFPSSENVKYFBSINDHTMAHRKAYAFDK VRDQYMWFCLARPTTFALIBNLXYTLLKXDPSQPFYLGHTIKSG DLBYVGMGGIULSYSGMRLANSLILNI PEKCEPBGGGMIKKISED OLBYVGMGGIULSYSGMRLANSLILNI PEKCEPBGGGMIKKISED CRANCLKYAGFFABRAEDADGROUPWTKSVGISIKKAMTYBPN OVVECCSDMAYTPRGLIPPOMIVMWYGVYRLRAFGFYFO  1 570 LVGMSGGTETFVGCEAAFGGSKKRDLGTAGSAHLITRDIGG HERALDHRPVTQGGTETFYVGCEAAFGGSKKRDLSTRAMVLENIKMTHE TNEHTLPKCRDTMRDSISGVIQRLQAANDSVCRLQGREGERKX HDDILVASEKQIBHQDMIVMYGVYRLERDFOWNSKILCQGYQAVKE SCRALEFRINGDILTFTVVQHITACTIAATASVVRKKLATGGS SGATEMKKGLSDFLAVTSNOPDFPELFDAMLSGCCLEEK KGBISBLLVGSSFIRADTTRNPDGPPELFDAMLSGCCLEEK GGRISBLLVGSSFIRADTTRNPDGFRTYCORPDGPPELFDAMLSGCCLEEK KGBISBLLVGSSFIRADTTRNPDGFRTYFCSSESISISUT		l		OKORLINGYRRYDPARGMEYTLDLLLECVTQRGHRRALARRVSL
NVLEPREBIALITLILVYGPREGGRGAPPPELGYRAAAAELERRYY PGTRLAMILAVRABAPSQVRIMIDVYSKHEPUDTJEPUTTYWTPDG PSWLANKCRMALGORQAPPPUHTGEFRATAUS PGRSPPGPPGAGP DPPSPPGADPSRGAPIGGRPDRGASAEGCTYNADTLAARARLAG ELAGGRERERALEGELWUDVFLEPSGLHIPRAVSPGLVQKFSIRD DPSPPGADPSRGAPIGGRPDRGASAEGCTYNADTLAARARLAG ELAGGRERERALEGELWUDVFLEPSGLHIPRAVSPGLVQKFSIRD GRANGUPVLREQUSGGGAMPDVFLIRSALGAGARQLAMALFROEGDANST CSPRLSBELYHRCRISNLEGLAGRAQLAMALFROEGDANST GCSADTREPSGQAMPTVGLRAAAGAFRTGSPJALIGPETPQVACLP GCSADTREPSGQAMPTVGLRAAAGAFRTGSPJALIGPETPQVACLP GCSADTREPSGQAMPTVGLRAAAGAFRTGSPJALIGPETPQVACLP GCSADTREPSGQAMPTVGLRAAAGAFRTGSPJALIGPETPQVACLP GCSADTREPSGQAMPTVGLRAAAGAFRTGSPJALIGPETPQVACLP GCSADTREPSGQAMPTVGLRAAAGAFRTGSPTALIGAG GKAHCGPAELCEPYSRPDGLPCHURKPCGTYALIGLUM ADGI-FILRQCLSELGGYULSUHDURFHHPP IS ERQLANGTYALIG GKAHCGPAELCEPYSRPDGLPCHURKPCGTYALIGLUM FWINSSLTEBERABRKLYSGAQTUGKFLLRPRKRSGGTYALISLIYG KTYYHKLISODRAGKYCI PEGTKPTTITAQUUVTLKLKKAGGLIYC LKRACPNSSASNASGAAAPTLPAHPSTTLTHQGTRIDTINSDGYT DEPARITSODKPRPMPDTSVYSSPYSDPELKOKLILLKRDNL LIADI BLGCGSRGSVRGGYYRRKKQIDVAIKVLKQGTBKADTE BWRGEQQIHPQLDMPYSVYSSPYSDPELKOKLILLKRDNL LIADI BLGCGSRGSVRGGYYRRKKQIDVAIKVLKQGTBKADTE BWRGEQQIHPQUNDYSVYTARSAGRQFLKMYAPBCCINF RKFSSRSDVWSGYTMMSALSYGAPYXKNRGFSVMAPIBGGKR MECPBECPPELYALMSCMITYKHQUVALRARMGGPVHAPBCGKR MECPBECPPELYALMSCMITYKHQUSPDFLITVRQBMRACYYSLA SKVBGPPGSTQKARAACA  1773 726 TGPTHASADAWGJVBSVTBECANVKGBPPCAALISCPQAVLDAGK MLSESSSPLKGVMLGSIFCALITMLGHIRIGHCRMMHHBIBHH. QAPNKEDILKISEDERHELSISFRYVCILLVRCDVSLGAAAVK TWTHCHCKAEFFSSENVKVSESINDITDMMLAMRKAYKARDDK YRDQYNN*FLARPTTFAI IRBILKYFLLKXDPSQFTICHTIKSG DLEYVGMEGGIVLSVSSMKLINSLIN IPRKCPBGGGMIKISED VRDQYNN*FLARPTTFAI IRBILKYFLLKXDPSQFTYIGHTIKSG DLEYVGMEGGIVLSVSSMKLINSLIN IPRKCPBGGGAHKISED KGLACKLKYAGVFARNABADAAGKOVFNTRASVCESISITUTTNEHPAGFYFQ 1 LVGMSGGFTETPVCGEAAPGGGSKKBGLGGAGAHITIKDIGB HSHLLDHRPVLQGETRYFVKEPERKRGLEGVAGAGHITIKDIGB SCHACHKKGLSDFLGVVSDTRAPSGDKTICDVITLMGTPSGT- TABSTLIPKCRDTMRDSISGVIQACAANBSVCGLAGERHITIKDIGB SGATEMKKGLSDFLGVVSDTRAPSGDKTICDVITLMGTPSGT- AEPYDGTKARLYSLQSDPATYCREPGDRTICDVITLMGTPSGT- AEPYDGTKARLYSLQSPRATYCRE	1		<b>!</b>	LRPLSRVETLPMPYVTRATRVQLVLPLLVAKAAAAPAFLEAFAA
PGTRLAMILAVRARAPSQVKLMUVUSKKREPUTFLFTTTVMTRE PEVLINCCRMIA ISGNQAPPPVHRORPRALS PORSEPOPPORAGE PEVLINCCRMIA ISGNQAPPVHRORPRALS PORSEPOPPORAGE DPSSPEGADESGRAPIGGRPDRQASAEGCFYNADYLARARLAG ELAGOERERALBEGLEVMUVFLIRESGLHIJRAVERSULTARALAG ELAGOERERALBEGLEVMUVFLIRESGLHIJRAVERSULTARALAG ELAGOERERALBEGLEVMUVFLIRESGLHIJRAVERSULTARARLAG ELAGOERERALBEGLEVMUVFLIRESGLHIJRAVERSULTARARLAG GERAPSGRAPPTVELRAÄAGAPRTOSEPLAUGPETPOVACLE GEPRISEBLIJRAGGERSULTARALEREHLIJAGA ADGLIPLIRGCERSLIGSVUSLIVEBUVRFHHPP IERQLINGTVALAG GRAHCGPARLCEPYSRDPDGLLEVILREVCKREDELEFORGVUSL LARDAWNGVVRQTYNKERGERALGALT ISGAPQVEKLLATTAHERM PWYHSSLTRERBERLINGGANGTOGRPLIREPKERGTVALSLIVG KTVYHYLLISQDRGKYCI PEGTKEPTLINQLIVELKLAGGLIYC KTVYHYLLISQDRGKYCI PEGTKEPTLINQLIVELKLAGGLIYC KTVYHYLLISQDRGKYCI PEGTKEPTLINQLIVELKLAGGLIYC KTVYHYLLISQDRGKYCI PEGTKEPTLINGLIVELKALPILKEDNIL LIADI ELGCGMEGSVIRGVYNRIKKI JOPAT KVILKGGTEKAGT PEPAR TYSEDKER PMPMDTISVYESP YSDPEELLKKALPILKEDNIL LIADI ELGCGMEGSVIRGVYNRIKKI JOPAT KVILKGGTEKADTE EMMREAQIHHQUAMPYJVULI GUCQABRIAMIVNEMBAGGOPLHKF LVOKRRE IPVSRVAELHIQVSMGMKYLLEKMPYHRULARRIVLL VINRHYAKLSDFGLSKALGADDSYYTRARGESEVIARIVAPBECINF RKFSSRSDWSGYTMMEALSYGORYYRKKINGSEVVAFIEGCEK MECPBECPBENJAMINGSTFCALTIMGHTRIGHGRMRHEHEHHHL RKFSSRSDWSGYTMMEALSYGORYYRKKINGSPEVVAFIEGCEK MECPBECPBENJAMINGSTFCALTIMGHTRIGHGRMRHHEHHHHL GEPBENDENSKENTENGUNGSTFCALTIMGHTRIGHGRMRHHEHHHHL GEPBENDENSKENTENGUNGSTFCALTIMGHTRIGHGRMRHHEHHHHL GEPBENDENSKENTENGUNGSTFCALTIMGHTRIGHGRMHHEHHHHL UNDHAVASERSPSSENVEVESINDTIDMHUMMKYAYTALKARYAPDK YRDQYNWFFLARPTTFALIENLKYFLLKXDPSOEPYLGHTI ISG DLSYVGMEGGIULSYSSMREIABILLI I PEKCPEDGOMINKTENG KOLKYAGPGSTFVYGCEAAPGGSKKROLSGISTAGSAHLI TUDIGB HERILDHRPVIGGETFFYGCEAAPGGSKKROLSGISTAGSAHLI TUDIGB HERILDHRPVIGGETFFYGCEAAPGGSKKROLSGAMRINGSTFCAGGAMITENGUNG HERSTIPKCROTMRDSISGOVIGALOAANDSVCHOQREGERKKI HSDHLVASEKGHMIGNINFNKEOPNKRAVGENINKSHLOQSYQAVE KSSRALEFHMROLTSFTYQVOHINTACTIAATASVVREKLATGGS GATERMKGLSOPLAVISDTPAPSBURT GOTOTTIMGTPSGT- AEPYDGTKARLYSLOSEPINTSOFTARTSTVRENDENTYPSKUPGCLEEK KGRISHLIVGSSEIRADTTROVPREDOTVENDENTINGOCCLEEK KGRISHLIVGSSEIRADTTR		· ·	f	
PBULINCRIMAL ISONQAPPPUHPCBENDALS PGRSPOPPOAGE DPPS PPGADPSEGAP IGGREDROAS ABGCTYMADULARRALIAG ELAGGEEREALEGLEVINDVFLRPSGLHLPRAVEPGLVQKFSLRD ESPRISBELTIRCRISHLEGLGGRQLAMALEPGSDANST CSPRIJEBELTIRCRISHLEGLGGRQLAMALEPGSDANST GRANCEPPUNGGRAAGAPRITSSPLAUGETPOVACLE GHPVRPQVSGGPGAMPDPAAHLPPFYGSISRABEBEHLKLAGM ADDLIFLLRCCLESLGGYVLSLUHDVRFHHSP IERQLINGTYALAG GRANCEPPELCEPYSRDPDGLPCHLKKPCNRPSGLEPOPGVFDC LRDAMWRDVVRQTWILISGBALEQAILSQAPOUKLLATTAHERM PWYHISSLITRRBABERLYSGAQTUGKFLLRPRENGGTYALISLIYG KTVHHLISQDKAGKYCIPEGTKFDTLMQLVEYLLKADGLIYC LKBRCENSSASMASGAAAPTLPAHESTLTHDGRIDTINSDGYT PEPARTTSPDKPRPHMDTSVISSPYSDPEBLEDKALFLKRDNL LIADIBLGCGNEGSVRQGVYRMRKKQIDVAIKVLKQATEKADTE PMREAQIMHQLDNPYIVRLIG VCQABAIMLJWEMBANGGOPLIKF RKPSSRSDWWSYGVTYMBRLSYGGATKANGAGGPPLKKF RKPSSRSDWWSYGVTYMBRLSYGKYKINKGPEWAMFIGGGKR KKVGGPPGSTIGARAACA RKVGGPPGSTIGARAACA SKWGGPPGSTIGARAACA GSRSSPLKGWMLGSIPCALITMLGHIRIGHGNNHHHBHHHL QANNKEDILKISEDBERMELSKSPRVYCIILVRROUSLABAVKE THTRHCDKAGFFSSENVKVFSIINDUTNDWLMMKKAYKYAFDK YRDQYNNFFLARPTTFAIIBMLKYFLLKKDPSOPFYLGHTIKSG DLEYVGMEGGTITSYGCFAARGGGSKRDDSLGTAGSAHLITKDIGG KQLAVCLKYAGVFAENAEDADGKDVFTKSVGLSI KEAMTYHDN QVVBGCCSDMAVTFRGLIPTNOMHVMMTGVYTRAFGFYFG KQLAVCLKYAGVFAENAEDADGKDVFTKSVGLSI KEAMTYHDN QVVBGCCSDMAVTFRGLIPTNOMHVMMTGVTRAFGFYFG FRENCHINGERGFILTSVSSMRILNSLIP PRICEPPGGGMIKKISED KGRAVCLKYAGVFAENAEDADGKDVFTRKSVGLSI KEAMTYHDN QVVBGCCSDMAVTFRGLIPTNOMHVMMTGVTRAFGFYFG FRENCHINGHER FRENCHINGH FRENCHERGERGHERKNIL KSBLLANSRGMHLONDFMERGOPRKRAVUERNILMTHR TNERTLIPKCROTMENDSLSGVUQRUADANDSVCRLQQREGERKKIL HSDILLANSRGMHLONDFMERGOPRKRAVUERNILMTRG SGATEKMKKGLSDFLGVTGTFAPSPBRTTLDCVTTLMFFTSG- AEPYDGTKARLYSLQSDPATYCNEPDGFPBIFDAWINGGCLLEKK KSBLISBLLVGSPSI RALTTRWPAAVSHSEFWHRYFYKVHQLEO- KGRISBLLVGSPSI RALTTRWPAAVSHSEFWHRYFYKHQLEO- KGRISBLLVGSPSI RALTTRWPAAVSHSEFWHRYFYKHQLEO- KGRIBBLIVGSPSI RALTTRWPAAVSHSEFWHRYFYKHQLEO- KGRIBBLIVGSPSI RALTTRWPAAVSHSEFWHRYFYKHQLEO- KGRIBBLIVGSPSI RALTTRWPAAVSHSEFWHRYFYKHQLEO- KGRIBBLIVGSPSI RALTTRWPAAVSHSEFWHRYFYKHQLEO- KGRIBBLIVGSPSI RALTTRWPAAVSHSEFWHRYFYKHQLEO- KGRIBBLIVGSPSI RALTTRWPAAVSHSEFWHRYFYKHQL			ł	DCTRLAWLAVRARAPSOVRLMDVVSKKHPVDTLFFLTTVWTRPG
DPPSPGADPSRGAP IGGRFDRQASAEGCFYRAD/ILARARILAG ELAGQEKEEALBEGLEVMOVFLRFSGLH-LIPRAVEPOLOVGFSIRD CSPRISBEILYRRCCILSILBGIGGRAQLAMALFEQEQANST 6499 3 2040 SCSADTRPSGQAMPTVGLRAAAGAFRTGSFLAGFET POVACLE GHPVRPQVSGGGGAMPDPAAHLP PFYGSISRABAEBLIKLAGA ADGI-FILRQCLRSLGGYVLSLVHDVRFHHFP IERQLNGTYALAG GKAHCGPAELGEFYSRDPDGI-CCHLKRPCRRSGLEPOGYVTDC LRDAWNDVWRQTWLBGEAL-EOGAI ISQAPOVEKLIATTAHERM PWYHSSLTRBEABERLLYSGAQTOGKFLLFPRESGGTYALSLIYG KTYYHYLISQDFAGKYCIPEGTKFDTLNQLVEYLKLKADGLIYC LKRACFRSSASNASGAAAPTI-PAHPSTLTHDQRRIDTILISDGYT PEPARTTSPDKRPRMPMTSVYESPYSDPEELEDKALFIKRDNL LIADIELGCGNFGSVRQGVYRMKYDLDVAIKVLKGYFTKADTE PWRFAQIHHQLDNPYIVRLIGVQARALMIVMEMAGGGPLHKF LVGKREB IFVSNVASLLHQVSMGMKYLERRNFVHRDLAARNVLL VNRHYAKISDPGISKANGADDSYVHKRASAKKPLKNYAPECINF RKFSSRDVWSYGVTMWBALSYGQKPYKMKGPBVMAPIEQGKR MECPPRCPPELVALMSDCM IYKMEDRPDFLTVRQBWRACYYSLA KVKGPPGSTQKAKAACA  6500 1773 726 TGPTHASADAWGLVRSVTEWCANVRGNFCAAALSCCPOAVLDAGK MLSESSSFLKGWMLGSIFCALITMLGHIRIGHCRNMHHBEHBHL QAPNKEDILKISEDBEMBLSSFRVYCILIVKREVOYSLMAAVKS TWTKHCDKASFFSSRNVKVFSINDMYNDMHLMRKAYKYAFDK YRQQYNWFFLARPTTFAIIBNLKYFLIKDPSQPFYLGHTIKSG DLBYVGMEGGIVSSYSSMRLUSLINIPRRCYKGFSTGGAHKISED KQLAVCLKYAGVFARNAEDADGKUVFATTSVGLSI KEAMTYHPN QVVEGCCSDMAVTFNGLTPNOMHVMMYGVYRLARFOFFYO UVEGCCSDMAVTFNGLTPNOMHVMMYGVYRLARFOFFYO LUCHSGGGTTSTVGCEAAPGGGSKKRDSLGTAGSAHLIIKDIGB HSBLLDHRPVLQGSTRYFVKRFEREGLARRWLENLKNMTHE TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQGREGEKKI HSDHLVASRGQHLGNDRFMKEQPNKRAEVDEERKAMSRLKEO YABMEKDLAKFSTF  6502 213 1650 AGNRPDFWAGGNETAVLPDVSVYHREDVGWRSWLQQSYQAVKE KSSRALBFMRRDLTBFTQVVQHDTACTIAATASVVKBKLATEGS SGATEKMKKGLSDFLGVISDTPAPSPBRTLDCVVITIMGTPSGC- ARPYDGTKARLYSLODPATYCNRPGSFFSIFPAPFREKERISPRGACHERSKELKEO KGRISBLLVGSFSIRALYTKNVPAAVSHSBFWHRYYKVHQLEO- KGRISBLLVGSFSIRALYTKNVPAAVSHSBFWHRYYFYKVHQLEO- KGRRIBBLIVGSFSIRALYTKNVPAAVSHSBFWHRYFYKVHQLEO- KGRRIBBLIVGSFSIRALYTKNVPAAVSHSBFWHRYFYKVHQLEO- KGRRIBBLIVGSFSIRALYTKNVPAAVSHSBFWHRYFYKVHQLEO- KGRRIBBLIVGSFSIRALYTKNVPAAVSHSBFWHRYFYKVHQLEO- KGRRIBBLIVGSFSIRALYTKNVPAAVSHSBFWHRYFYKVHQLEO- KGRRIBBLIVGSFSIRALYTKNVPAAVSHSBFWHRYFYKVHQLEO- KGRRIBBLIVGSFSIRALYT	1	ł	l	PRVINRCRMNAISGWOAFFPVHFOBFNPALSPQRSPPGPPGAGP
ELAGQERERALEGLEVMUVFLRPAGIHLFRAVEPGLVQKFSLRI  CSPRLSBELYHRCRLSNILBGLGGRAQLAMALF PEGEOANST  GSPRLSBELYHRCRLSNILBGLGGRAQLAMALF PEGEOANST  GENDYRPGVGGGGAMPDVGLRAAGAFRTVGSPLALGPETPQVACLE  GHDPVRPGVGGGGAMPDPAAHLPFFYGSSTBRARAEBHLKLAGM  ADGLPLLRQCLBSLGGYVSLUHDVRFHHFPIERGLANTVALAG  GKAHCGPAELCEPYSRDPDGLPCNLRKPCNRPSGLEDOFGVPDC  LRDAMVBDVVRQTWKLBGRAEQATLSQAPOVEKLIATTAHERM  PWHISSLTRBRABRKLYSGAQTOGKFLLRPRKEGGTVALSLIVG  KTVYHYLLSQDKAGKYCI PEGTKFDTLNQLVBYLKLKADGLIVG  LKBACPNSSASNASGAAPTLPAHPSTLTHPQRRIDTINSGYT  DEPARTTSDPKDRPPMEMDTSVYSEPYSDFEELKDKKLFLKRDNL  LIADIELGCONFGSVRQGYVRWRKGIDVALKVLKQGTBKADTE  EMSRESQIMSIGNDPYIVELIGVCQABAIMLVMBAGGGPLKKF  LVGKRBEIPVSNVABELHQVSMGMKYLERKNFVHEDLAARNVLL  VNRHYKKISDFGLSKALGADDSYYTARAGKQLKWYABECINF  RKPSSRDVMSYGVTWMBALSTGOKFYKMMGDFRWAPIEGGKR  MECPPBCPBLYALMSDCMIYKWEDRPDFLTVRQBMRACCYYSLA  KVEGPPGCPBLYALMSDCMIYKWEDRPDFLTVRQBMRACCYYSLA  KVEGPPGCPBLYALMSDCMIYKWEDRPDFLTVRQBMRACCYYSLA  KVEGPPGCPBLYALMSDCMIYKWEDRPDFLTVRQBMRACCYYSLA  MESESSFLKGVMLGSIFCALTTMLGHIRIGHGRMHHBHBHHH-  QAPNKEDILKISEDERMEIJSBFYCYLCILLVKRDVSLMAAVKE  TWTKHCDKABFFSSENVKVFESINMIYTDMHLMMRKAYKYAFDK  YRDQYNN#FLARFTTFALIBNLKYFLLKDPSQEFYLHTIKSG  DLBEVGMEGGTISLVSYSMKRINSLIAN IP BKCCPBQGGMIWKISED  KQLAVCLKYAGVFAENAEDADGKDVFNTRSVGLSIKERAMTVEPN  QVVBGCCSDMAVTFNGLITNQMHVMYGVYRLRAFGPYFQ  6501  1 570  LVGMSGGTTSTPVGCRAPGGGSKKRDSLGTAGSAHLITNDLGG  HSRLLDHRPVIGGBTRFVVKBFEERKGLRRMRVLENLKNMTHE  TNEHTLPKCRUTMRDSLSQVLQRLDAANDSVCRLQQREOGERKKI  HSDHLVASEKQHALQMDNTMIKGDPMRARVUEBERKAMERKEG  YABMEKDLAKFSTF  6502  213  1650  AGNKPDPWGGRONTAVLPDVSVFHREDVGMWRSMLQQSYQAVKE  KSSRALEFMKRDLTBFTQVVQHDTACTIAATASVVKBKLATEGS  SGATEKMKKGLSDFLGVISDFTAPSPDKTDCDVITLMTPSGC-  AEPYDGTKARLYSLQSDPATYCNRPDGPPELFDAMISOFCLBEK  KGELSBLLVGSPSIRALYTMVPAAVSHSBFWHRYFYKVHQLEO  RQARRDALKQRACGSISBEGMBEEBERKMGISDFJSRAKVPV  AT 15 TEPTPERBRDDGSPGCREMUSRYBPPARSYSSSESISLVT	ĺ	ĺ	•	DDDSDDGADDSRGAPIGGRFDROASAEGCFYNADYLAARARLAG
CSPRLSEELYHRCRISHLEGLGGRAQLAMAFFEQEQANST  SCADTRPSGQANPTVGLEAAAGAPTGSPLALGPETPOVACLE GHPVRPQQVSGGGMMPDPAAHLPFYSGSLSRABABEHLKLAGM ADGI-FLIRQCLRSLGSYVI-SLVHDURFHHPFIERQLINGTVALAG GKAHCGPAELCEFYSRDPDGILECVIR.KPCNRPSGIBPOPGVFDC LRDAMWRDVRQTWKLBGEALEQAIISQAPQVEKLIATTAHERM PWHISSLTREBABRKLYSGAQTDGKFLILFRKEGGTVALSLIVG KTV4VTVLSQTMGAKVC1PEGFKPDTLMQLWSYLLKABGLIYC LKBACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTINSDGYT PEPARITSPDKPRPMEMDTSVYESPYSDFBELKDKKLFLKRDNL LIADIELGCCINGSVRQGVYRMRKQIDVALKVLKQGTBKADTE EMMREAQIMHQLDNPYLVILIGVCQABALMLVMEMAGGGPLHKF LVGKREBIEVSNVABLLHQVSMGMKYLEEKNFVHRDLAARNVLL VNRHYAKISDFGISKALGADDSYYTARSAGKQLKWYAPBCINF RKFSSRSDWSYGVTYMBALSTGOKPYKKMKGFBWAAFIEGGKR MECPPBCPPELYALMSDCWIYKMEDPPDFLTVRQRMRACYYSLA SKVUGGPPGSTGKABAACA GGPTHASADAGUVRSUTEWCANVKGNPCAAALSCPQAVLDAGK MLSESSFLKGVMLGSIFCALITMLGHIRIGKNRMHHBEHBHL QAPNKEDILKISCDEMBELSSFRVYCIILVKPKDVSLMAAVKE TWTKHCDKARFFSSEAVKVFSINMITHINMLMMKKAKXAFDK KROLDENSTANDENSTANDENSTANDHINMLWMYGVYRLKABFTTIKG GLEVVGMEGGIVLSVSSMKRLMSLLNIPEKCPBQGGMIWKISED KQLAVCLKYAGVFARBAEDADGROUPMTRSVGLSIKARATYHPN QVVBGCCSDMAVTPNGLTIPNGHUVMYGVYRLRAFGPYFO  570 LVGMSGGTETFVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGB KGLAUCLKYAGVFARBATSPGSLSGVLORLORANDSVCRLQGREDERKKI HSBLLDHRPVIGGBTRYFVKBFEKRGRRMRVLEENKMMIHB HSBLLDHRPVIGGBTRYFVKBFEKRGRRMRVLEENKMMIHB HSBLLDHRPVIGGBTRYFVKBFEKRGRRMRVLEENKMMIHB HSBLLAHRPVIGGBTRYFVKBFEKRGRRMRVLEENKMMIHB HSBLLAHRPVIGGBTRYFVKBFEKRGRRMRVLEENKMMIHB KSSRALEFMKROLTBFTGVVQHDTACTIAATASVVKBKLATEGS SGATEKMKKGLSDFLGVISDTPAPSDEWITCDCUTITLGTFEGG- AEPYDGTKARLUSLGSDFLGVISDTPAPSDFRICTDCUTITLGTFEGG- AEPYDGTKARLUSLGSDFLGVISDTPAPSDFRICTDCUTITLGTFEGG- AEPYDGTKARLUSLGSDFLGVISDTPAPSDFRICTDCUTITLGTFEGG- AEPYDGTKARLUSLGSDFLGVISDTPAPSDFRICTDCUTITLGTFEGG- AEPYDGTKARLUSLGSDFLGVISDTPAPSDFRICTDCUTITLGTFEGG- AEPYDGTKARLUSLGSDFLGVISDTPAPSDFRICTDCUTITLGTFEGG- AEPYDGTKARLUSLGSDFLGVISDTPAPSDFRICTDCUTITLGTFEGG- AEPYDGTKARLUSLGSDFLGVISDTPAPSDFRICTDCUTITLGTFEGG- AEPYDGTKARLUSLGSDFLGVISDTPAPSDFRICTDCUTITLGTFEGG- AEPYDGTKARLUSLGSDFRICHSERPERLERGISDFISDFAKUP	1	}	· '	RT.AGORRERAT.RGI.EVMDVFLRFSGLHLFRAVEPGLVQKFSLRD
6499  3 2040  SCSADTRPSGQAMPTVGLERÄÄÄGARTTSSPLALGPBTPQVGCLE GHPVRPQVSGGPGAMPDPAHLPPTYGSISRABABEHLKLÄGM ADGI-FLIRQCLESLGGYVLSLVHDVRFHHPPI ERQLAGTYALAG GKAHCGPAELCEPYSRDPDGLPCNLRKPCNRPSGLEPOPGYPDC LRDAMVRDYVRQTWKLEGRALGOATUGKFLERRREGGTYALSLIYG KTVYHYLISQDKAGKYCI PEGFKFDTILNQUBYLKLKADGLIYC LKBACPNSSASNASGAAPTLPAHPSTLTHPQRETDTINSGYT PEPARTTSPDKRPPMEMDTSVYESPYSDPEELKDKKLFLKRONL LIADIELGCONFGSVRQGYRWRKKQIDVAIKVLKQGJFYGKADTE EMMREAQIMHQLDNPYIVLLIQOABAIMLUMEMAGGGPLIKF KPSRSDVWSYGVTMRRAGISPYTARSAGKYQLKNYAPBCINF RKPSRSDVWSYGVTMRALSYGGVYRKMKSPEWMAFEGSKR MECPPKCPPELYALMSDCHIYKWEDRPDFLTVRQBWRACYYSLA SKVEGPPGSTQKABAACA MESSSPLAGWMLGSIFCALTMIGHIRICHGMRMHHEHHHL QAPNKEDILKISKDESMEISKSPRVYCIILVKPKDVSLWAAVKE TWTKHCDKAEFFSSENVKVFESINMITMIGHIRICHGMRMHHEHHHL QAPNKEDILKISKDESMEISKSPRVYCIILVKPKDVSLWAAVKE TWTKHCDKAEFFSSENVKVFESINMITMIGHIRICHGMRMKLSKYAFDK YRDQYNWFPLARFTTFALIENLKYFLLKKDPSQPFYLGHTIKSG DLEVVGMEGGIVLSVSSMKRLUSLLNIPKCPGGGGMIKKISED KQLAVCLKYAGVFFAENAEDDAGKDVSTNTSVGLSIKEAMTYBPN QVVBGCCSDMAVTFNGLTROMHVMMYGVYRLRAFGPYFQ  6501  1 570 LVGMSGGGTEFPVSCEARAGGGSKRDSIGTAGSAHLITKDIGH HSRLLLDKRDTIDRGLSQVLQRLQAANDSVCELQQREDBRKKI HSDHLVASEKQHBLQWDNFMKSQPNKRAEVDEEHRKAMIHB TNEHTLPKCRUTHREBLSGVLQGHKKAERD YABMEKDLAKFSTP AGNERDLAKRSTP AGNERDAGRAGGSTPAGGBREREBERGSBRIGH AGNERDALKRSTP AGNERDLAKRSTP AGNERDLA	į	<u> </u>		CODDI. SREI. VERCRI SNI RGLGGRAOLAMALFEQEQANST
GHPVRPQVSGSGRAMPDPAAHLPFYYGSISRABABEHLKIAGA ADGLFLLRQCLRSLGSYVLSLVHDVRFHHPPIERQLMGTYALAG GKAHCGPAELCEFYSRDPDGLPCNLRRPCRRPSGLEPOPGVFDC LRDAMVRDYVRQTVKLEGALEQAIISQAPQVERLIATTAHERM PWYHSSLTRBEABRKLYSGAQTOGKFLLRPRKSGGTYALSLIYG KTYYHYLISQDKAGKYCIPBGTKPDTLNQLVEYLKLKADGLIYC LKRACPNSSASNASGAAPTLPAHBSTLTHQRINIDTINSDGYT PEPARITSPDKPRPMPMDTSVSSPYSDPBELKUKKLFKRDIL LIADIELGCSNFGSVRQGVYRMKKQIDVAIKVLKQGTBKADTE BMREAQIMIQLDNPYLVRLIGVCQABAIMLVMEMAGGGLMKK LVGKRBIPVSVVABLHHQVSMGMKYLEEKRYVIRDLAARNVLL VORRHIYAKISDFGLSKALGADDSYYTARSAGKQLKWYAPBCINF RKFSSRSDVWSYGYTMMBALSYGCKPYKNMGFBVMAFIEGGEN MCCPPBCPBRIYALMSDCUIY IKMEDRPDFLTVBQRMRACYYSLA SKVEGPPSGTQKABAACA  1773 726 TGPTHASADAMGLVRSVTEWCANVRGNPCAAALSCPQAVLDAGK MLSESSFLKGVMGSIPCALITVHLGHIRIGHGRMMHHBKHHL QAPNKEDILKISEDERMELSKSPRVYCILLVKPROVSLWAAVKE TWTKHCKAEFFSSENVKVESILNDIVNDMHLMMRKAYKYAFDK YRDQYNMFFLARFTTFAIIBLKYFLLKKDPSQPFYLGHTIKSG DLEYVGMEGGIVLSVSSMKRLNSLLN TPKCPEGGGHIWKISED KQLAVCLKYAGVFRABABCDADGKDVFNTKSVGLSIKEAMTYHPN QVVBGCCSDMAVTFNGLTPROMHVMMYCVYRLRAFGFYFQ  6501 1 570 LVGMSGGGTETPVGCEAAPGGGSKKRDSGIGTAGSAHLTIKDIGH HSBLLDHRPVIQGKTRYFVEFFEKRGLREMRVLENLKNMIHB LHSBLLDHRPVIQGKTRYFVEFFEKRGLREMRVLENLKNMIHB TINEHTLPKCROTMRDISIGSVLQRLQAANDSVCRLQQRGGRKKXI HSDHLVASEKQHMLQWDNFMKBQPNKRAEVDEEHRKAMERLKEQ YABMEKDLAKPSTF 6502 213 1650 AGNRCDFAGRGRRTTAVLFDVSVFHREDVGWWRSMLQQSYQAVKE KSSBALRFMKRGLSDFLGVISDTFADSPDRTIDCDVITLMGTPGGS GATEKMKGLSDFLGVISDTFADSPDRTIDCDVITLMGTPGGS GATEKMKGLSDFLGVISDTFADSPDRTIDCDVITLMGTPGGS GATEKMKGLSDFLGVISDTFADSPDRTIDCDVITLMGTPGGS GATEKMKGLSDFLGVISDTFADSPDRTIDCDVITLMGTPGGS GATEKMKGLSDFLGVISDTFADSPDRTIDCDVITLMGTPGGS GRATEKMKGLSDFLGVISDTFADSPDRTIDCDVITLMGTPGGS GATEKMKGLSDFLGVISDTFADSPDRTIDCDVITLMGTPGGC ABPYDGTARRLYSLGSDPATYCNEPDGSPERFDRAUSGGCCLEBK KGELSELLVGSPSIRALYTKMVPAAVSHSEFWHRYTYMHOLEQ KGRISBLLVGSPSIRALSGOSS ISEEPGMEEREERBIMGISPIDRIAKVDV AKISCPPREMBEDADGOS CERENLVTSVEPPARVPGSSSSSISLUVT			2040	CCANTEDECOANDIUGI.PAAAGAPRIGSPLALGPETPOVACLP
ADGLPILRQCLRSLGGYVLSLVBDVRPHHPPIRRQLNGTYAIAG GKAHCGPAELCEPYSRDPDGLPCVLRKKPCNRFSGLEPOPGVPDC LRDAWNDYVQTVKLLGBALEQAIISQAPQVEKLIATTAHERM PWYHSSLTRBABRKLYSGAQTGKPILRPKKBGGTYALSLIYG KTYYHYLISQDKAGKYCIPEGTKPDTLNQLVBYLKLKADGLIYC LKERCPMSSASNASGAAPTLPHPSTLTHPQRRIDTINSDGYT PEPARITSPDKPRPMPDTSVYESPYSDPESLKDKKLFLKRDNL LIADIELGCGNFGSVRQGYYMRKKQIDVAIKVLKQGTBKADTE EMPREAQIMHQUNPYIVELHIGVCQABAIHLVHEMAGGGPLHKF LVGKRBEIPVSNVABLLHQVSMGMKYLEEKNFVHRDLAARNVLL VNRHYAKISDFGLSKALGADDSYYTARSAGKWPLKNYAPBCINP RKFSSBOVWSYGTYMBALSYGCKPYKKNKGFSVMAPHECINP RKFSSBOVWSYGTYMBALSYGCKPYKKNKGFSVMAPHECINP RKFSSBOVWSGPPGSTQKARAACA GFPHASSADAGA GSPHASSADAGA MLSESSSFLKGVMLGSIFCALITMLGHTRIGHGRMHHHBHHH- QAPNKEDILKISEDERMELGKSFRVYCILVKKRCDSHAAVKE WTHTHCDKABFPSSENVKYFSINMOTNOMHIMMRKAYKYAFDK YRDQYNWFPLARPTTFAIIBNLKYFLLKKDPSQPFYLGHTIKSG DLBYVGMEGGTVLSVSSMKRLINSLIN TEKCPRGGMIWKISE WQLAVCLKYARGYFSENWKYSISMVTSUCKINSULSIKBAMTYHPN QVVBGCCSDMAVTPNGLTPNQMHVMMYGVYRLRAFGPYFQ  LVGMSGGTETPVGCGEAAPGGGSKKRDSLGTAGSAHLITKDLGB KQLAVCLKYARGVFABNABDGKDVFNTKSVGLSIKBAMTYHPN QVVBGCCSDMAVTPNGLTPNQMHVMMYGVYRLRAFGPYFQ  LVGMSGGTETPVGCGEAAPGGGSKKRDSLGTAGSAHLITKDLGB TNERTLEKCROTMBDSLSQVIQRIQAANDSVCRLQQREQERKKI HSDHLVASEKCHMLQNDNFMKSQPNKRAEVDEERKAMERLKEQ YABMEKDLAKPSTF ASNRCDPÄGGRNTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSBALBFMKROLSDFLGVISDTFAPSPBKTIDCDVITLMGTPSG- SGATEKMKGJSDFLGVISDTFAPSPBKTIDCDVITLMGTPSG- SGATEKMKGJSDFLGVISDTFAPSPBKTIDCDVITLMGTPSG- AEPPYGTKARLYSLGSDPATYCNRPDGFPERFDAWLSGCFCLEEK KGELSELLVGSPSTRALYTKMVPAAVSESEFMHRYTYKVHOLBO- RQARRDALKQRAEQSISEEPGWEERERBIMGISPISPKEAKVUP KTSCPPFRENGDADGS SEEPGWEERERBIMGISPISPKEAKVUP KTSCPPFRENGDADGS SEEPGWEERERBIMGISPISPKEAKVUP KTSCPPFRENGDADGS SEEPGWEERERBERMGISPISPKEAKVUP KTSCPPFRENGDADGS SEEPGWEERERBERMGISPISPKEAKVUP KTSCPPFRENGDADGS SEEPGWEERERBERMGISPISPKEAKVUP KTSCPPFRENGDADGS SEEPGWEERERBERMGISPISPKEAKVUP KTSCPPFRENGDADGS SEEPGWEERERBERMGISPISPKEAKVUP KTSCPPFRENGDADGS SEEPGWEERERBERMGISPISPKEAKVUP KTSCPPFRENGDADGS SEEPGWEERERBERMGISPISPKEAKVUP KTSCPPFRENGDADGS SEEPGWEERERBERMGISPISPKEAKVUP	6499	, 3	2040	CHDDUDDOVSGGDGAMPDPAAHLPFFYGSISRAEAEEHLKLAGM
GKAHCGPAELCEFYSRDPDGLPCNILKPCNRFSGLEPOFOYFDC LRDAMWRDYVRQTNKLEGEALEQAIISQAPQVEKLIATTAHERM PWYKISSITREBAERKIJSQAPTOGKFLIAFREGGTYALSLIVG KTVYHYLISQDKAGKYCIPEGTKFDTLMQLVEYLKLKADGLIYC LKERCPNSSASNASGAAAPTIPAHPSTLTHPQRRIDTLNSDGYT DEPPARITSPDFKPRMPMDTSVYESPYSDPEELKDKALFLKRONL LIADIELGCGNFGSVRQGVYRMRKKQIDVAIKVLKQGTBKADTE BWMREAQIMHQLDMPYIVRLIGVCQABALMLVWEMAGGGPLHKF LVGKRBEIPVSNVASLLHQVSMGMKYLIERENTPVIRPDLAARNVLL VNRHYAKISDFGLSKALGADDSYYTARSAGKWPLKWYAPBCINF RKFSSRSDVWSYGYTYMBALSYGORFYKMKGPEVMAFIRQGKR MECPPECPPELYALMSDCWIYKWEDRPDFLTVRQRMRACYYSLA SKVUGPPGSTQKARAACA  6500 1773 726 TGPTHASADAWGLVUSVTEWCANVKGNPCAAALSCPQAVLDAGK MLGESSSPLKGVMLGSIPCALITMLGHIRIGHCRMHHHBHHHL QAPKKEDILKISEDERMELSSFRYVCIILVKPKDVSLMAAVKE TWTKHCDKAEPFSSENVKVPESINMININHMKKAYKYAPDK YRDQYNWFFLARPTIFALIBNLKYFLLKKDPSQPFYLGHTIKSG DLBYVGMEGGIVLSVSSWRLMSILMIPRKCPBGGGMIWKISED KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN QVVBGCCSDMAVTFWGLTTNQHHVMYGVYRLRAFGFYFQ LVGMSGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLITKDLGB HSBLLDURPVIQGETRYFVKBFERKRGLRRMRVLENLKNMIHB TNEHTLPKCRDIMRDSLSQVLQRLQAANDSVCRLQQREQBRKKI HSDILVASEKQHMLQWDMFMKSQPNRRAEVDEEHRKAMERLKEQ YAPBEKDLLAKFSTF AGNRDDWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSRALBFMKRDLTBFTQVVQHDTACTIAATASVVKRKLATEGS GGATEKMKRGLSDFLGVISDTFPAPSPDKTIDCDVITIMGTPSG- AENYPDFWARLILKFSTFTVCREPDGPPBLFDAWLSQFCLEEK KGELSELLVGSPSIRALYTKMVPAAVSHSRFWHRYFYKVHOLBO- BARRDALKGRAPGDGSISBEPGWEEBEBERLMG ISPISPKRAKVPV ALSSYPPBGRARDGDGSPERSILVTSVEPPABFTPSTSPSSESSISLVT		,		ADGLELL ROCLES LGGYVLS LVHDVR FHHFPIERQLNGTYALAG
LRDAMVRDYURÇITKILGGRA-EQALISOAPOURKLIATTAHERM PWHISSLTREBAERKLYSGAQTDGKFILRPKEGGTYALSLIYC KTYYHYLISODKAGKYCI PEGTKFDTLMQLURYLKKADGLIYC LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTINSDGYT PEDARITSPDKPRPMPMDTSVYSPYSDPEELKDKKLFLKRDNL LIADIELGCGNFGSVRQGVYRMRKQIDVAIKVLKQGTBRADTE EMMREAQIMHQLDNPYIVRLIGVCQABALMLVWEMAGGGILKF LVOKRBEIPVSNVARALLHQVSMGMKYLEEKNPVHRDLAARNVLL VNRHYAKISDFGLSKALGADDSYYTARSAGKRALKWYAPBCINF RKPSSRSDVWSYGVTMWBALSYGOKPYKKMKGPBVMAFIEQKR MECPPGCPPELYALMSDCWIYKWEDRPDPLITVEQRWRACYYSLA SKUKGPPGSTQKRAAACS MECPSCPFELYALMSDCWIYKWEDRPDPLITVEQRWRACYYSLA SKUKGPPGSTQKRAAACS MESESSFLKGVMLGSIPCALTTMLGHIRIGHGNRMHHBEHHL QAPKEDILKISEDERMELSKSPRYVCIILVVPROVSUMAAVKE TWTKHCDKARFFSSENVKVFESINMUTNDMWLMMRKAYKYAPDK YRDQYNWFPLARPTTFALIBNLKYFLLKKDPSQFFYLGHTIKSG DLBYVGMEGGIVLSVZSMKRLNSLLNIPRCPEGGFMIKKISED KQLAVCLKYAGVFAENAEDADGKDVENTKSVGLSIKEAMTYHPN QVVEGCCSDMAVTHWGLTPNQMEVMMYGVYRLARAFGPYFQ LVGMSGGGTETPVGCCBAAFGGSKKRDSLGTAGSAHLITKDLGB KQLAVCLKYAGVFAENAEDADGKDVENTKSVGLSIKEAMTYHPN QVVEGCCSDMAVTHWGLTPNQMEVMMYGVYRLARAFGPYFQ LVGMSGGGTETPVGCCBAAFGGSKKRDSLGTAGSAHLITKDLGB KGLAVCLKYAGVFAENAEDADGKDVENTKSVGLSIKEAMTYHPN QVVEGCCSDMAVTHYGLTPNQMEVMMYGVYRLARAFGPYFQ LVGMSGGGTETPVGCCBAAFGGSKKRDSLGTAGSAHLITKDLGB KGLAVCLKYAGVFAENAEDADGKDVENTKSVGLSIKEAMTYHPN QVVEGCCSDMAVTHYGLTPNQMEVMMYGVYRLARAFGEYFQ LVGMSGGGTETPVGCCBAAFGGSKKRDSLGTAGSAHLITKDLGB KGLAVCLKYAGVFAENAEDADGKDVENTKSVGLSIKEAMTYHPN QVVEGCCSDMAVTHYGLTPNQMEVMYGVRLARAFGSHKKILKNIHR TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQBERKKI HSDHLVASEKQHMLQNDNFMKSQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKPSTF AGNREDPFAGRIRRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSRALEFMKROLTBFTQVVQHITACTIAATASVVKRKLATEGS SGATEKMKRGLSDFLGVUSDTFAAPSPDKTIDCDVITLMGTPSG- AEPPYDGTKARLNSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK KGELSELLVGSPSIRALYTKMVPAAVSHSFFMRYFYKVHOLBO- AERPYDGTKARLNSLQSDPATYCNEPDGPPELFPRAWLSQFCLEEK KGELSELLVGSPSIRALYTKMVPAAVSHSFFMRYFYKVHOLBO- BQARRDALKQRAEQGSISEEPGMLGEEBERLMG ISPISPKRAKVPV ALSSPPERGROPPGDGOSPERENLUYSSVEPPAEVTPSESSESISLVT	l .	· ·	1	GKAHCGPAFLCEFYSRDPDGLPCNLRKPCNRPSGLEPOPGVFDC
PWYHSSLIREABERLYSGAQTDGKFLLEPRESGGTYALSLIVG KTYYHYLISQDKAGKYCIPEGTKFDTLNQLVEYLKLKADGLIYC LKERCPMSSASNASGAAAPTLPAHPSTLTHDQRRIDTLNSDGYT PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKALFLKRDNL LIADIBLGCGNFGSVRQGVYRNEKRQIDVAIKVLKQGTBKADTE EMMEAQIMHQLDNPYIVRLIGVCQABALMLVMEMAGGGFLHKF LVOKRBE LPVSNVARLLHQVSMGMKYLEEKNPVHRDLAARNVLL VNRHYAKISDFGLSKALGADDSYYTARSAGKRQLKWYAPECINF RKPSSRSDVWSYGVTMWBALSYGQKPYKRMKGFBVMAPFECINF RKPSSRSDVWSYGVTMWBALSYGGKPYKMKGFBVMAPFECINF RKPSSRSDVWSYGVTMWBALSYGGKPYKMKGFBVMAPFECINF RKPSSRSDVWSYGVTMWBALSYGGKPYKMKGFBVMAPFECINF RKPSSRSDVWSYGVTMWBALSYGGKPYKMRGFBVMAPFECINF RKPSSRSDVWSYGVTMWBALSYGGKPYKMRGFBVMAPFECINF RKPSSRSDVWSYGVTMWBALSYGGKPYKMRGFBVMAPFECINF RKPSSRSDVWSYGVTMWBALSYGGKPYKMRGFBVMAPFECINF RKPSSRSDVWSYGVTMWBALSYGGKPYKMRAPECYSLA SKVEGPPGSTQKABAACA MECEPPECPPELNAMACOMIVENTRAGHPRINAMHBRHHHL QAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSLWAAVKE TWTKHCDKABFFSSENVKVFSSINNDINDINMHLMRKAYKYAFDK YRDQYNMYFLARPTTFAIIBNLKYFILKKDPSQPFYIGHTIKSG DLBYVGMRGGIVLSVSSMRLLMSLLNI PEKCPEQGGMIWKISED KQLAVCLKYAGVFAENAEDADGKDVNTKSVGLSIKRAMTYHPN QVVSGCCSDMAVTFWGLTPNQHIVMYGVYRLRAFGPYFQ  6501  1 570 LVGMSGGGTETPVGCBAAGGGSKRADSLGTAGSAHLJIKDLGBE HBRILDINFPVIQGSTRYFVKEPEKRGLREMRVLENLKNMIHE TNEFTLPKCRDIMRDSLSQVLQRLQAANDSVCRLQQREQBRKKI HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMGRLEQ YABMEKDLAKPSTF  6502 213 1650 AGNKPDFWAGRIRTAVLPDVSVFHREDVGWNRSMLQQSYQAVKE KSSRALEFMKRGLITBFTQVVQHITACTIAATASVVKKKLATEGS SGATEKMKKGLSDFLGVISDFTYADSPPKTICDCDVITMGTPSG- AEPPYDGTKARLYSLQSDPATYCMEPDGPPBLFDAWLSQFCLEEK KGELSBLLVGSPSIRALYTKMVPAAVSHSKFWHKYFYKVHOLEQ- BQARRIDALKQRAEQSISBEPGWEEEBERLMGISPISPKRAKVPV ALTSCPPERGROPGPGPGERENLVYSVEPPABVTPSSSSESISLVT	ł			LRDAMVRDYVROTNKLEGEALEQAIISQAPQVEKLIATTAHERM
KTVYHYLISQDKAGKYCIPEGTKPDTLMQLWEYLKIKADGLIYC LKRACPNSSASMASGAAPTLPAHPSTLTHPQRRIDTLNSDGYT PEPARITSPDKRPPHPMDTSVYESPYSDPEELKDKALPLKRONL LIADIELGCGNFGSVRQGVYMRKKQIDVAIKVLKQGTEKADTE EMMREAQIMHQLDNPYIVELIGVCQABALMLVMEMAGGGPLHKF LVGKREEIPVSNVABLLHQVSMGMKYLEEKNPVHRDLAARNVLL VNRHYAKISDFGISKALGADDSYYTARSAGKWLKNYAPECINP RKPSSRSDVWSYGVTMWEALSYGQKPYKKMKGPEVMAFIEQGKR MECPPBCPPELYALMSDCMIYKMEDRPDFLTVRQRMRACTYSLA SKVEGPPGSTQKABAACA  6500 1773 726 TGPTHASADAWGLVRSVTEWCANVRGNPCAAALSCPQAVLDAGK MLSESSSPLKGVMLGSIFCALITMLGHIRLGHGNRMHHHRHHLL QAPNKEDTLIKISEDERMELSKSPRVYCIILVKPKDVSLWAAVKE TWTKHCDKABFFSSENKVPESINMDTNDMYLMMRKAYKVAFDK YRDQYNWFFLARPTTFALIENLKYFLLKXDPSQFYLGHTIKSG DLBYVGMEGGIVLSVSSMRRINSLINIPRKCPEQGGMIWKISED KQLAVCLKYAGVFAENAEDADGKDVPNTKSVGLSIKBAMTYHPN QVVBGCCSDMAVTPHGLIPROMHVMYGYVRLRAFGPYFQ QVBGCCSDMAVTPHGLIPROMHVMYGYVRLRAFGPYFQ UVGGCSDMAVTPHGLIPROMHVMYGYVRLRAFGPYFQ LVGMSGGGTETFVGCEAAFGGGSKKRDSLGTAGSAHLITKDLGB HSRLLDHRPVIQGETRYFVKEPEKRGLRKHRVLENLKNMIHE TNEHTLPKCRDTMRDSLSQVIJRLQAANDSVCRLQQREQBRKKI HSDHLVASSKQMHLQNDNFMKEQPNKRAEVDEEHRKAMERLKEQ YABMEKDLAKFSTF 6502 213 1650 AGNKPDPWAGRRITAVLPDVSYHREDVGWMRSMLQQSYQAVKE KSSRALEFMKRDLTBFTQVVQHDTACTIAATASVVKKELATEGS GGATEKMKKGLSDFLGVIJSDYFPABPDRTIDCDVITLMGTPSGC- AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLBEK KGELSELLVGSPSIRALYTKNVPAAVSISBFWHRKYFYKVHQLEQ. BQARKDALKQRAEQSISEEPGWEEEEBRLMGISPISPKREKVPU  ANTSTPPERFREPROMOSPORGENIVTSVEPPARBTESESSESISLVT		1		PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYALSLIYG
LKEACPNSSASNASGAAPTIPAHPSTLTHPQRRIDTINSDGYT PEDARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLPLKRONL LIADIELGCANFGSVRGGVYRMRKGIDVAIKVLKQGTEKADTE EMMREAQIMHQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHKF LVGKREETPVSNYABLLHQVSMGMKYLEERNFVHEDLAARNVLL VNRHYAKISDFGLSKALGADDSYYTARSAGKWPLKMYAPECINF RKFSSRSDVWSYGVTMMEALSYGGKPYKKMKGPEVMAFIEQGKR MECPPECPPELYALMSDCWIYKWEDRPDFLTVEQBWRACYYSLA SKVBGPPGSTQKARAACA  6500 1773 726 TGPTHASADAWGLVRSVTEWCANVKGNPCAAALSCPQAVLDAGK MLGESSSFLKGWMLGSIPCALITMLGHIRIGHGNRMHHEHHHL QAPMKEDILKISKDERWELSKSFRVYCILLVKPKDVSLMAAVKE TWTKHCDKRAEFFSSENVKVFESINMDTNDMMLMMRKAYKYAFDK YRDQYNWFFLARFTTFALIBNLKYFLLKNDPSQFFYLGHTIKSG DLBYVGMEGGIVLSVSSMKRLNSLLNIPKCPGGGGMIMKISED KQLAVCLKYAGVFAENAEDJADCKDVENTKSVGLSIKEAMTYPHD QVVEGCCSDMAVTFNGLTFNQMEVMFYGVYRLRAFGPYFQ LVGMSGGGTETFVGCEAAPGGGSKKRDSLGTAGSAHLITKDLGB HSRLLDHRPVIQGBTRYFVKEFEERGLREMRVLENLKNMIHE TNEHTLPKCRDTMRDSLSQVIQRLQAANDSVCRLQQRQDRKKL HSDHLVASEKQHMLQWDDFMKBQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKPSTF  6502 213 1650 AGNKPDPWAGRNRTAVLPDUSVPHREDVGWWRSWLQQSYQAVKE KSSRALEFMKRDLTEFTQVVQHDTACTIAATASVVKKKLATEGS GGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVTTLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK KGELSELLVGSPSIRALTKMVPAAVSHSEMHRYTYTKVRQLEQ AKTSDHALKQRAEQSISEEGBERMGISPJSPKRAKVPV AKTSTPPERFREDGROSPCERNLVYSVEPPABYTPSSSSSISLIVT	1	1	1	KTVYHYLISODKAGKYCIPEGTKFDTLWQLVEYLKLKADGLIYC
DEPARITSPDKPRPMPMDTSVYESPYSDBEELRUKKLFLKROMIL LIADIELGCGNFGSVRQGVYRMRKKQIDVAIKVLKQGTBKADTE BMMREAQIMHQLDNPYIVRLIGVCQABAIMLVMEMAGGGGFLHKF LVGKREETPVSNVABLLHQVSMGMKYLEEKNPVHRDLAARNVLL VNRHYAKISDFGLSKALGADDSYYTARSAGKQLKNYAPBCINF RKFSSRSDVMSYGVTAWBALSYGQKPYKKMKGFBVMAFIEQKK MECPPBCIPBLYALMSDCWIYKMEDRPDFLTVEQBWRACYYSLA SKVBGPPBSTQKARAACA  6500 1773 726 TGPTHASADAWGLVRSVTEWCANVKGNPCAAALSCPQAVLDAGK MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHBHHLL QAPNKEDILKISEDERMELSKSFRVVCIILVKPKDVSLMAAVKE TWTKHCDKARFFSSENVKVFESINMDTNDMWLMMRKAYKYAFDK YRDQYNWFPLARPTTFALIBNLKYFLLKKDPSQPFYLGHTIKSG DLBYVGMEGGIVLSVSMKRLNSLLNIPBKCPEQGGMIWKISED KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN QVVBGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ  6501 1 570 LVGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLITKDLGB HSRLLDHRPVIQGSTRYFVKBFEEKRGLEMRVLENLKNMIH TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQGKKK HSDHLVASSKQHMLQDNFMKBQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKPSTF  6502 213 1650 AGNKEDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALEFMKRGLSDFLGVTSDTFAPSPDKTIDCDVTTLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLBEK KGSLSELLVSSPSTRALTTKMVPAAVSHSKFMHRYTYKVHQLBE KGSLSELLVSSPSTRALTTKMVPAAVSHSKFMHRYTYKVHQLBE KGSLSELLVSSPSTRALTTKMVPAAVSHSKFMHRYTYKVHQLBE KGSLSELLVSSPSTRALTTKMVPAAVSHSKFMHRYTYKVHQLBE KGSLSELLVSSPSTRALTTKMVPAAVSHSKFMHRYTYKVHQLBE KGSLSELLVSSPSTRALTTKMVPAAVSHSKFMHRYTYKVHQLBE KGSLSELLVSSPSTRALTTKMVPAAVSHSKFMHRYTYKVHQLBE KGSLSELLVSSPSTRALTTKMVPAAVSHSKFMHRYTYKVHQLBE KGSLSELLVSSPSTRALTTKMVPAAVSHSKFMRYSKSTRALVPV AKTSPPERGREGROSPCKERNLVTSVEPPAEVTPSSSSSSISLVT	!		1	LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTLNSDGYT
LIADIELGCGNFGSVRQGVYRMRKKQIDVAIKVLKQGTBKADTE  BMMREAQIHHQLDNPYIVLIGVCQABAIMLVMEMAGGGPLHKF  LVGKREEIPVSNVABLLHQVSMGMKYLEERNFVHRDLAARNVLL  VNRHYAKISDFGLSKALGADDSYYTARSAGKWPLKMYAPECINF  RKFSSRSDVWSYGVTMWBALSYGQKPYKKMKGPEVMAFIRQGKR  MCCPPBCPPBIYALMSDCWIYKMEDRPDFLTVRQRWRACYYSLA  SKVBGPPGSTQKABAAS.  TGPTHASADAWGLVRSVTBWCANVKGNPCAAALSCPQAVLDAGK  MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHBEHHLL  QAPNKEDILKISEDERMELSKSPRVYCIILVKPKDVSLAAAVKR  TWTKHCDKABFFSSENVKVFSINMDTNDMWLMMRKAYKYAFDK  YRDQYNWSPLARPTTFAIIBNLKYFLLKKDPSQFPYLGHTIKSG  DLBYYGMEGGIVLSVSSMKRLUSLLNIPKCPBGGGMIWKISED  KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN  QVVEGCSDMAVTFMGLTFNQMHMMMYGYVRLARAFGPYFQ  LVGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIKDLGB  HSRLLDHRPVIQGBTRYFVKEFEBKRGLREMRVLENLKNMIHE  TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKKI  HSDHLVASEKQHMLQWDNPMKEQPNKRAEVDEEHRKAMERLKEQ  YABMEKDLAKFSTF  6502  213  1650  AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE  KSSFALBFMKRDLTBFTQVVQHDTACTIAATASVVKBKLATEGS  SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT-  AEPYDGTKARLYSLQSDPATYCNEPDGPPBLFDAMLSQFCLBEK  KGRISBILVGSPSIRALYTKNYPAAVSHSEFWHRYFYKVHQLEQ  ARYSTPWGRRDSLKQRAEQSISBEPGWEEKEBRLMGISPISPKRAKVPV  ANYSTPPWGRRDSPOSPCREMLVTSVEPPARSVTPSESSESISLVT				PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLFLKRDNL
EMMREAQIMHQLDNPYIVRLIGVCQARAIMILVMEMAGGGPILHKF LVGKRERIFVSNVARLHIQVSMGMKYLEEKNFVHRDLAARNVIL VNRHYAKISDPGLSKALGADDSYYTARSAGKWPLKMYAPECINF RKFSSRSDVWSYGYTMWRALSYGCKPYKKMKGFEVMAFIEQGKR RKFSSRSDVWSYGYTMWRALSYGCKPYKKMKGFEVMAFIEQGKR MECPPECPPELYALMSDCWIYKWEDRPDFLTVEQRWRACYYSLA SKVBSPPGSTQKARAACA  6500 1773 726 TGPTHASADAWGLVRSVTEWCANVRGNPCAAALSCPQAVLDAGK MLSESSFILKGVMLGSIFCALITWLGHIRIGHGMRMHHEHHHL QAPNKEDILKISEDERMELSKSPRVYCIILVKPKDVSLWAAVKE TWTKHCDKARFFSSENVKVYESINMDTNDMMLMMKKAXKYAFDK YRDQYNWFFLARPTTFALIENLKYFLLKKDPSQPFYLGHTIKSG DLEYVGMEGGIVLSVSSMKRLUSLINIPKKCPEQGGHIMKISED KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN QVVEGCCSDMAVTFNGLTPNQMHVMMYGYVRLRAFGPYFQ VVEGCCSDMAVTFNGLTPNQMHVMMYGYVRLRAFGPYFQ UGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGB HSGLLVASSKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKFSTF AGNKEDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSPALBFMKRDLTBFTQVVQHDTACTIAATASVVKEKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT- AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAMLSQFCLBEK KGELSELLVGSPSIRALYTKNVPAAVSHSEKPWHRYFYKUHQLEQ GQRRDALKQRAPQSISBEPGWEEEEBRLMGISPISPKRAKUPV ANTSTPPGGRRGDOSPCRENLVTSVEPPARSVTPSESSESISLVT	1		1	LIADIELGCGNFGSVRQGVYRMRKKQIDVAIKVLKQGTBKADTE
LVGKRBE I PVSNVAELLHQVSMGMKYLEEKNEVHRDLAARNVLL VNRHYAKI SDFGLSKALGADDSYYTARSAGKQLKWYAPBCINF RKFSSRSDVMSYGVTMWBALSYGQKPYKKMKGFBVMAFIRQGKR MECPBECPBELYALMSDCWI YKWEDRPDFLIVEQRMRACYYSLA SKVBGPPGSTQKABAACA  6500 1773 726 TGPTHASADAWGLVRSVTEWCANVRGWPCAAALSCPQAVLDAGK MLSBSSFLKGVMLGSIFCALITMLGHIRIGHCRNRHHEHHHL QAPNKEDILKISEDBSMELSKSFRVYCTILVKPKDVSLWAAVKE TWTKHCDKABFFSSENVKVFRS INMOTINDMMLMMRKAYKYAFDK YRDQYNWFFLARPTTFALIBNLKYFLLKKDPSQFFYLGHTIKSG DLBYVGMEGGIVLSVSMKRLINSLLN I PRKCPRGGGMIWKISED KQLAVCLKYAGUFARBADDAGGKUVFNTKSVGLSI KRAMTHPN QVVEGCSGMAVTFNGLTPNQMHVMYGVYRLRAFGPYFQ VVEGCSGMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFD LVGMSGGGTEFPVGCBAPGGGSKKRDSLGTAGSAHLIIKDLGB HSRLLDHRPVIQGBTRYFVKEFEKRGLREMRVLENLKNMIHE TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQBRKKI HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ YABMEKDLAKPSTF 6502 213 1650 AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSRALBFMKRDLTEFTQUVQMDTACTIAATASVVKBKLATEGS GGATEKMKKGLSDFLGVISDTPAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNBPDGPPELFDAWLSQFCLBEK KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ EQARRDALKQRAEQSISEEPGWEEEEBLMGISPISPKRAKVPV AKISTTPEGRPGPDOSPCRENLYTSVEPPARVTPSSSSSESISLIV	j .			RMMREAOIMHOLDNPYIVRLIGVCQABALMLVMEMAGGGPLHKF
VNRHYAKISDFGLSKAIGADDSYYTARSAGKQLKWYAPBCINF RKFSSRSDVWGYGVIMWEALSYGCKPYKKNKGPEVMAPIEQGKR MECPPECPPELYALMSDCWIYKWEDRPDFLIVRQRMRACYYSLA SKVEGPPGSTQKABAACA  1773  726  TGPTHASADAWGLVRSVTEWCANVRGNPCAAALSCPQAVLDAGK MLSESSSPLKGVMLGSIFCALITMLGHIRIGHRMHHHHHHHHL QAPAKEDILKISEDEMELSKSFRYYCIILVKPKDVSLWAAVKE TWTKHCDKABFFSSENVKVPESINMDTNDMHLMMRKAYKYAFDK YRDQXNWFYLARPTTFAIIENLKYFLLKKDPSQPFYLGHTIKSG DLBYVGMEGGIVLSV3SMKRLNSLLNIPRKCPEQGGMIWKISED KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ LVGMSGGGTETPVGCEAAFGGGSKKRDSLGTAGSAHLIIKDLGBE HSRLLDHRPVTQGBTRYFVKBFEEKRGLREMRVLENLKNMIHE TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQBRKKI HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKFSTF  6502  213  1650  AGNKPDDWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALBFMKRDLTEFTQVVQHDTACTIAATASVVKBKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGSPBLFDAWLSQFCLBEK KGEISBLLVGSPSIRALTTKMVPAAVSHSBFWHRYFYKVHQLEGK EQARRDALKQRAEQSISEEPGWEEEEBLMGISPISPKBAKUPV AKISTPPEGRPGDDSPCERNLVTSVEPPAEVTPSESSESISLVT				LVGKRBEIPVSNVABLLHQVSMGMKYLEEKNFVHRDLAARNVLL
RKFSSRSDVWSYGVTMWBALSYGQKPYKRMKGPBVMAPIRQGKR MECPPBCPPBLYALMSDCWIYKWEDRPDFLTVRQRMRACYYSLA SKVBGPPGSTQKABACA  1773 726 TGPTHASADAWGLVRSVTEWCANVRGNPCAAALSCPQAVLDAGK MLSBSSSFIKKGVMLGSIPCALITMLGHIRIGHGNRHHHHRHHHL QAPNKEDILKISEDERMELSKSPRVYCIILVKPKDVSLWAAVKB TWTKHCDKABFFSSENVKVFESINMDTNDWHLMMRKAYKYAFDK YRDQYNWFFLARPTTFAIIBNLKYFLLKKDPSQFFYLGHTIKSG DLBYVGMEGGIVLSVSSMKRLNSLLNIPBKCPBGGGMIWKISED KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN OVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ  6501 1 570 LVGMSGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGB HHSRLLDHRPVIQGSTRYFVKEFEEKRGLRMRVLBNLKNMIHB TNEHTLPKCRDTMRDSLSQVIQRLQAANDSVCRLQQREQBRKKI HSDHLVASEKQHNLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKPSTF AGNKPDFWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSRALBFMKRDLTEFTQVVQHDTACTIAATASVVKBKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNRPDGPPBLFDAWLSQFCLBEK KGSLSBLLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLBEK EQARRDALKQRAEQSISEEFGWEEEBBLMGTSPISPKRAKVPV AKISTPPERSPGDDSPCERNLVTSVEPPAEVTPSESSESISLVT				VNRHYAKISDEGLSKALGADDSYYTARSAGKMELKNYAPECINE
MECPPECPPELYALMSDCWIYKWEDRPDFLTVRQRMRACYYSLA SKVBGPPGSTQKABAACA  TGPTHASADAWGLVRSVTEWCANVRGNPCAAALSCPQAVLDAGK MLSESSPILKGVMLGSIPCALITMLGHIRIGHGNRMHHBHHHL QAPAKEDILKISEDERMELSKSPRVYCIILVKPKDVSLWAAVKE TWTKHCDKABFFSSENVKVPESINMDTNDMWLMMRKAYKYAFDK YRDQYNWFPLARPTTFALIENLKYFLLKKDPSQPFYLGHTIKSG DLBYYGMEGGIVLSVSMKRLNSLLNIPBKCPEQGGMIWKISED KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN OVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ LVGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGE HHSRLLDHRPVIQGETRYFVKEFEEKRGLREMRVLENLKNMIHE TNEHTLPKCRDTMRDSLSQVIQRLQAANDSVCRLQQREQERKKI HSDHLVASEKQHMLQNDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKPSTF AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSRALBFMKRDLTEFTQVVQHDTACTIAATASVVKBKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPBLFDAWLSQFCLBEK KGELSELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEGL EQARRDALKQRAEQSISEEFGWEEEEBLMGISPISPKRAKVPV AKISTPPERSPGDDSPCERNLVTSVEPPAEVTPSESSESISLVT	1			RKFSSRSDVWSYGVTMWEALSYGQKPYKKMKGPEVMAFIRQGKR
SKVEGPPGSTQKAEAACA  1773  726  TGPTHASADAMGLVRSVTEWCANVRGNPCAAALSCPQAVLDAGK MLSESSPLKGVMLGSIFCALITMLGHIRIGHGNRMHHERHHL QAPNKEDILKISEDERMELSKSPRVYCIILVKPKDVSLMAAVKR TWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKYAFDK YRDQYNWFPLARPTTFALIENLKYFLLKKDPSQPFYLGHTIKSG DLEYVCMEGGIVLSV3SMKRLNSLLNIPRKCPEQGGMIWKISED KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ LVGMGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGE IHSRLLDHRPVIQGETRYFVKEFEEKRGLREMRVLENLKNMIHE TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKKI HSDHLVASEKOMALQNDMFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKPSTP SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSGFCLBEK KGSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKBKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSGFCLBEK KGEISELLVGSFSIRALTTKMVPAAVSHSEFWHRYFYKVHQLEEK EQARRDALKQRAEQSISEEFGWEEEEBRLMGISPISPKRAKUPV AKISTPPERPRGGDDSPCERNLVTSVEPPAEVTPSESSESISLVT	l .			MECPPECPPELYALMSDCWIYKWEDRPDFLTVEQRMRACYYSLA
TGPTHASADAWGLVRSVTEWCANVRGNPCAAALSCPQAVLDAGK MLSESSSPLKGVMLGSIPCALITMLGHIRIGHGRMHHHHHHHHHL QAPNKEDILKISEDERMELSKSPRVYCIILVKPKDVSLWAAVKE TWIKHCDKABFFSSENVKVFBSIMMJYNDMHLMMRKAYKYAFDK YRDQYNWFFLARPTTFALIBNLKYFLLKKDPSQPFYLGHTIKSG DLBYVGMEGGIVLSV3SMKRLNSLLNIPRKCPEQGGMIWKISED KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ LVGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIKDLGE HSRLLDHRPVIQGBTRYFVKBFEEKRGLREMRVLENLKNMIHE TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQBRKKI HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ YABMEKDLAKFSTF AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALBFMKRDLTEFTQVVQHDTACTIAATASVVKBKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPBLFDAWLSQFCLBEK KGEISBLLVGSPSIRALTTKMVPAAVSHSBFWHRYFYKVHQLEQ EQARRDALKQRAEQSISBEPGWEEEBBLMGISPISPKBAKUPV AKISTPPEGRPGDDSPCERNLVTSVEPPAEVTPSESSESISLVT	1	1		SKVRGPPGSTOKARAACA
MLSESSPIKGVMLGSIPCALITMIGHIRIGHERRMHHERHHIL QAPAKEDILKISEDEMELSKSPRYYCIILVKPKDVSLWAAVKE TWIKHCKARFFSSENVKYPESINMOTNDMMLMMRKAYKYAFDK YRDQVNWFYLARPTIFAIIENLKYFLIKKDPSQPFYLGHTIKSG DLBYVGMEGGIVLSV3SMKRLNSLLNIPBKCPBQGGMIWKISED KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ LVGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGB HSRLLDHRPVIQGBTRYFVKBFEEKRGLREMRVLENLKNMIHE TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQBRKKI HSDHLVASEKQHMLQWDNFMKBQPNKRAEVDEEHRKAMERLKEQ YAEMBKDDLAKFSTF 6502 213 1650 AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALBFMKRDLITBFTQVVQHDTACTIAATASVVKBKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPBLFDAWLSQFCLBEK KGEISBLLVGSPSIRALTTKMVPAAVSHSBFWHRYFYKVHQLED EQARRDALKQRAEQSISBEPGWEEEEBLMGISPISPKBAKUPV AKISTPPERPRGGDOSPCERNLVTSVEPPABEVTPSESSESISLVT	6500	1773	726	TGPTHASADAWGLVRSVTBWCANVRGNPCAAALSCPQAVLDAGK
QAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSLMAAVKE TWTKHCDKAEFFSSENVKVFSIAMDTNIMMLMMRKAYKYAFDK YRDQYNM*FLARPTTFAIIBNLKYFLLKKDPSQFFYLGHTIKSG DLEYVGMEGGIVLSV3SMKRLNSLLNIPBKCPEQGGMIMKISED KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ  LVGMSGGGTETFVGCEAAFGGGSKKRDSLGTAGSAHLIKDLGE HSRLLDHRPVIQGBTRYFVKEFEEKKGLREMRVLENLKNMIHE TNEHTILPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKKL HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKFSTF  AGNKEDDWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSPBATYCNEPDGPPBLFDAWLSQFCLBEK KGEISBLLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ EQARRDALKQRAEQSISEEFGWEEEEBLMGTSPISPKRAKVPV AKISTPPERSPGDSPCERNLVTSVEPPAEVTPSESSESISLVT	6500	1	720	MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHL
TWTKHCDKAEFFSSENVKVFESINMDTNDMMLMMRKAYKYAFDK YRDQYNW#FLARPTTFAIIENLKYFILIKKDPSQPFYLGHTIKSG DLEYVGMEGGIVLSV3SMKRLNSLLNIPBKCPEQGGMIWKISED KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN OVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ  LVGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGE HHSRLLDHRPVIQGBTRYFVKEFEEKRGLRMRVLENLKNMIHE TNEHTLPKCRDTMRDSLSQVIQRLQAANDSVCRLQQREQERKKI HSDHLVASEKQHMLQMDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKPSTF AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSRALBFMKRDLTEFTQVVQHDTACTIAATASVVKBKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPBLFDAWLSQFCLBEK KGEISBLLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ EQARRDALKQRAEQSISEEFGWEEEBBLMGISPISPKRAKVPV AKISTPPERSPGDOSPCERNLVTSVEPPAEVTPSESSESISLVT	1	[		OAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSLWAAVKK
YRDQYNWFFLARPTTFALIENLKYFLLKKDPSQPFYLGHTIKSG DLEYYCMEGGIVISVSSMKRLNSLLNIPRKCPEQGGMIWKISED KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ LVGMGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGE IHSRLLDHRPVIQGETRYFVKEFEEKRGLREMRVLENLKNMIHE TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKKI HSDHLVASEKOMMLQNDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKPSTP 6502 213 1650 AGNKPDFWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSRALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSGFCLBEK KGEISELLVGSFSIRALTTKMVPAAVSHSEFWHRYFYKVHQLEG EQARRDALKQRAEQSISEEFGWEEEEBRLMGISPISPKRAKVPV AKISTPPERSPGDDSPCERNLVTSVEPPAEVTPSESSESISLVT	i			TWIKHCDKARFFSSENVKVFESINMDTNDMWLMMRKAYKYAFDK
DLEYVGMEGGIVLSV3SMKRLNSILNIPRKCPEQGGMIMKISED KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ LVGMCGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGE IHSRLDHRPVIQGBTRYFVKBFEEKRGLREMRVLENLKNMIHE TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKKI HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKFSTFP AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALBFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPBLFDAWLSQFCLBEK KGEISBLLVGSPSIRALTTKMVPAAVSHSEFWHRYFYKVHQLED EQARRDALKQRAEQSISBEPGWEEEKBLMGISPISPKBAKUPV AKISTPPEGRPGGPOSPCERNLVTSVEPPAEVTPSESSESISLVT	l	1		YRDOYNWFFLARPTTFALIENLKYFLLKKDPSQPFYLGHTIKSG
KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN QVVEGCCSDMAVTFNGLTPNQMHVMYGVYNLRAFGFYFQ  LVGMGGGTETFVGCERAFGGGSKRDSLGTAGSAHLIKDLGE IHSRLLDHRPVIQGETRYFVKEFEEKRGLREMRVLENLKNMIHE TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKKI HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKFSTF  6502 213 1650 AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALEFMKRDLTBFTQVVQHDTACTIAATASVVKEKLATEGS SGATEKMKKGLSDFLGVISDTFABSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSPBATYCNEPDGPPELFDAWLSQFCLBEK KGEISBLLVGSPSIRALYTKMVPPAVSHSEFWHRYFYKVHQLEQ EQARRDALKQRAEQSISEFGWEEEBELMGISPISPKRAKVPV AKISTPPGRPGGPOSPCERNLVTSVEPPAEVTPSESSESISLVT	i			DURYUGMEGGIVLSV3SMKRLNSLLNIPEKCPEQGGMIWKISED
QVVEGCCSDMAVTFNGLTFNQMHVMMYGVYRLRAFGFYFQ  6501 1 570 LVGMSGGGTETFVGCEAAFGGGSKRGSLGTAGSAHLIKDLGE	1	1		KOLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN
1 570 LVGMSGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGE IHSRLLDHRPVIQGBTRYFVKEFEKKGLRMRVLERLKNMIHK TNEHTILPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKK HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKPSTP  6502 213 1650 AGNKEDDWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS 9GATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSPEATYCREPDGPPELFDAWLSQFCLBEK KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLBEG EQARRDALKQRAEQSISEEFGWEEEEBLMGTSPISPKRAKVPV AKISTPPERSPGDSPCERNLVTSVEPPAEVTPSESSESISLVT	1			OVVRGCCSDMAVTFNGLTPNOMHVMMYGVYRLRAFGPYFQ
IHSRLIDHRPVIQGSTRYFVKEFEEKRGLRMRVLENILKNMIHE TNEHTIJPKCRDTMRDSISQVIQRIQANDSVCRLQQREQERKKI HSDHLVASEKQHMLQMDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKPSTF  6502 213 1650 AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSRALBFMKRDLTEFTQVVQHDTACTIAATASVVKBKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPBLFDAWLSQFCLBEK KGELSBLLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEG EQARRDALKQRAEQSISBEFGWEEEBBLMGISPISPKRAKUPV AKISTPPERSPGDSPCERNLVTSVEPPAEVTPSESSESISLVT	C 5703	<del> </del>	E70	LUCMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLTIKDLGE
TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKKI HSDHLVASEKOMIQMDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKPSTP 6502 213 1650 AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSRALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPBLFDAWLSQFCLBEK KGELSBLLVGSPSIRALTTKMVPAAVSHSEFWHRYFYKVHQLEV EQARRDALKQRAEQSISBEPGWEEEEBLMGISPISPKBAKVPV AKISTPPERGPGDSPCERNLVTSVEPPAEVTPSESSESISLVT	9201	1	1 3,0	THERT TO THE DATE OF THE
HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKFSTF  6502 213 1650 AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALBFMKRDLTEFTQVVQHDTACTIAATASVVKBKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPKLFDAWLSQFCLKEK KGELSELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ- EQARRDALKQRAEQSISEFGWEEKEBELMGISPISPKRAKVPV AKISTPPKRPGGPOSPCERNLVTSVEPPAEVTPSESSESISLVT	ſ			THEFTI DECENTARDSI SOVI ORI OBANDSVCRLOOREOKRKKI
YAEMEKDLAKPSTF  6502 213 1650 AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALBFMKRDLTEFTQVVQHDTACTIAATASVVKBKLATEGS GGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK KGELSELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ EQARRDALKQRAEQSISEEFGWEEKEBELMGISPISPKRAKVPV AKISTPPEGRPGPOSPCERNLVTSVEPPAEVTPSESSESISLVT		1		HEDET VA SEKOFINI ONDNEMKROPNKRAKVDEEHRKAMERLKEO
6502 213 1650 AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALBFMKRDLTBFTQVVQHDTACTIAATASVVKBKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSG- AEPYDGTKARLYSLQSDPATYCNRPDGPPBLFDAWLSQFCLBEC KGELSBLLVGSPSIRALYTKMVPPAVSHSBFWHRYFYKVHQLEQ- EQARRDALKQRAEQSISBEFGWEEEBBLMGISPISPKRAKVPV AKISTPPEGRAGOSPCERNLVTSVEPPAEVTPSESSESISLVT	1		1	
KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS  9GATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT  AEPYDGTKARLYSLQSPRATYCMEPDGPPELFDAWLSQFCLEEK  KGELSBLLVGSPSIRALYTKMVPPAVSHSEFWHRYFYKVHQLEQ  EQARRDALKQRAEQSISEEFGWEEEEBLMGISPISPKRAKVPV  AKISTPPERSPGPOSPCERNLVTSVEPPAEVTPSESSESISLVT			I	THEFTE ADMINISTRATE DOUGH PURCHED CHIMDENT ON
SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCINEPDGPPBLFDAWLSQFCLBEK KGELSBLLVGSPSITAALYTKMVPPAVSHSBFWHRYFYKVHQLBEG EQARRDALKQRAEQSISBEFGWEEEBBLMGISPISPKRAKVPV AKISTPPERSPGDSPCERNLVTSVEPPAEVTPSESSESISLVT	6502	213	1650	MONAT DEMAND THE PROPERTY OF T
AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK KGELSELLVGSPSIRALYTKMVPAAVSHSEYMHRYFYKVHQLEK EQARRDALKQRAEQSISEEPGWEEEEBLMGISPISPKEAKUPV AKISTPPEGROGPOSPCERNLVTSVEPPAEVTPSESSESISLVT		,		KSSKALKFMKRULTSFTQVVQHUTACTIAATADVVAGRIFITEGO
KGELSELLVGSPSIRALYTKNVPAAVSHSEFWHRYFYKVHQLEQ  EQARRDALKQRAEQSISEEPGWEEEEBLMGISPISPKEAKVPV  AKISTFPEGRPGPOSPCRENLVTSVEPPAEVTPSESSESISLVT	1	1	1	SGATEKMKKOLSDELOVISUTFAPSPURITUCDVITIOGIPSG:
EQARRIBALKQRAEQSISEEPGWEEEEBBLMGISPISPKBAKVPV  AKISTPPEGRPGPOSPCRENLVTSVEPPABVTPSESSESISLVT				AEPYDGTKARLYSLQSDPATYCNKPLGYPBUFDAWDSQFCDBER
AKISTPPEGRPGPOSPCRENLVTSVEPPAEVTPSESSESISLVT	1		1	KGRISELLVGSPSIRALYTKMVPAAVSHSEFWHRIFIKVHQLEQ.
AKISTPPEGEPGPQSPCRENLVTSVEPPABVTPSESSESISLVI QIANPATAPEARVLPKDLSQKLLRASLEBQGLAVDVGETGPSPP	1			EQARRDALKQRAEQSISEEPGWEEKEKEKEMG-15P15PKBAKVPV
QIANPATAPEARVLPKDLSQKLLKASLBEQGLAVDVGEIGFSFF	1		1 .	AKISTPPEGEPGPQSPCKENLVTSVKPPAKVTPSESSESISDVI
· · · · · · · · · · · · · · · · · · ·	1		1	QIANPATAPEARVLPKDLSQKLLKASLKEQGLAVDVGEIGPSPP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ľ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotice insertion)
1		i	IHSKPLTPAGHTGGPEPRPPARVETLREKAPTDLRVFELNSDSG
			KSTPSNNGKKGSSTDISEDWEKDFDLDMTEEEVQMALSKVDASG
			EVSGPGGSEGSEPNGPGCESSPQPAQLSPQEGPCSCLR
6503	213	1650	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE
İ	ļ		KSSEALEFMKRDLTEPTQVVQHDTACTIAATASVVKEKLATEGS
l	1	İ	SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
		1	AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK
į		l	KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ
1			BQARRDALKQRAEQSISBEPGWEBEERKINGISPISPKRAKVPV
i	j	į	AKISTFPEGEPGPQSPCRRNLVTSVEPPAEVTPSESSESISLVT
l		l	QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP
1	!	}	IHSKPLTPAGHTGGPBPRPPARVETLREEAPTDLRVFELNSDSG
		1	KSTPSNNGKKGSSTDISEDWEKDFDLDMTBEEVQMALSKVDASG
L			BVSGPGGSBGSEPNGPGCESSPQPAQLSPQBGPCSCLR
6504	2131	1294	GKVC_VAHWVCLSILSPPPAGMKTPNAQEARGQQTRAAAGRATG
1	I	ľ	SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKEGDEPITQ
i			WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
]	İ		DRVASSHISDANLANTIIGKAVRHMFEGRHGSKDRWRGMVLAQA
1		İ	PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
			REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYPIKF
			DDDFHIYVYDLVKKS
6505	2131	1294	GKVCLVAHWVCL91L9PPPAGMKTPNAQBABGQQTRAAAGRATG
ì		1	SANNTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKPGDEPITQ
		•	WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
ŀ		,	DRVASSHISDANLANTIIGKAVEHNFEGEHGSKDEWRGMVLAQA
l	ł	}	PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
[	i		REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF DDDFHIYVYDLVKKS
6506	1	1350	EVSPPTSCCLTVAVADPGVSEGFRGFGAGCEMPGRGRCPDCGST
0300	1 *	1350	ELVEDSHYSQSQLVCSDCGCVVTEGVLTTTFSDEGNLRKVTYSR
	Ì	٠	STGENEQVSRSQQRGLRRVRDLCRVLQLPPTFEDTAVAYYQQAY
			RHSGIRAARLQKKEVLVGCCVLITCRQHNWPLTMGAICTLLYAD
			LDVPSSTYMQIVKLLGLDVPSLCLARLVKTYCSSFKLFQASPSV
			PAKYVEDKEKMISRTMQIVELANETWIVTGRHPLPVITAATPLA
1	]		WQSLQPADRLSCSLARFCKLANVDLPYPASSRLOBLLAVLLRMA
l	· .		EQLAWLRVLRLDKRSVVKHIGDLLOHROSLVRSAFRDGIAKVET
1			REKEPPOWGQQGEGEVGNINSLGLPQGKRPASPALILLPPCMLKS
1	ļ		PKRICPVPPVSTVTGDENISDSBIEQYLRTPQEVRDFORAQAAR
			OAATSVPNPP
6507	1878	929	RSHASRLPELPSGCLVLQVQELVONSGMEATVTIPIWONKPHGA
1			ARSVVRRIGINLPLKPCARASFETLPNISD_CLRDVPPVPTLAD
}			IAWIAADEEETYARVRSDTRPLRHTWKPSPLIVMORNASVPNLR
		1	GSEERLLALKKPALPALSRTTELODELSHLRSOLAKIVAADAAS
			ASLTPDFLSPGSSNVSSPLPCFGSSFHSTTSFVISDITEETEVE
			VPELPSVPLLCSASPECCKPEHKAACSSSEEDDCVSLSKASSFA
			DMMGILKDFHRMKQSQDLNRSLLKBEDPAVLISEVLRRKFALKE
ļ '			BDISRKGN
6508	862	342	WEARKRPORWPSERREVRVPPPHLORGRSGLEPGTFRKMAAARP
	. , , ,		SLGRVLPGSSVLPLCDMOEKFRHNIAYPPQIVSVAARMLKNTTL
			DLLDRGLQVHVVVDACSSRSQVDRLVALARMRQSGAFLSTSEGL
			ILQLVGDAVHPQFKEIQKLIKEPAPDSGLIGLFQGQNSLLH
6509	2	1053	FVNNPRGGRKRRQAAVTQAATRASGTPSPRDGTMTQGKLSVAN
	~	2000	KAPGTEGQQQVHGRKKRAPAVPSAPPSYERATSGEGMKAGAFPP
	1		APTAVPLHPSWAYVDPSSSSSYDNGFPTGDHELFTTFSWDDQKV
	i		RRVFVRKVYTILLIOLLYTLAVVALFTFCDPVKDYVQANPGWYW
			ASYAVFFATYLTLACCSGPRRHFPWNLILLTVFTLSMAYLTCML
ليسسما			19 TITLE COGERUIS AND THE ALTERNATION OF

	A. 2000		·	•
			.4	
	· · · · · · · · · · · · · · · · · · ·	1 Bar 30 and 1 and		<u>,</u>
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide	i
ID	beginning	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=	l .
NO:	nucleotide		Glutamic Acid, F=Phenylalanine, G=Glycine,	1
	location	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,	
	corresponding		L=Leucine, M=Methionine, N=Asparagine,	
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,	1
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,	}
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop	
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,	1
	sequence		\-possible nucleotide insertion)	
			SSYYNTTSVLLCLGITALVCLSVTVFSFQTKFDFTSCQGVLFVL	1
			LMTLFFSGLILAILLPFQYVPWLHAVYAALGAGVFTLPLALDTQ	1
		į	LLMGNRRHSLSPEBY I FGALNIYLDI IYI FTFFIQLFGTNRB	1
6510	37	1156	PCALDGCPQRGAVHPLLSSAMGLLAFLKTQFVLHLLVGFVFVVS	1
			GLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLVMLLEWW	}
	1		SCTECTLFTDQATVERFGKEHAVIILNHNFRIDFLCGWTMCERF	1
	ľ		GVLGSSKVLAKKBLLYVPLIGWTWYFLETVFCKRKWEEDRDTVV	ļ
			EGLRRLSDYPEYMWPLLYCEGTRFTETKHRVSMEVAAAKGLPVL	}
			KYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGIL	l.
	}		YGKKYEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIY	
			NOKEMFPGEOFKPARRPWTLLNFLSWATILLSPLFSFVLGVFAS	1
				l
CE-1-	3545	170=	GSPLLILTFIGFVGAGNGHCR	-
6511	2541	1425	GEEQPLAAAPTECLEQVIGGAGDPGTWASFPSPLPGPAPLKGGK	
	i	1	TMATNFSDIVKQGYVKMKSRKLGIYRRCMLVFRKSSSKGPQRLB	
		ļ	KYPDEKSVCLRGCPKVTEISNVKCVTRLPKETKRQAVAIIFTDD	Į.
		į.	SARTFTCDSELEABEWYKTLSVECLGSRLNDISLGEPDLLAPGV	I
			QCEQTORFNVFLLPCPMLDVYGECKLQITHENIYLWDIHNPRVK	1
	f		LVSWPLCSLRRYGRDATRFTFRAGRMCDAGEGLYTFQTQEGEQI	ļ
		]	YQRVHSATLAIABQEKRVLLEMBKNVRLLNKGTEHYSYPCTPTT	Ī
		1	MLPRSAYWHHITGSQNIABASSYAGEGYGAAQASSETDLLNRFI	ļ
			LLKPKPSQGDSSEAKTPSQ	]
6512	159	807	FGKKSTWPPLSRSLRVASGRSCKLGHGGYTGSGPGFGBPRDSGA	1
•	ļ		EVPSGSGRATGCERGGVRGARQGRAPGSSIWRKEPRMVCTRKTK	1
	}		TLVSTCVILSGMTNIICLLYVGWVTNYIASVYVRGQEPAPDKKL	ì
	ł	ļ	EBDKGDTLKIIERLDHLENVIKQHIQEAPAKPEEAEAEPFTDSS	
		l	LPAHWGQELSPEGRRVALKQFQYYGYNAYLSDRLPLDRP	
6513	2	756	FVSPEPGFSLAQLNLIWQLTDTKQLVHSPAEGQDQGSAYANRTA	} .
			LFPDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQV	1
			AAPYSKPSMTLE?NKDLRPGDTVTITCSSYQGYPEAEVFWQDGQ	
			GVPLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPV	·
			LQQDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSF	
		İ	SPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALF	]
	1		PDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAA	·
			PYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEARVFWQDGQGV	
	1	i	PLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQ	İ
			QDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSP	
	i		EPGFSLAQLNLIWQLTDTRQLVHSFTEGR	
6514	985	302	VGIPGPTISSAAEMEDIJDLDERLRYSLATSRAKMGRRAQQESA	†
	]		OAKNHLNGKNSSLTLTGRTSSAKLPRCROGGWAGDSVKASKFRR	
		i	KASERIEDFRLRPOSLNGSDYGGDIPIIPDLEEVOEEDFVLOVA	
	1	1	APPSIQIKRVMTYRDLDNDLMKYSAIQTLDGBIDLKLLTKVLAP	1
		·	EHEVRERNPSWQDDVGWDWDHLFTEVSSEVLTEWDPLQTEKEDP	İ
			AGOARHT	
6515	1225	305	GRVGSRRRGAAVPGGCGAGSTQLEVSASASCGALGSADMNPIVV	4
6515	1345	305	· · · <del>_</del>	1
	1	J	VHGGGAGPISKDRKERVHQGNVRAATVGYGILREGGSAVDAVEG	
		1	AVVALEDDPEPNAGCGSVLNTNGEVEMDASIMDGKDLSAGAVSA	
			VQCIANPIKLARLVMEKTPHCPLTDQGAAQFAAAMGVPEIPGEK	
	1	]	LVTERNKKRLEKEKHEKGAQKTDCQKNLGTVGAVALDCKGNVAY	!
		1 -	ATSTGGIVNKMVGRVGDSPCLGAGGYADNDIGAVSTTGHGESIL	
		1	KVNLARLTLFHIBQGKTVBBAADLSLGYMKSRVKGLGGLIVVSK	1
		]	TGDWVAKWTSTSMPWAAAKDGKLHFGIDPDDTTITDLP	
6516	1	1402	FRRLRYLGODATAAARDLRTRGLOGYCPSATARQQVLVSALQQL	1
	_	1	KGRRSEHRNENOEMPYSTNKELILGIMVGTAGISLLLLWYHKVR	
		1	KPGIAMKLPBFLSLGNTFNSITLQDEIHDDQGTTVIFQBRQLQI	
	1	1	LEKLNELLINMERLKEEIRFLKEAIPKLEEYIODELGGKITVHK	
		1	ISPOHRARKERLPTIOSSATSNSSEEAESEGGYITANTDTKEQS	

27.7			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
I	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			FPVPKAFNTRVEELNLDVLLQKVDHLRMSESGKSESFELLRDHK
i			EKPRDEIEFMWRFARAYGDMYELSTNTQEKKHYANIGKTLSERA
1			INRAPMMGHCHLWYAVI.CGYVSEFEGLQNKINYGHLFKEHLDIA
İ			IKLLPREPFLYYLKGRYCYTVSKLSWIEKKMAATLFGKIFSSTV
l .	l .		QRALHNFLKAERLCPGYSNPNYMYLAKCYTDLEENQNALKFCNL
Į .	ļ		ALLLPTVTKEDKEAQKEMQKIMTSLKR
6517	3	1414	GRVWGGSSSLNAMVYVRGHAEDYERWQRQGARGWDYAHCLPYFR
	1	}	KAQGHELGASRYRGADGPLRVSRGKTNHPLHCAFLRATQQAGYP
ł	j		LTEDMNGFQOEGFGWMDMTIHEGKRWSAACAYLHPALSRTNLKA
1	į	{	<b>EARTLYSKYLFEGTRAVGVEYVKNGQSHRAYASKEVILSGGAIN</b>
1	1	:	SPQLLMLSGIGNADDLKKLGIPVVCHLPGVGQNLQDHLBIYIQQ
1	I		ACTRPITLHSAQKPLRKVCIGLEWLWKFTGEGATAHLETGGFIR
l	<b>[</b>	l	SQPGVPHPDIQFHFLPSQVIDHGRVPTQQEAYQVHVGPMRGTSV
1	1	1	GWLKLRSANPQDHPVIQPNYLSTETDIEDFRLCVKLTRBIFAQE
i	}	1	ALAPPRGKELQPGSHIQSDKEIDAFVRAKADSAYHPSCTCKMGQ
1	1	I	PSDPTAVVDPQTRVLGVENLRVVDASIMPSMVSGNLNAPTIMIA
ł	4	I	BKAADIIKGQPALWDKDVPVYKPRTLATQR
6518	242	1098	PAWNPGSEPRTRVRPRARSFPLPPPRAPRRRHRLLRAVPGPSR
1			RHRCRRRAPPPPSTMGDAGSERSKAPSLPPRCPCGPWGSSKTMN
1	Ì	Ī	LCSKCFADFQKKQPDDDSAPST9NSQSDLFSEETTSDNNNTSIT
Į.		1	TPTLSPSQQPLPTBLNVTSPSKEECGPCTDTAHVSLITPTKRSC
} .	ł	}	GTDSQSENEASPVKRPRLLENTERSEBTSRSKQKSRRRCFQCQT
Į	1	1	KLELVQQRLGSCRCGYVFCMLHRLPEQHDCTFDHMGRGREEAIM
{		1	KMVKLDRKVGRSCQRIGEGCS
6519	3	1113	BRKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS
j .	<u> </u>	1	AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPQSYGSPAS
1	Ï	`	wsfaplsaapspsssrssfsfsagtavpssasaslsqpgprkll
I			VPPTLLHAQPHHLLLPAAAAAASANAKSRRPKEKREKERRHGL
}	1	}	GGARRAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK
l	į	)	VMNBIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKK
i	į.	}	ENRKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG
			KNLDTKNYDSKIPENSRFPFVSLKEPRVQNNLKRLDTLBFKQLI
<u>L</u> .	l	L	HIEHQPNGGASVIHCLQ
6520	3	1113	ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQL99RDPPGSLS
1	1		AKKVRTEEKKAPRRVNGBGGSGENSRQLQPPAAPSPQSYGSPAS
1	1	1	WSFAPLSAAPSPSSSRSSPSFSAGTAVPSSASASLSQPGPRKLL
		1	VPPTLLHAQPHHLLLPAAAAAASANAKSRRPKBKRRRHGL
1	1	ļ	GGAREAGGASRBENGEVKPLPRDKIKDKIKERDKEKEREKKKHK
1		1	VMNBIKKENGEVKILLKSGKEKPKTNIRDLQIKKVKKKKKKHK
ŀ	1	[	ENEKRERPKMYSKSIQTICSGLLTDVBDQAAKGILWDNIKDYVG
1	1	1	KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI
L	1	L	HIRHQPNGGASVIHCLQ
6521	184	1798	KLPKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP
}			IRRTVNSTRETPPKSKLAEGEBEKPBPDISSEESVSTVEEQENE
ļ	(	1	TPPATSSRABOPKGEPKNEBKEENKSSEBTKKDEKDQSKEKEKK
1		ļ	VKKTIPSWATLSASQLARAQKQTPMASSPRPKMDAILTBAIKAC
l			POKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKREINRGVI
1			KQVKGKGA9GSFVVVQK6RKTPQKSRNRKNRSSAVDPEPQVKLE
			DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA
{	1	1	LORAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS
1	•	1	ALAAMNEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCK
[	l	!	KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE
1	Į.	1	DEDESSEEDSEDEEPPPKRELQKKTPAKSPGKAASVKORGSKPA
	ļ	1	PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS
)	1	1	KKPATSARKE
6522	1042	391	NKWLRPSPRSHRTPESGRVLSLFRLPPPGMALSGSTPAPCWEED
	<u> </u>		<u></u>

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *⇒Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
j	1	ļ	ECLDYYGMLSLHRMFEVVGGQLTECELELLAFLLDEAPGAAGGL
			SRARSGLKLLLELERRGQCDESNLRLLGQLLRVLARHDLLPHLA
1	j		RKRRRPVSPERYSYGTSSSSKRTEGSCRRRRQSSSSANSQQGSP
<u> </u>			PTKRQRRSRGRPSGGARRRRRGPQPHPSSSQSPPDLPLKAK
6523	2	1097	ASCQTRRRTAALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI
1			RSRKLGIFRRCWLVFKKASSKGPRRLBKFPDEKAAYFRNFHKVT
1			ELHNIKNITRLPRETKKHAVAIIPHDETSKTFACESELEAREWC
1		1	KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN
			LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
1	}		WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHBR
Ī	İ		LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGE
			IYSLQGNHENRHSDLTGKSCKTSENRFLEENAPLVMYGITHHLF
L			MDTSTCKVVHDLE
6524	2	1097	ASCQTRRRTAALDSGERLAGRRSPIALAMASNFNDIVKQGYVKI
			RSRKLGIFRRCWLVFKKASSKGPRRLEKFPDEKAAYFRNFHKVT
ł			BLHNIKNITRLPRETKKHAVAIIPHDETSKTFACBSBLEAEEWC
			KHLCMECLGTRLNDISLGBPDLLAAGVQREQNERFNVYLMPTPN
			LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
i			WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER
i			LMLEMBQKARLQTSLTEPMTLSKS1SLPRSAYWHHITRQNSVGB
1			IYSLQCNHENRHSDLTGKSCKTSENRFLBENAPLVMYGITHHLF
			MDTSTCKVVHDLB
6525	1	1859	GESPFSEESIEFNPSSSGRSARTVSSNSFCSDDTGWPSSQSVS
1			PVKTPSDAGNSPIGFCPGSDEGFTRKKCTIGMVGEGS1QSSRYK
			KBSKSGLVKPGSEADFSSSSSTGSISAPEVHMSTAGSKRSSSSR
١.		•	NRGPHGRSNGASSHKPGSSPSSPREKDLLSMLCRNQLSPVNIHP
1			SYAPSSPSSSNSGSYKGSDCSPIMRRSGRYMSCGENHGVRPPNP
			EQYLTPLQQKEVTVRHLKTKLKESERRLHERESEIVELKSQLAR
1 :			MREDWIEEECHRVEAQLALKEARKEIKQLKQVIETMRSSLADKD
		,	KGIQKYEVDINIQNKKLESLLQSMKMAHSGSLRDELCLDFPCDS
ł i	•		PEKSLTINPPLDTMADGLSLEEQVTGEGADRELLVGDSIANSTD
[			LFDBIVTATTTESGDLELVHSTPGANVLELLPIVMGQEEGSVVV
j l			ERAVQTDVVPYSPAISELIQSVLQKLQDPCPSSLASPDESEPDS
	i		MESPPESLSALVVOLTPRNPNSAILLSPVETPYANVDAEVHANR
			IMRELDFAACVEERLDGVIPLARGGVVRQYWSSSFLVDLLAVAA
			PVVPTVLMAFSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR IKT
6526	2	2034	SGRAGEPEEWRGRQIIDSKETWIPFNSEDSOOLERAYSSGKGCN
5525	~	2032	GRVVPTDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD
[			NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREIIILHNP
] ]			KLMVHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDIHCGBP
			LQIDHLVFVVHGIGPACDLRFRSIVQCVNDFRSVSLNILOTHFK
1			KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLORITLPSINRLRH
			FINDTILDVFFYN8PTYCQTIVDTVASEMNRIYTLFLQRNPDFK
( . )			GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD
1 1			TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLOEIGIP
į i			LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN
			TRNGDYLDVGIGOVSVKYPRLIYKPRIFFAFGSPIGMFLTVRGL
, 1		!	
			KRIDPNYRPPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI
j			PHHKGRKRMHLBLREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY
j			PALQASETPRETRABPESTSEKPSDVNTERTSVAVKEEVLPINV
] [		İ	GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV
F 6537 -			LKRIYQTQGIFLDQPLQ
6527	1	922	GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCQRGDLS
1 1	j.		fifngdaapsesfvvloneqkvyqrihheesemeteebvdilms
, ,			SDIYSATLSTKSISFTRAQTGWLFREDKTERVCNFLADFYLVNG

SEQ Predicted predicted end nucleotide location nucleotide location for first amino acid segment containing significant corresponding to first amino acid residue of amino acid sequence sequenc	G=Glycine, sine, ragine, ine, nown, *=Stop
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Serie, residue of sequence Sequ	G=Glycine, sine, ragine, ine, nown, *=Stop
location corresponding to first amino acid residue of amino acid sequence    Codon, /=possible nucleotide del   Codon /=possible nucleotide del   Codon /=po	gine, ragine, ine, nown, *=Stop
corresponding to first amino acid residue of amino acid residue of amino acid sequence Codon, /=possible nucleotide del sequence LVLESRKRREHLSEEDILRNKAIMESLSKOGG SLTPPPONTITWEEYISAENGKAPHLGRELVC MSQBFPLGIELLLAVULBVVAPFKHFMKLREFF DIPVFPTITATVTPQEFRYDBFDGSIFTIPDI LTGPAAAEPRCAADAGMKRALGRRKGVWLRLE LQPEEDVTIGVWHTVPAVWKNAQGKDQMWYE LHGNAGTRGGDHRVELYKVLSSLGYHVVTFDN RGMTYDALHVFDN KHRSCPLLILHARBDPVVE PARSFRDFKVQFVPFHSDLGYRHKYIYKSPEI PEHQH  6529 363 2215 THIRYNKIGVVKTMSCGNEFVETLKKIGYPKF GSVEDESFLKKIGYPKFL RGVEDESFLKKIGYPKF RGVEDESFLKKIGYPKF RGVEDESFLKKIGYPKF RRKCQLMASVTSHKSLRIKHERER ALDBALKICKTSDLKTPRLDDKELEKLEDEVC RRKCQLMSVTSHKSLRIKHERER ALDBALKICKTSDLKTPRLDDKELEKLEDEVC RRKCQLMSVTSHKSLRILNAKEEBATKKLKGS NELQALTDEVTOLMMFFRHSNLGQGTNPLVFI	ragine, ine, nown, *=Stop
to first amino acid residue of amino acid residue of amino acid sequence    Codon, /=possible nucleotide del   Codon, /=possible nucleotide del   Codon, /=possible nucleotide del   Codon, /=possible nucleotide insertion	ine, nown, *=Stop
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, residue of amino acid sequence Codon, /=possible nucleotide del \=possible nucleotide insertion)  LVLESRKREBHLSEBILRNKAIMESLSKOGN SLTPPPQNTITWEBYISAENGKAPHLGRELVC MSQBPPLGIELLLNVLBVVAPFKHFNKLREFV DIFVFPTTTATVTFQEFRYDSFUGSIFTIPDI LTGPAAAEPRCAALGRRKGVWLRLE LQPEEDVTICVWHTVPAVWWXNAQGKDQMWYE LHGNAGTRGODHRVELYKVLSSLGYHVVTFDY RGMTYDALHVFDW KARSGNPVYIGGHSLGT RETPPDALILESPTNIREBAKSHPFSVITY TSSGIKFANDENVKHISCPLLILHAEDDPVVE PARSFROFKVQFVFFHSDLGYRHKYTYKSPEI PEHQH  6529 363 2215 THIRYNKIGVVKTMSCONEFVETLKKIGYPKF BGVEDESFLKWFCGNVNEQNVLESRELEAFSI ALDBALKICKTSDLKTPRLDDKELEKLEDEVC RNKCQLMSVTSHKSLRILNKKEEBATKKLKGS NELQALTDEVTOLMMFFRHSNLGQGTNPLVFF	nown, *=Stop
residue of amino acid sequence Codon, /=possible nucleotide del sequence Codon, /=possible nucleotide del sequence LVLESRKRREHLSEBDILRNKAIMESLSKOGM SLTPPPQNTITWEBYISAENGKAPHLGRELVC MSQEFPLGIELLLNVLEVVAPFKHFNKLREFV DIPVPPTITATVTPQEPRYDSFDGSIFTIPDI IPVPPTITATVTPQEPRYDSFDGSIFTIPDI LTGPAAAEPRCAADAGMKRALGRRKGVWLRIL LGPELVTLGVWHTVPAVWANAQGEDQMWYE LHGNAGTRGGDHRVELYKVLSSLGYHVVTFD RGMTYDALHVFDWIKARSGDNPVYIWGHSLGF RETPPDALILESPFINIRERAKSHPFSVIYRY TSSGIKFANDENVKHISCPLLILHAEDDPVVE PARSFRDFKVQFVPFHSDLGYRHKYIYKSPEI PEHQH  6529 363 2215 THIRYNKIGVVKTMSCGNEFVETLKKIGYPKA EGVEDESFLKWFCGNNEGNVLSERELBAFSI ALDBALKICKTSDLKTPRLDDKELEKLEDEWG RNKCQLMASVISHKSLRINAKEEBATKKLKGS NELQALTDEVTOLMMFFRHSNLGQGTNPLVFI	nown, *=Stop
amino acid sequence Codon, /=possible nucleotide del    -possible nucleotide insertion	
Sequence   Sequence   Sequence   Sequence   SULTERKRERHLSEEDILRNKAIMESLSKOGK	
LVLESRKRREHLSEEDILRNKAIMESLSKOGE SLTPPPQNTITWEEYISAENGKAPHLGRELVC MSQBFPLGIELLLNVLBVVAPFKHFMKLREF DIPVPPTITATVTPQBFRYDBFDGSIFTIPDI 6528 1 1073 LTGPAAABPRCAADAGMKRALGRRKGVWLRLE IPPLIKLCPGIQAKLIFLNFVRVPYPFIDLKKE LQPEEDVTIGVWHTVPAVWKNAQGKDQMWYE LHGNAGTRGGDHRVELYKVLSSLGYHVVTFDX RGMTYDALHVFDWIKARSGDNPVYIWGHSLGT RETPPDALILESPFINIREBAKSHPPSVIYRY TSSGIKFANDENVKHISCPLLILHABDDPVVE PARSFRDFKVQFVPFHSDLGYRHKYIYKSPEI PEHQH 6529 363 2215 THIRYNKIGVVKTMSCGNEFVETLKKIGYPKR EGVEDESFLKWFCGNVNEQNVLSERELBAFSI ALDBALKICKTSDLKTPRLDDKELEKLEDEVC RNKCQLMSVTSHKSLRILNKKEEBATKKLKCS	
SLTPPPQNTITWEBYISAENGKAPHLGRELVC MSQBFPLGIELLLNVLBVVAPFKHFMKLREF\ DIFVFPTTTATVTFQBFRYDSFDGSIFTIPDI 6528  1 1073 LTGPAAAEPRCAADAGKRALGRRKGVWLRLE IPPLIKLCEGIQAKLIFLNFVRVPYFIDLKKE LQPEEDVTIGVWHTVPAVWWKNAQGKDQMWYE LHGNAGTRGODHRVELYKVLSSLGYHVVTFD\ RGMTYDALHVFDWIKARSGDNPVYIWGHSLGT RETPPDALILESPFTNIREBAKSHPPSVIYR\ TSSGIKFANDENVKHISCPLLILHAEDDPVVE PARSFRDFKVQFVFFHSDLGYRHKYIYKSPEI PEHQH 6529 363 2215 THIRYNKTGVVKTMSQGNEFVETLKKIGYPKR EGVEDESFLKWFCGNVNEQNVLSERELBAFSI ALDBALKICKTSDLKTPRLDDKELEKLEDEVC RNKCQLMSVTSHKSLRILNKKEEBATKKLKGS	
MSQBFPLGIELLLNVLBVVAPFKHFNKLREFV DIFVFPTITATVTFQBFRYDSFDGSIFTIPDE 6528  1 1073 LTGPAABEPRCAADAGMRALGERKGVWLERLE LOPELIKLCPGIQAKLIFLNFVRVPYFIDLKKE LOPEEDVTIGVWHTVPAVWWXNAQGEDQMWYE LHGNAGTRGGDHRVBLYKVLSSLGYHVVTFDY RGMTYDALHVFDWIKARSGDNFVYIWGHSLGT RETPFDALILESFFINIRERAKSHPFSVIYRY TSSGIKFANDENVKHISCPLLILHAEDDPVVE PARS FROFKVQFVPFHSDLGYRHKYIYKSPEI PBHQH 6529 363 2215 THIRYNKIGVVKTMSCGNEFVETLKKIGYPKF BGVBDESFLKWFCCNVNBQNVLSBRELBAFSI ALDBALKICKTSDLKTPRLDDKELEKLEDBVQ RNKCQLMSSVTSHKSLRILNAKEEBATKKLKGS	
6528 1 1073 LTGPAAAEPRCAADAGMKRALGRRKGVWLRLE LTGPAAAEPRCAADAGMKRALGRRKGVWLRLE LQPEEDVTIGVWHTVPAVWKKAAQGKDQMYY LHGNAGTRGODHRVELYKVLSSLGYHVVTFD) RGMTYDALHYDW IKARSGDNPVYIWGHSLGT RETPPDALILESPFINIRERAKSHPFSVIYRY TSSGIKFANDENVKHISCPLLILHAEDDPVVE PARSPROFKVQFVPFHSDLGYRHKYIYKSPEI PERIQH  6529 363 2215 THIRYNKIGVVKTMSCGNEFVETLKKIGYPKA EGVBDESFLKWFCGNVNEQNVLSERELBAFSI ALDBALKTCKTSDLKTPRLDDKELBKLEDRVC RNKCQLMASVTSHKSLRLNAKEEBATKKLKQS NELQALTDEVTQLMMFFRHSNLGQGTNPLVFI	
6528 1 1073 LTGPAAAEPRCAADAGMKRALGRRKGVWLRIL IPPLIKLCPGIQAKLIPLNFVRVPYFIDLKKE LQPEEDVTIGVWHTVPAVWWXNAQGKDQMWYE LHGNAGTRGODHRVELYKVLSSLGYHVVTFD RGMTYDALHVPDWIKARSGDNPVYIWGHSLGI RETPPDALILESPFINIREBAKSHPPSVIYR) TSSGIKFANDENVKHISCPLLILHAEDDPVVE PARSPROFKVQFVPFHSDLGYRHKYIYKSPEI PBHQH 6529 363 2215 THIRYNKIGVVKTMSCGNEFVETLKKIGYPKF EGVBESFIKWFCGNVNEQNVLSERELBAFSI ALDBALKICKTSDLKTPRLDDKELEKLEDBVC RNKCQLMSVTSHKSIRLMAKEEBATKKLKCS	
IPPLIKLCPGIQAKLIPLNFVRVPYFIDLKKE LQPEEDVTIGVWHTVPAVWWKNAQGKDQMWYE LHCNAGTRGGDHRVELYKVLSSLGYHVVTFDY RGMTYDALHVFDWIKARSGNDPVYIWGHSLGI RETPPDALILESPFINIREBAKSHPPSVIYRY TSSGIKFANDENVKHISCPLLILHAEDDPVVE PARSFRDFKVQFVPFHSDLGYRHKYIYKSPEL PEHQH  6529 363 2215 THIRYNKIGVVKTMSCGNEFVETLKKIGYPKA EGVBDESFLXWFCGNVNEQNVLSERELBAFSI ALDBALKICKTSDLKTPRLDDKELBKLEDBVC RNKCQLMSVTSHKSLRIMAKEEBATKKLKCS NELQALTDEVTQLMWFFRHSNLGQGTNPLVFI	
LQPEEDVTIGVWHTVPAVWKNAQGKDQMWYE LHGNAGTRGGDHRVELYKVLSSLGYHVVTFD) RGMTYDALHVFDWI KARSGDNPVYIWGHSLGT RETPPDALILESPFINIREBAKSHPPSVIYR) TSSGIKFANDENVKHISCPLLILHAEDDPVVE PARSFRDFKVQFVPPHSDLGYRHKYIYKSPEI PEHQH 6529 363 2215 THIRYNKIGVVKTMSCGNEFVETLKKIGYPKF EGVBDESFLKWFCGNVNEQNVLSERELBAFSI ALDBALKICKTSDLKTPRLDDKELEKLEDEVC RNKCQLMSVTSHKSLRILNAKEEBATKKLKCS	
LHGNAGTRGODHRVELYKVLSSLGYHVVTFDY RGMTYDALHVFDWIKARSGDNPVYIWGHSLGT RETPPDALILES?FTNIREBAKSHPFSVIYRY TSSGIKFANDENVKHISCPLLILHAEDDPVVE PARS FROFKVQFVPFHSDLGYRHKYIYKSPEI PEHQH 6529 363 2215 THIRYNKIGVVKTMSCSNEFVETLKKIGYPKF BGVBDESFLKWFCGNVNEQNVLSERELBAFSI ALDBALKICKTSDLKTPRLDDKELEKLEDEVC RNKCQLMASVISHRSLRILNAKEEBATKKLKGS NELQALTDEVTQLMFFRHSNLGQGTNPLVFI	
RGMTYDALHVFDWIKARSGDNPVYIWGHSLGT RETPPDALILESPFINIREBAKSHPPSVIYRY TSSGIKFANDENVKHISCPLLILHAEDDPVVE PARSFRDFKVQFVPFHSDLGYRHKYIYKSPEI PBHQH 6529 363 2215 THIRYNKIGVVKTMSCGNEFVETLKKIGYPKA BGVBDESFIKWFCGNVNBQNVLSERELBAFSI ALDBALKTCKTSDLKTPRLDDKELBKLEDBVQ RNKCQLMASVISHKSLRLNAKEEBATKKLKQS NELQALTDEVTQLMMFFRHSNLGQGTNPLVFI	
RETPPDALILES?FINIREBAKSHPPSVIYRY TSSGIKFANDENVKHISCPLLILHAEDDPVVE PARS FROFKVQFVPFHSDLGYRHKYIYKSPEI PEHQH 6529 363 2215 THIRYNKIGVVKTMSCGNEFVETLKKIGYPKA BGVBDESFLKWFCGNVNBQNVLSERELBAFSI ALDBALKTCKTSDLKTPRLDDKELBKLEDBVQ RNKCQLMASVTSHKSLRLNAKEEBATKKLKQS NELQALTDEVTQLMMFFRHSNLGQGTNPLVFI	
TSSGIKFANDENVKHISCPLLILHAEDDPVVE PARS PROFKVQFVPFHSDLGYRHKYTYKSPET PERIQH 6529 363 2215 THIRYNKIGVVKTMSCGNEFVETLKKIGYPKA EGVBDESFLKWFCGNVNEQNVLSERELBAFSI ALDBALKTCKTSDLKTPRLDDKELBKLEDBVC RNKCQLMASVTSHKSLRLMAKEEBATKKLKQS NELQALTDEVTQLMMFFRHSNLGQGTNPLVFI	
PARS PROFKVQFVPFHSDLGYRHKYTYKSPEI PBHQH 6529 363 2215 THIRYNKIGVVKTMSCGNEFVETLKKIGYPKF EGVBDESFLKWFCGNVNBQNVLSERELBAFSI ALDBALKICKTSDLKTPRLDDKELBKLEDBVC RNKCQLMSVTSHKSLRLMAKEBBATKKLKCS NELQALTDEVTQLMMFFRHSNLGQGTNPLVFI	
PBHQH  6529 363 2215 THIRYNKIGVVKTMSGGNEFVETLKKIGYPKF  BGVBDESFLKWFCGNVNEQNVLSERELBAFSI ALDBALKICKTSDLKTPRLDDKELEKLEDBVG RNKCQLMASVTSHKSLRLNAKEEBATKKLKGS NELQALTDEVTQLMMFFRHSNLGQGTNPLVFI	
6529 363 2215 THIRYNKIGVVKTMSCGNEFVETLKKIGYPKA  BGVEDESFLKWFCGNVNEQNVLSERELBAFSI ALDBALKICKTSDLKTPRLDDKELEKLEDEVC RNKCQLMASVTSHKSLRLNAKEEBATKKLKQS NELQALTDEVTQLMMFFRHSNLGQGTNPLVFI	
BGVBDESFLKWFCGNVNBQNVLSERRLBAFSI ALDBALKTCKTSDLKTPRLDDKELEKLÆDBVC RNKCQLMASVTSHKSLRLNAKEEBATKKLKQS NELQALTDEVTQLMMFFRHSNLGQGTNPLVFI	DNI-NGEDPDWI.P
ALDRALKTCKTSDLKTPRLIDDKELEKLEDBYC RNKCQLMASVTSHKSLRLNAKEEBATKKLKQS NELQALTDEVTQLMMFFRHSNLGQGTNPLVFI	
RNKCQLMASVTSHKSLRLNAKEEBATKKLKQS NELQALTDEVTQLMMFFRHSNLGQGTNFLVFI	
NELQALTDEVTQLMMFFRHSNLGQGTNPLVFI	
, ,	
EQSTAALTLYTKKOFFOGIHEVVESSNESOFF	
NQEILEERRLEMARLQLAYICAQHQLIHLKAS	-
RSLHSLTSKAVDKENLDAKISSLTSEIMKLEK	
VVRENAQLIAMPVVKGDFDLQIAKODYYTARO	
SFBLLQLSYEIELRKHRDIYRQLENLVQELSQ	SNMMLYKQLEML
TDPSVSQQINPRNTIDTKDYSTHRLYQVLEGE	NKKKELFLTHGN
LEEVAEKLKQNI9LVQDQLAVSAQEHSFFLSK	RNKDVDMLCDTL
YQGGNQLLLSDQELTEQFHKVESOLNKLNHLL	TDILADVKTKRK
TLANNKLHOMBREFYVYFLKDEDYLKDIVENL	ETQSKIKAVSLE
D	
6530 128 2986 GAAHHGAIVQVHPLLPGSSTIMIHDLCLVFPA	PAKAVVYVSDIQ
BLYIRVVDKVBIGKTVKAYVRVLDLHKKPFLA	KYFPFMDLKLRA
ASPIITLVALDEALDNYTITFLIRGVAIGQTS	
INSAPQQIBVFPPFRIMPRKVTLLIGATMQVT	
FSISNESVALVSAAGLVQGLAIGNGTVSGLVQ	
SQDLVQVEVLLLRAVRIRAPIMRMRTGTQMPI	-
SFGNAVPGLTFHWSVTKRDVLDLRGRHHEASI	_
LGRVKGRTGLRAVVKAVDPTSGQLYGLARELS	
LINPKIEAEQIIMSPNSYIKLQTNRDGAASLS	
VHVDBKGPLASGSMIGTSTIEVIAQEPPGANQ	
YLRVSMSPVLHTQNKEALVAVPLGMTVTFTVH	
SSVLNPATNRDDFVQIGKGPTNNTCVVRTVSV	
PGLSDFMPLPVLQAISPELSGAMVVGDVLCIA	
NSSSANSILHIDPKTGVAVARAVGSVTVYYEV	
SVPQRIMARHLHPIQTSFQRATASKVIVAVGD	
QREVIQALHPETLISCQSQFKPAVFDFPSQDV	
QYFCSITMHRLTDKQRKHLSMKKTALVVSASL	
EVPFSPGLFADQAEILLSNHYTSSEIRVFGAP	
PAVLAFAKEKSFGWPSFITYTVGVLDPAAGSQ	
VTNQAIAIPVTVAFVVDRRGPGPYGASLFQHF	
ALLAGTAVMIIAYHTVCTPRDLAVPAALTPRA	SPGHSPHYFAAS
SPTSPNALPPARKASPPSGLWSPAYASH	
6531 845 1425 PSASIPPSASPDPVPDIRTCHFCLVEDPSVGC	
SLCMVITIYYDVKVRPIVRGCGQYISYRCQEKI	
QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPL	
NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSF	
SGLLVLPQAGLLTPHPS	AELRRMYLFLNS
6532 2 954 AAGPPSEVVNQDSLFPEPEPGPAPQVLLGPQGI	1

		·	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
I	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
<u> </u>	amino acid'	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
1	ļ		ITDSTGTHLVLTVTNKNAHSPGLSRGSPQQPSSQPGSPAPAPSA
	}	i	QMDLEHPLQPLFGTPTSLLKKEPPGYEEAMSQQPKQQENGSSSQ
			QMDDLFDILIQSGEISADFKEPPSLPGKEKPSPKTVCWSPLAAQ
I	ľ		PSPSAKLPQAAPPPPGSPSLPGRLRDFLESSTGLPLLTSGHDGP
1	ļ	•	EPLSLIDDLHSQMLSSTAILDHPPSPMDTSELHFVPEPSSTMGL
		l	DLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLFSTDFLDGHD
			LQLHWDSCL
6533	1798	373	STISWLARVEPPRRSSGVGAARURFPGGSRPLRARACVLALAVL
		[	ALLERNNADSMSAHSMLCERIATAKELIKRAESLSRSRKGGIEG
		ł	GAKLCSKLKABLKFLQKVRAGKVAIKESHLQSTNLTHLRAIVES
		1	AENLEEVVSVLHVFGYTDTLGEKQTLVVDVVANGGHTWVKAIGR
		1	KARALHNIWLGRGQYGDKSIIEQARDFLQASHQQPVQYSNPHII
			FAFYNSVSSPMAEKT,KEMGISVRGDIVAVNALLDHPEBLQPSES
j	•	1	ESDDEGPELLQVTRVDRENILASVAFPTBIKVDVCKRVNLDITT
			LITYVSALSYGGCHFIFKEKVLTEQAEQERKEQVLPQLEAFMKD
		]	KELFACESAVKDFQSILDTLGGPGERERATVLIKRINVVPDQPS
l			ERALRLVASSKINSRSLTIFGTGDTLKAITWIANSGFVRAANNO
			GVKFSVFIHQPRALTESKEALATPLPKDYTTDSEH
6534	47	596	KATRFISAAFVVLNKQGVSPAKLPHTSWSWSLQTLSFLFSCDLA
1			EKSLQCFPCSAMLLELIPLLGIHFVLRTARAQSVTQPDIHITVS
j			EGASLELRCNYSYGATPYLFWMERTVEEAFILLVCLKPWRVASS
		ļ	LEKKEKEDESFQLLLGSRYNVLKAHCLLPLIRWLTSGDSLLSAQ
			PHCPQGL
6535	250	964	LIKTFFRDVAIQRDLLPKBKNLETLLTLAFLEIDKAFSSHARLS
1 :			ADATILTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL
	!		TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD
1			LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIN
1			DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN
C-36	242	3374	SEINFSFERSFASSGRWA
6536	242	1174	SLVKEMTNOYGILFKOBOAHDDAIWSVAWGTNKKENSETVVTGS
			LDDLVKVWKWRDBRLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDAHIRLWDLKNGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV
			GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI
			INIFDIATGKILHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK
			I YDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW
			DVGTRTCVHTPFDHQDQVWGVKYNGNGSKIVSVGDDQBIHIYDC
1			PI
6537	1638	921	NRFNPPPTQGPDFSLVYRPDVDPEVAKDKASFRNYTSGPLLDRV
' ' '	1030	741	PTTYKLMHTHOTUDFURSKHAOFGGFSYKKMTVMEAUDLLDGLU
			DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV
			LALFGEPQWAVVGDTPPVGCRPQASVVFCDSTFQDNPDLQDPRY
1			STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG
			AEAVPAGDTISPOSTCTR
6538	3345	2412	PYLYDFLDALITCOTAPERAFIKLDGLAGMLTEGLERLTKQVQK
0550	3343	6716	ARHNRODEAIKKAVNKYDETMEKYIPVLMAQAKIYWNLENYPMV
1			RKIPRKSVBFCNDHDVWKLNVAHVLFMQBNKYKEAIGFYEPIVK
1			KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEQL
			SYDDPNRKMYHLCIVNLVIGTLYCAKGNYRFGISRVIKSLEPYN
			KKLGTDTWYYAKRCPLSLLENMSKHMIVIHDSVIQBCVQPLGHC
			BLYGTNIPAVIEQPLEEERMHVGKNTVTDBSRQLKALIYEIIGW   NK
			DK.
6520	210	770	DECA DESCRIPTION ADVIDED DESCRIPTION OF PARKET GENERAL
6539	218	339	FLGAASPHPHFSSLAPHPDQPEFTPVQDELRAMELWGPGV
6539 6540	218 3	339 391	LERLWLLLLRRPEDAMAECPTLGEAVTDHPDRLWAWEKFVYLDE

SEQ	Predicted	Predicted end	Dmine acid common control in cional montida
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A-Alanine, C-Cysteine, D-Aspartic Acid, E=
, MO:	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
l	sequence	sequence	\=possible nucleotide insertion)
6541	1165	536	RTLVORRILMLLRKPARGRDLRGRGRGTPRGGRKGLLPTPDRFP
6241	1103	336	RFEGGRKPDSWDGNREPGPGHEHFRDTPRPDHPPHDGHSPASRE
ļ			RSSSLOGMDMASLPPRKRPWHDGPGTSEHREMEAPGGPSEDRGG
l			KGRGGPGPAORVPKSGRSSSLDGEHHDGYHRDEPFGGPPGSGTP
ļ	1		SRGGRSGSNWGRGSNMNSGPPRRGASRGGGRGR
6542	3	3775	SWPRGRGETGGHPGALRTRTMQKSVRYNEGHALYLAFLARKEGT
6542	,	3775	•
ľ	i	i	KRGFLSKKTAEASRWHEKWPALYONVLFYFEGEQSCRPAGMYLL
	!		EGCSCERTPAPPRAGAGQGGVRDALDKQYYFTVLFGHEGQKPLE LRCEEEQDGKEWMEAIHQASYADILIEREVLMOKYIHLVOIVET
1	1		EKIAANQLRHQLEDQDTEIBRLKSEIIALNKTKERMRPYQSNQE
l			
1	1		DEDPDIKKIKKVQSFMRGWLCRRKWKTIVQDYICSPHAESMRKR NQIVFTMVEAESEYVHQLYILVNGFLRPLRMAASSKKPPISHDD
1	1	I	VSSIPLNSETIMFLHEIPHQGLKARIANWPTLILADLFDILLPM
			LNIYQEPVRNHQYSLQVLANCKQNRDFDKLLKQYEANPACEGRM
1	1	[	LETFLTYPMFQIPRYIITLHELLAHTPHEHVERKSLEFAKSKLE
		ŀ	ELSRVMHDEVSDTENIRKNIAIERMIVEGCDILLDTSQTFIRQG
		l	SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLFTKHFLICTRS
j	ļ	i	SGGKLHLLKTGGVLSLIDCTLIERPDASDDDSKGSGOVFGHLDF
1			KIVVEPPDRAAFTVVLLAPSRQEKAAWMSDISQCVDNIRCNGLM
1			TIVFEENSKVTVPHMIKSDARLHKDDTDICPSKTLNSCKVPQIR
1	}	1	YASVERLLERLTDLRFLSIDPLNTFLHTYRIFTTAAVVLGKLSD
}	}	1	TYKRPFTSIPVRSLELPFATSONNRGEHLVDGKSPRLCRKFSSP
		·	PPLAVSRTSSPVRARKISLTSPINSKIGALDLTTSSSPTTTTQS
	<u> </u>		PAASPPPHTGQIPLDLSRGLSSPEQSPGTVEKNVDNPRVDLCNK
1		·	LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPSTPRHLR
1	į	ļ	YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNNTÉRTC
l .	1		DKEFI IRRTATNRVLNVLRHWVSKHAQDFELNNELKMNVLNLLE
l	İ		EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDIIQMTDC
l .		ľ	MKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLGQGWMKLDK
ŀ			NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIBKWVAV
l		Ì	ADICRCLHNYNGVLEITSALNRSATYRLKKTWAKVSKOTKALMD
{	}		KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAFIEEGT
<u> </u>			PNFTEEGLVNPSKMRMISHIIREIRQFQQTSYRIDHQPKVAQYL
L			LDKDLIIDEDTLYELSLKIEPRLPA
6543	1857	950	FVSGCGRAGIGLSWAMAABARVSRWYPGGLASCGAACCTHPLDL
	[		LKVHLQTQQEVKLRMTCMALRVVRTDGILALYSGLSASLCRQMT
	]		YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLAGGFVG
ł			TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEGLRRLF
			SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIFTHFVA
	1		SFIAGGCATFLCQPLDVLKTRLMNSKGRYQGVFHCAVETAKLGP
	ļ		LAFYKGLVPAGIRLIPHTVLTFVFLEQLRKNFGIKVPS
6544	630	79	PSPCFIRSRLDGQPWMAGLEAWLSQNFSLHQPQSRVRVRRASIS
1			BPSDTDPEPRTINPSPAGWFVQQHPBIJEIMSSFRERFGRNWLQY
			RSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRPSPPQEEAR
1	ł		GPQESPQKMSEKVRAKPQKEKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
			EGKQKECP
6545	176	560	PPHSHAALLPAAMTPLLTLILVVLMGLPLAQALDCHVCAYNGDN
<u> </u>			CFNPMRCPAMVAYCMTTRTYYTPTRMKVSKSCVPRCFETVYDGY
			SKHASTTSCCQYDLCNGTGLATPATLALAPILLATLNGLL
6546	1657	364	HLLNGLDEVAAFFVADLGAIVRKHFCFLKCLPRVRPFYAVKCNS
1			SPGVLKVLAQLGLGFSCANKARMELVQHIGIPASKIICANPCKQ
			IAQIKYAAKHGIQLLSFDNEMELAKVVKSHPSAKMVLCIATDDS
1			HSLSCLSLKFGVSLKSCRHLLKNAKKHHVEVVGVSFHIGSGCPD
1	ł		PQAYAQSIADARLVFEMGTELGHKMHVLDLGGGFPGTEGAKVRF
l	İ		REIASVINSALDLYFPEGCGVDIFAKLGRYYVTSAFTVAVSIIA
L	L		KKEVLLDQPGREEENGSTSKTIVYHLDEGVYGIFNSVLFDNICP

Deginning   Docation   Cortesponding to first   amino acid   amino acid   residue of amino acid   amino acid   amino acid   sequence   Period   P	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Mociocation   Corresponding to first amino acid residue of amino acid residue of amino acid sequence   Seque	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Coetson   Coffee   Leterice   L	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
Corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence   Section T-Threonine, V-Valine, amino acid sequence   Section T-Threonine, V-Valine, Section, V-Pooline, G-Quituanine, R-Argainine, P-Proline, G-Quituanine, R-Argainine, Sequence   Sequence   Sequence   Section, V-Poosible mucleotide deletion, V-Poosible mucleotide insertion   V-Poosible mucleotide deletion, V-Poosible mucleotide insertion   V-Poosible mucleotide deletion, V-Poosible mucleotide insertion   V-Poosible mucleotide deletion, V-Poosible mucleotide deletion, V-Poosible mucleotide deletion, V-Poosible mucleotide deletion, V-Poosible mucleotide insertion   V-Poosible mucleotide deletion, V-Poosible mucleot	ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine,
to first amino acid residue of amino acid amino acid residue of amino acid amino acid sequence    Hottprophan, Y-Tyroonine, X-Unknown, *estop   Codon, /-possible muleotide deletion,   Codon, /-possible muleotide deletion,   Codon, /-possible muleotide deletion,   Codon, /-possible muleotide deletion,   Codon, /-possible muleotide deletion,   Codon, /-possible muleotide deletion,   Codon, /-possible muleotide deletion,   Codon, /-possible muleotide insertion)   TFI (CORRESTEED/INSESSIMOPANICACHITYAMSRVAMERALERQLAMA ROBEDVEOVER/SECORE TOTAL COPENTYPIASIM   FOR COMMISSION   COMMISSION   COMMISSION   COMMISSION   COMMISSION	ł	corresponding		L=Leucine, M=Methionine, N=Asparagine.
amino acid residue of maino acid sequence (Ptytophana, T-Threonine, V-Valine, amino acid sequence (Ptytophana, T-Threonine, V-Valine, amino acid sequence (Ptytophana, T-Threonine, V-Valine, Sequence (Ptytophana, T-Threonine, V-Valine, Sequence (Ptytophana, T-Threonine, V-Valine, Sequence (Ptytophana) (P	1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
residue of amino acid sequence  amino acid sequence    F-Tryptophan, Y-Trytooine, X-Unknown, *-stop code, *-possible mucleotide deletion, *-possible mucleotide deletion, *-possible mucleotide deletion, *-possible mucleotide deletion, *-possible mucleotide insertion)   TPILOKRESTEPDYSSSIMCPANOGICPMAGNITQLINGDN     TVENNKAYTUMGSPRWITGACHITYMSRYAMFALERQLMAA     ROEDDWOVCKICLOKREITDTLICUSPYTPASIM   POSSIBLE		amino acid		
Sequence   Codon, /-possible mucleotide deletion,	I	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
A-possible nucleotide insertion	i	amino acid		Codon. /=Dossible mucleotide deletion
### INTERPREDUKSSING PAUTOCU VARCHIFOLIUM LUFPINNINGATURUS PRIMINGATUTU (ITTAMIS VANARLIREQUAMA ROBODURS PRIMINGATUTU (ITTAMIS VANARLIREQUAMA ROBODURS PRIMINGATUTU (ITTAMIS VANARLIREQUAMA ROBODURS PRIMINGATUTU (ITTAMIS VANARLIREQUAMA ROBODURS PRIMINGATUTU (ITTAMIS VANARLIREQUAMA ROBODURS PRIMINGATUTU (ITTAMIS VANARLIA (ITTAMIS VANARLIRE) (ITTAMIS VANARLIREQUAMA PRIMINGATURUS PR	ì	sequence		\=possible nucleotide insertion)
LVFINNGATTUCHGSPRHGTOACHITYMISEVAMERLERQLHAA	<u> </u>	<del> </del>		
SCIEDURGEVCREISCRETTOTLCVGFVPTPASIM	1			
6547   1		1		
PPLABAJAGYPRICUTTYGGRACULRUGBMGRGEGLETICESW NDPHRCASQVISGCPEBAAVWRSIQGRAGARPRINAITHCGA PVHVRRRTGTGSRTNGSTHRATAPALPHADAPPLICABALATATIL RPLA  6548  2 219 PVSRISVEDVRPFTFIGGHGADAMHTDPDYSAAVVPIETDAEDG I KGGGTFFTLGKGTEVGELKILGERQUA  6549 73 1490 BTGRVCEDARPACGSSERIRRKSRAPGIFFSPSSSSPTSSERA ARAPSRAPAGISSPRARESPADGGRATIQBE I IOARIKHI, IMC SSVAAKUMFILDRIRRIBENPODGGRATIQBE I IOARIKHI, IMC SSVAAKUMFILDRIRRIBENPODGGRATIQBE I IOARIKHI, IMC SSVAAKUMFILDRIRRIBENPODGGRATIQBE I IOARIKHI, IMC SSVAAKUMFILDRIRRIBENPOKETIARIAKKGEBELDPPAVWI DEVVILTBGGBIGSHENGRILTATPOVVVVVPTPWQGSDGIT VLRHERRGGLAMPROALINCUMPETPUBGIGVPLDPTPS VGGRAPPARMIDBARVLSPFWVVWITSGGBGKAVPLANDHHILA DLSHLIFBERAPYLPORTVRESHGGVAVFLANDHHILA DLSHLIFBERAPYLPORTVRESHGGVAVFLANDHHILA DLSHLIFBERAPYLPORTVRESHGGVAVFLANDHHILA DLSHLIFBERAPYLPORTVRESHGGVAVFLANDHHILA BURLLTRIBARITY OR STANDHHILABE KILLVU  RRINGSGROUS GROUPEN STANDHHILABE KILLVU PRITARRSLIDGFLGWGGARRGGSYRANGSSERGGWYTIRVPF LPYSLIGPILI ILGIULMVCSUNHWSTESNLQATERRRBGLYSQ COGGRUTYTWINGRWAALITERSTVANDHHILABE KILLVU NOKWATLEVE IRAKENTICTKORADITMOSHMISGOSSERGCWYTIRVPF LPYSLIGPILI ILGIULMVCSUNHWSTESNLQATERRRBGLIVGQ COGGRUTYTWINGRWAALITERSTVANTHMINGS II PRS LDNILGTRSGLARKGOLOKVOALCLEPIDDGKFENDIRNIMGS GIPALIPMI NOKWATLEVE IRAKENTICTKORADITMOSHMISGOSSERGUMPCUNTAPTE LOHGEGGLAKROLOKVOALCLEPIDDGKFENDIRNIMGS GIPALIPMI NOKWATLEVE IRAKENTICTKORDHANIKSULARUSLASILABA LERVARENSOLOKOKLEROGGERASGGRAGKVEKRAQBERALIQ AEGSROTIGLABERKOMA KRENGALERIKKERADELARULA AEGSROTIGLABERKOMA KRENGALARUKERADARUKELABSLERA  6551 157 748 TOPPDFRIMTIAAYKERKRKELPUSLFCSCFLADPLINKSYKYE ADTVOLINKVI SIMMEVI HLINKCTSOGSFEVI LIKPPSFDCVPEFM ASLPRRDPSLEB I KOKKLAASERRKYOGRAFILAHALARURELIG EKKRABEVERNINELKERASS  6552 157 748 TOPPDFRIMTIAAYKERKRELPUSLFCSGGFADPLINKSYKYE ADTVOLINKVI SIMMEVI HLANGTSGGFFEVI LIKPPSFDCVPEFM ASLPRRDPSLEB I KOKKLAASERRKYOGRAFILAHALARURELIG EKKRABEVERNINELKERASGER  6553 2 1807 FVWSKRBAHHISAN KERKRELERSHERANTWERE KREOTEGORGHI VIVD EKKRGBMININ TARABELLAQWESSKENRERHIDAN VIVLDERKSTATION VVLLPERKFADILLIDRINVILERGORGDVALTUPPRIBLIDTY VVLLPERKFADILLIDRI	6547	<del>                                     </del>	541	
DIPHIACRSQVILSGCPERABAUWSSICODERROAPRENILHTICGA PVHVERGTGSTRNGSTIRATAPALMADAPPILAAALALAYLI RPLA 6548 2 219 PVSRISVROFTFTGGGGADMHTDEPTSAGVAVPIETDAEDG IKGGGITFTIGKSTRVGELKILSRYQNA 6549 73 1490 ETGRVCEDARPAGGSSRRRRKEAAFGIFFSPSSSSPTSSKPA ARAPSKAPARIASRKERABGIFFSPSSSSPTSSKPA ARAPSKAPARIASRKERABGIFFSPSSSSPTSSKPA ARAPSKAPARIASRKCCEERLDPRAVN DEVVLITSGGRIGHGIBTINGELIATAYDVVVVEYHVGSRIVATARAKKCCEERLDPRAVN DEVVLITSGGRIGHGIBTINGELIATAYDVVVVEYHVGSRIVATARAKKCCEERLDPRAVN DEVVLITSGGRIGHGIBTINGELIATAYDVVVVEYHAVGSDIVT VLERILERRGCLEMRPOALINCVMKPWPORLAGGGVPLDPTFS VGGRENPAKINGBARVEFTHAVYONTVORGRVVGTMLRCST DGEMGSNCSLGGVGRINGSLAGGVRUGTMLRCST DGEMGSNCSLGGVGRINGSLAGGVRUGTMLRCST DGEMGSNCSLGGVGRINGSLAGGVRUGTMLRCST DGEMGSNCSLGGVGRINGSLAGGVRUGTMLRCST DGEMGSNCSLGGVGRINGSLAGGVRUGTMLRCST DGEMGSNCSLGGVGRINGSLAGGVRUGTMLRCST REFTREILITLICHLURWVVGNVATSCRAGGVRUGTMLRCST LUGITASGSNLTTKKINFTTRANDATMOMINARRDLDRINASFR COCGERVITYMRNORMANILISKECADLEPMINASFR COCGERVITYMRNORMANILISKECADLEPMINASFRECTALLPMI NOKVKTLRVBIAREKTICTKDRSSVLIKKRVAREDOLVECVKYRE LURIGYRIJMPLGSKIASIERRAGGBVRRUGTMRRAKACQ AECSRCTULLBERKVAURKRRUNLAKEREKREREGLIMELATI REVARENSDLOKQRUGRAGGGRAGGVRRAGGVRRAGARRAKACQ AECSRCTULBERKVAURKRUNLAKEREREREGLIMELATI REVARENSDLOKGRURAGGSRAGGVRRAGGRAGGVRRAGARRAKACQ AECSRCTULBERKVAURKRUNLAKEREREREGLIMELATI RENSALDTCIKTRSQVMMPVSRPMGPVPNPOPTDPASLEBRIKKT APTVOLINNCVI SUMMVILSKAVICSGGSFRUINDENSSYKYE ADTVOLINNCVI SUMMVILSKAVICSGGSFRUINDENSSYKYE ADTVOLINNCVI SUMMVILSKAVICSGGSFRUINDENSSYKYE ADTVOLINNCVI SUMMVILSKAVICSGGSFRUINDENSSYKYE ADTVOLINNCVI SUMMVILSKAVICSGGSFRUINDENSSYKYE ADTVOLINNCVI SUMMVILSKAVICSGGSFRUILHHAARKERER FVTQRALEERING INGRVENSKARRERERERIGHER FVTQRALEERING INGRVENSKARRERERERERIGHER FVTQRALEERING INGRVENSKARRERERERERERERE FVTQRALEERING INGRVENSKARRERERERERERERERERERERERERERERERERERER	031.	1 -	542	
PVHURERGTGSETNQSTIRATAPALPMAPAPPLLAAALALAYLL RPLA  6548  2 219 FVSRLSVRDVRPFTFLGGEGADAMHTDEDYSAAVVPIETDAEDG 1KGCGITFTLGKSTRVGELKILSGRQVBA  6549  73 1490 RTGRVCEDARBAGGSSERRRRKEAAFGIPTFSPSSSSPTSSRPA ARAPSRAPAGISSRPRRRREKEAAFGIPTFSPSSSSPTSSRPA ARAPSRAPAGISSRPRRRREKEAAFGIPTFSPSSSSPTSSRPA ARAPSRAPARISRPRARBEPPDDGRRYIQBEIJORAKHKI, IMC SSVAAKIMFLIDRIRIEDTVGREITUNGELTGAGUVVUVUVPTFWUGSDJIT VLRRLRRIGGLAMPROALITUNGHFWTFGBLAGGGVPLDPTFS YGGHEMPAKHIDRAEVLEFFMVVRTRGRRGKAVPLARDKHILA DLSELLIRREAPTLFORTVRSSHGEBURVIVVOGRVOTHRICST JGGRINGSNCSLGGVGMCSLGGGGRGLAIQVSLIGHDVGGIDLI MEDDGSPCVCRAMANUGILAPBKACHLOVAGITADVAGSLUFSG REITRMSLLSVSTATSBTSBEBEIGPPASTANDVAGSSSSVDSD PBSTRREILTKLPGGLFMMNGLLABBKKLLVD  RYSKRGAADGEIGMGGAMBRGGSVAARGSSSGCGVYIRFPF LFVSLIGHLITLGLJUFMVYGNYHVSTESKLQATERRARGLYSQ LLGLTASGSNLTKKLNPTTRAKAAIMGMNRSCGLALFMI, NGKVKTLEVBIARBKTICTKDKRSVLINKRVABEQLIVECVKRRE LQHGGRQLAKRGQCVQALCLEDDKFFEDHMSSCGLALFMI, NGKVKTLEVBIARBKTICTKDKRSVLINKRVABEQLIVECVKRRE LDRLGGRADJARGQCVQACLCLEDDKFFEDHMSSCCALLFMILA RNSAALDTCITKKSQOMMPUSGRASGKKRGKAAGARRALQ ABCSROTOLIALBEKAVIRKRRNILAKSLEKKRRRARGLHRULAI RNSAALDTCITKKSQOMMPUSGRASGKKRGKAAGARRALQ ABCSROTOLIALBEKAVIRKRRNBLPLVSLFCSCFLADPLNKSSYKYE ADTVOLINKCVISIMSVIHLINKCTSGQSFSVILKPPSSDCVPEFR ASLPRRRDPSLBEIGRKLBAABERRKTGRBELLKHLARKREBER EVIGRALBERENNFIKMRELPLVSLFCSCFLADPLNKSSYKYE ADTVOLINKCVISIMSVIHLINKCTSGQSFSVILKPPSSDCVPEFR ASLPRRRDPSLBEIGRKLBAABERRKTGRBELLKHLARKREBER EVIGRALBERNNFIKMRSLERASGRAFARIGAMER EVIGRALBERNNFIKMRSLERASGRAFARIGAMER EVIGRALBERNNFIKMRSLERASGRAFARICH LGRUBPFFFFF LGRUBPHTARVFFRENSELLEFIDKCAGSKATVWD EYLTGPFGLIAQYSLLKRBASGRAFRETORBELLKHLARAKERBER EVIGRALBERVRNTELKBRASG  6552  157  748 1GPPDFRRMTLAATSGRRGFTROPRHILEVPRSSLCCGCRUBPHTAR ASLPRRRDPSLEBIGRKLAGABERRKTGGRBLIKHLARKREBER EVIGRALBERVRNTELKBRASG  6553 2 1807  PWSKMAAHLSTAAVEGKORGFTROPHILEVPRSSLCCGCRUBPHGAA RGSLANHTSTABLIKUTTEGGGGFTROPHILEVPRSSLCCGCRUBPHGAA RGSLANHTSTABLIKUTTEGGGGGGGRUBTRAKTGLONGLEHVARIBRA RGSLANHTSTABLIKUTTEGGGGRSTEEVURTLEGGGTDFHWN TIEDGLAGKGGGGGRUBTTRAKTGLONGESHENDENGENGENDENGENGENGENGENGENGENGENGENGENGENGENGENGE			•	
6548 2 219 FYSRLSVEDVRPPTFLIGHEGADAMETUDDYSAAVYPIETDAEDG IKGGITPTLEKSTEVGELKILERPONA 6549 73 1490 ETGRVCEDARPACGERSRRRREARFGIPTSPSSSSPTSSRPA ARAPSKAPARLSSPRARESPPDEGRTYLGEIIOARCHKLIKMC SSVAAKHFLIDERIREDYPOKRSILRALKAKCCEERLDPFAAVM DEVVLTIRGGHILGHIRMGELIATYPOVVVEYPWQGSDUTT VLEHLEKMGCHIANRPOAIINCVRFWTPGELAGHGVPLEDTPS VGGENPAAN IDERKVLESPPWVRTSTGEREGKAVPLARDKHILA DLESILIBHEAPVILFOKYVKESHGEDVRVIVVGGRVOTTHIRCST DGRMONGLGGGVANGLSLEGGORQLAIOVSHILMDVCGIDLI MENDGSPCVCENNANVGPIAPDEACHDVAGIIADVAASILPSG RITRRELITKLEGGINMSGLAGGORQLAIOVSHILMDVCGIDLI MENDGSPCVCENNANVGPIAPDEACHDVAGIIADVAASILPSG RITRRESITKLEGGINMSGLAGGORQLAIOVSHILMDVCGIDLI MENDGSPCVCENNANVGPIAPDEACHDVAGIIADVAASILPSG RITRRESITKLEGGINMSGLAGGORQLAIOVSKESTYIRVFF LFVSLIQPILIILILULMVVAVVSHONGLAGTERRAGGISSOVSD PRSTREBLITKLEGGINMSGLAGGORGLAIOVAGATERRAGGISSQ COCGRUTYTMORPMAAIIILSBECGCOPORAGTERRAGGISSQ COCGRUTYTMORPMAAIIILSBECGCOPORAGTERRAGGISSQ COCGRUTYTMORPMAAIIILSBECGCOPORAGTERRAGGISSG COCGRUTYTMORPMAAIIILSBECGCOPORAGTERRAGGISG COCGRUTYTMORPMAAIIILSBECGCOPORAGTERRAGGISG COCGRUTYTMORPMAAIIILSBECGCOPORAGTERRAGGISG COCGRUTYTMORPMAAIIILSBECGCOPORAGTERRAGGISG COCGRUTYTMORPMAAIIILSBECGCOPORAGTERRAGGISG COCGRUTYTMORPMAAIIILSBECGCOPORAGTERRAGGISG COCGRUTYTMORPMAAIIILSBECGCOPORAGTERRAGGISG COCGRUTYTMORPMAAIIILSBECGCOPORAGTERRAGGISG COCGRUTYTMORPMAAIIILSBECGCOPORAGTERRAGGISG COCGRUTYTMORPMAAIIINTORYMORPMAAIINTORSCOLUTERRAGGISCOLUTERRAGGISG COCGRUTYTMORPMAAIINTORYMORPMAAIINTORSCOLUTERRAGGISCOLUTERRAGGIA COCGRUTYTMORPMAAIINTORYMORPMAAIINTORSCOLUTERRAGGIAMILAGA ROSKUMIYHPIGASILASILARACGMRONGKARAGCOLUTERRAGGIAMILAGA ROSKUMIYHPIGASILASILARACGARGAKVERAGGIAMILAGA ROSKUMIYHPIGASILASILARACGARGAKVERAGGARAAKIQ ABCSROJULABANAIRMAAIAGAGARGAKVERAGAGARAKIQ ABCSROJULABANAIRMAAIAGAGARGAKVERAGAGARAKIQ ABCSROJULABANAIRMAAIAGAGARGAKAKARAALAGARGAKAAIAGAA ASLPRREDPSILBSIORULABARGREKYOGABGILAHILAGARGERKEBE EVIQALAGAGAAIAGAAAAAAAAAAAAAAAAAAAAAAAAAAA	Į.	i		
6548 2 219 FYERLSVEDVRPPTFLCCHGADAMHTDDYSAAVVPIETDAEDG 6549 73 1490 RTGRVCEDARPACGSESRRRRREAAPGIPTESPSSSPTSSRPA ARAPSKAPARLSRPARKEPAPPORRITARIARUCGERIADPRAVA SVAAKLMPLITORIREDDYDGRITARIALGAEGUPLESPSSSSPTSSRPA ARAPSKAPARLSRPARESPPDRGRYTQBEI IQARRHKLI KMC SVAAKLMPLITORIREDDYDGRITARIALGAEGUPLPDTPE VGERBPARM IDRARVLEPPMVVUNTRGRRCKAVPLARDKHELA DEVULTIEGGRIGIRINGELITAYPQVVVVRVPTPMVQSDSDIT VLERHERMOCKIAMPOPALINCVUKPETVJCRGRVYDTHECST DGRMQSNGSLGGVGHACSLISBQGKQLAIJQNNILGHDVCGIDLL MEDDGSFCVCENANNUGFIAPDRACHLOVAGI IADVAASLLESG RLTRRRSLLSVVSTASRTEBPLIPPASTUNGSSSSGCMYVILRPPF LFVSLIGPLITALIAUVSVSTASRTEBPLIPPASTUNGSASSSVDSD PBSTRRELLITALPAGDLYSMWINGLABBIKLLUD PREVENGABOULSKOMGLAMBIGGSVARAGSSSSGCMYVILRPPF LFVSLIGPLITALIAUVSPWYZONVINSTESNIQATERRAGILYSQ LLGILTASSGNLTUKELMPFTPARDATMOMMINARSCISSLLPML NGKVKTLEVBIAKKRTICTKOKRSVLANMENGSSSRGCMYVILRPPF LFVSLIGPLITALIAUVSPWYZONVINSTESNIQATERRAGILYSQ CQGDRYTYTNNQNYMAAIILSERQCROOPKOMMSCISALLPML NGKVKTLEVBIAKKRIJCTKOKRSVLANMENGSSRGCMYVILRPPF LORRAGIAKRQLAVOALCLPLDKNOKFEDDIRNINGSI IPRS LDMLGYNLYHPLGSBLASIRRACDHPSIMSSKVEELARSIRAD IRRVARRRSDLOQKOKLEAGQGLRNSQGRAVVERRAQARERALQ AECSROTQLALBERAVLRKERINIAKELSEKKRRAGKUREVILAURALSI RNSALDTCILKYKSCOPHDYSRPMOVPNPQFIDPASLBEFKRKI LESGRPPAGIJVANSSG  6551 157 748 IQPPDPRANTLAAYKERMELPLUSLFCSCFLADPINKSSYKYE ANTVOLINMCVISIOMEVIBLINKCTSGQSPEVILKPSFDCUVEEPN ASSLPRRIPPSSLEEIGKKLAARBSRRRYQBAELLKHLAERRHIER EVYQRAIBENNFINARKEKLAQMESSKRRRHALAAMLERLG EKKHABEVRRINKELKBRASR  6552 157 748 IQPPDPRANTLAAYKERKERLPLUSLFCSCFLADPINKSSYKYE ANTVOLINMCVISIOMEVIBLINKCTSGQSPEVILKPSFDCUVEEPN ASSLPREDPSLEEIGKLAAABERRYQBAELLKHLAERRHIER EVYQRAIBENNFINARKEREPLUSLEGREPEDOKCAGSKATVWD EVILOPFGLIAQVSLLKRHEVENNFILRAURRIBLANMINGRFTC SQNSIFPVPONLALLARVLERGPPTDPH ILPPPRSLLCEGQLKD LGVLGSFTHREYSLDLIPTGGIGNSTVKTETJETTGGTMS VVLLPPEKFAPKKGGGGGKOLPTFAKKLQILMSAERLYARIBORN VILLPPEKFAPKKGGGGGKOLDPTRAKKLQILMSAERENIAGRINGRETTGGNS VVLLPPEKFAPKKGGGGGKOLDPTRAKKLQILMSREGAPTECYLLEGTOTS LYMAGNUSLKKKAKITISABERRHINATVELGIDETYGGTMS VVLLPPEKFAPKKGGGGGKOLDPTRAKKLJUNSAERLYRRIBORN VILDPEKFAPKKGGGGGKOLDPTRAKKLJUNSAE				
1 1490 ATTACHCE PLANTER POR ATTACHCE AND ATTACHCE PLANTER PROPERTY OF STATEMENT AT THE PROPERTY OF STATEMENT AT THE PROPERTY OF STATEMENT AND ATTACHCE PLANTER PROPERTY OF STATEMENT AND ATTACHCE PLANTER PROPERTY OF STATEMENT AND ATTACHCE PROPERTY OF STATEMENT AN	6548	<del> </del>	21.0	
1490   STGRUCEDARPACISSERRIRIERARAPGI PTESESSEPTESERA     ARAPSKAPARLSPRARESPPDGRAYIQEE I LORKHKLIKMC     SYAAKLWFLITURI IRBDYPQKBLIRAKAKCEBBLDPRAVW     DRVILTIBGGRIGIR INGELITAT PQUVUVEVPTPWUGSEDIT     VLEHLEKMGCHMRPOLIKOWKWWFUGHUGHUGHDLIK     DESHLIRHERAPYLPKYVYVESSIGDUNYLGHUGHUGHDLIK     DESHLIRHERAPYLPKYVYVESSIGDUNYLGHUGHUGHDLIK     DESHLIRHERAPYLPKYVYVESSIGDUNYLGHUGHUGHUGHLIK     MKDGSPCLCRANNWGSLASBORGIAJQVANILGHUGHUGHLIK     MKDGSPCLCRANNWGSLABBIKLIADGI TADYAASILPSG     RITERMSLLSVVSTASBTSEPELOPPASTAVDMSASSSSVDSD     PRITERBILITELPGGLYMMIGHIGHAGAGISAKAGUSKYRJEPF     LFVSLIGPLI ILGILVLPMYYCNVUNSTESILQATERRAGIJVSQ     LLGILTASGSINLIKKLAFTTRAKDAINGMAINARRIGUSTRANSFR     QCGGRUTYTNNORWAATILSBGCGLOFKUNINKSSSSEGWYYLRYPF     LFVSLIGPLI ILGILVLPMYYCNVUNSTESILQATERRAGIJVSQ     LLGILTASGSINLIKKLAFTTRAKDAINGMAHARRIGUSTRANSFR     QCGGRUTYTNNORWAATILSBEGCHOOFKUNINKSCOLLLPHI     NQKYNTARVE LARKHTICTKOKSEYLILINABERJULGUCKYKTE     LORIGYMLYIPLGSBIASI TRACCHMPSIMSSKVEELARSIKAD     TRVARENSDLORKUKEAQGLGKRAGGGRAKVEKRAQARERAKLQ     ARCSROTULALBERAVIRKERINILAKKLEKKERAQUKHKEAQUKHKEAA     RESALDTCILKYKSCOPHUPUSPPMOPUPUPASLEBEYKKI     LBSQRPPAGIIVAPSSG     LBSQRPPAGIIVAPSSG     TARABIKANDA SHAND	3370	<b>_</b>	213	
ARAPSKAPARLSRPRAREEPPDFGRRYTQBEITQARKHELIKME SSVAARLSWILTDRRIEDYPQKEILRALKARKCCEEBEDFRAUW DEWVLITEGGRIGIGINGERINGELITARPQUVUVEPPPWQGSDIT VLEHLEKMGCKIMKRPQATIANCVEKEPEDPADVER VGGRIBPFARM IDERAULE BEPWUVENTREIGKAPHGAPLAPHEN DLEHLIRREAPYLPQKYVEKESHGBUVEVLVUGGRVUGTHIRGST VGGRIBPFARM IDERAULE BEPWUVENTREIGKAPHGAPLAPHEN DLEHLIRREAPYLPQKYVEKSHGBUVEVLVUGGRVUGTHIRGST DGRWOSNCSLGGVGMMCSLSBGGKQLAIQVSHILMDVCGIDLI MKDDGSPCVCRANNNYGPTAPDRACHLOVAGITADVAASLLPSG RLTRRNSLLSVVSTASEKTBEPELOPPASTAVDINNSASSSSVDSD PSSTRREILTKLLGOLJFMRNQLIANBILGSVARAGGSSGEGVYTLRYPF BSTRREILTKLLGOLJFMRNQLIANBILGSVARAGGSSGEGVYTLRYPF BSTRREILTKLLADGJFMRNQLIANBILGSVARAGGSSGEGVYTLRYPF PSSTRREILTKLLADGJFMRNQLIANBILGSVARAGGSSGEGVYTLRYPF QCQGDRYTYTNRQTMAATITLSEKQCROQFKONNKSCLSVALLADG NQKVKTLEVBLAKERTICKKDKRSVILINKVABEOLJVECVKTRE LONIGGRQLAKEQLGKVQALCLFLDKDKFFEDIRINHDSITERS LONIGGRQLALEKKALIRGERRACHMPSIMSKVEBLABSLGAD TERVARENSDLQKOKLEAQOGIARSGEAKOKVEKRAQAREAKIQ ABGCSROTULALBEKALIRAKERINLAKELEKRABOLARMELSITERS LONIGGRUJAHRGGEGKVQALCLFLDKKFRENDIKTERSITERS LONIGGRUJAHRGGEGKVQALCLFLDKKFRENDIKTERSITERS LONIGGRUJAHRGGEGKVQALCLFLDKKFRENDIKTERSITERS LONIGGRUJAHRGGEGKVQALCLFLDKKFRENDIKTERSITERS LONIGGRUJAHRGGEGKVQALCLFLDKKFRENDIKTERSITERSITER LBSQRPPAGITVAAPSSG 1ERVARENSELBERKRENDIKTERSPRSKVEELABSLGRAD TERVARENSELBERGKRUSKERRINLAKELEKREADGLARMELG ABCGSROTULALBEKALIRKERRINLAKELEKRABOLKREIGE BVJQKALBERNINTHAKERKILAGMESNKENRRAHLAAMLERLQ KKOKHBERVERKKELEKRASS  6551 157 748 1QPPDFRRNTLAAYKERKKELEKRASS  6552 157 748 1QPPDFRRNTLAAYKERKKELEKRASS  6553 2 1807 FVINSMAAHLSYGRVELNVLREAVRRELEEFLOKCAGSKAIVWD ENITGPFGLIAQVSLLKERHVENOMTSLKKRAHLAAMLERLQ KKOKHBERVRINKELEKRASSR  6553 2 1807 FVINSMAAHLSYGRVELNVLREAVRRELEEFLOKCAGSKAIVWD ENITGPFGLIAQVSLLKERHVENOMTSLKKTGGGFFWGALTHYNTITFYCTGUS VVLLPPEKFAPKKGGGGKOLDPTRAKKLQUINSBERGLKARIEDHT VRANGSVLUSKKALTISARFERPRINKTVLEEGEDOTS LYHAARGILATULAQLVYCHT DFFGRECARGVANMTRMREPTC SQNSIFPVPDNILLLDERNVLLIFPPENGLICHGOOTS LYHAARGILATULAQLVYCHT DFFGRECARGKRYOLDYKRETLGGO VVLLPEKFAPAKKGGGGGKOLDPTRAKKLUMDSABERSLEGGN PROTODONN VIELPERKFAPAKKGGGGKOLDPTRAKKLUMD	6549	72	1400	
SSVARKLWFLITDRIRREDYPOREILRALNARCCEBELDPRAVVM DEVVLTIEGGNIGELITAPQVVVVRYPTPWQSDDIT VLEHLERMGCRIMMRPQATINCVNIKWTPGBLAGHEVPLPDTPS VGGHRIPFARMIDERAVLEPTMVVRSTHGHRGKAVPLARDKHELLA DESHLIRHERAPYLEPKVVRSHGHRDKVAVPLARDKHELA DESHLIRHERAPYLEPKVVRSHGHRDKVAVPLARDKHELA MKDDGSPCVCRNANNVQPTAPDRACHLDVANILAGHDVGTDLL MKDDGSPCVCRNANNVQPTAPDRACHLDVANILAGHDVGTDLL MKDDGSPCVCRNANNVQPTAPDRACHLDVANILAGHDVGTDLL MKDDGSPCVCRNANNVQPTAPDRACHLDVANILAGHDVGTDLL MKDDGSPCVCRNANNVQPTAPDRACHLDVANILAGHDVGTDLL MKDDGSPCVCRNANNVQPTAPDRACHSGVSRGCWYYLRYPF PSTBRELLTKLIPGGLINMNQDLAWEIKGLVD PRYSERGAPDCG1EMGLAMBIGGGYAGGGSSRGCWYYLRYPF LFVSLLQPLITLIGLVLFMVYGNVHVSTESKLQATRRARGGLYSQ LLIGITASQOSILTKKEINFTTEAKDAIMQMKNARRDLDRINASFR QCQGDRVIYTNNQRYMAAIILSERCCRQPKDMNKSCDALLFML NQRVKTLRVBLAKBKTICTTCDKBSVLINKRVBAEDQIVECVETTRE LDRIGGTNLYHDLGGSELASILRRACDBMPSIMSSEVEBLARSIRAD TERVARENDLQKORGLERQOGLRASPEDLANNMNSSITPRS LDRIGGTNLYHDLGGSELASILRRACDBMPSIMSSEVEBLARSIRAD TERVARENDLQKORGLERQOGLRASPEDLANNMNSSITPRS LDRIGGTNLYHDLGGSELASILRRACDBMPSIMSSEVEBLARSIRAD TERVARENDLQKORGLERQOGLRASPEDLARPDHANSSEVEL ABCRPPADIIVPASSE ABTYDLINGVISTBMCTORYBETHLAPPSTOPPEPPH ASLPRRDPSILBEIQKKLBABBERRKYQEABLLKHLARKREBER EVIQRAIBENNINFIKMARKKLAQKNESNKRRAHLAAMLERIQ EKNKHABEVRINKELKBRASR 6552 157 748 TQPPDPRINTIAAVKERMKKLLPUSLFCSCFLADPINKSSVKYE ADTYDLINGVISTBMCTOSGOSFEVILKPPSFPORVPEPPH ASLPRRDPSILBEIQKKLBABBERRKYQEABLLKHLARKREBER EVIQRAIBENNINFIKMARKKLAQKNESNKRIRBALLAMMERIQ EKNKHABEVRINKELKERASR 6553 2 1807 FVMSKWAAHLSYGRVINNVIRRAVBREIRBFLDKCAGSKAIVMD EKNKHABEVRINKELKERASR 6553 748 FVMSKWAAHLSYGRVINNVIRRAVBREIRBFLDKCAGSKAIVMD EKNKHABERTITQALYGTIQFTGGTEARCYLEGGOCTSKON VVGSPHIBERTSLDLIPPODLLISPESGARRCYLEGGOCTSKON VVGSPHIBERTSLDLIPPODLLISPESGARRCYLEGGOCTSKON VVGLSPHIBERTSLDLIPPODLLISPESGARGUTAETDRIN TIFDCTARGCAGATATURGTKOPTGGINNYPTIRRTGRINDVNB TRAVEGSCAGATATURGTKOPTGGLARGUTANTERTLORGUTAPGGLADPUNB TRAVEGRAMATURGALGYGGRNNYPTIRRTGRINDVNB TRAVEGSCAGATATURGGUTAPGGTANTYPTIRRTGRINDDVNB GNSTLAMTTSLABLLKDVTTSBDFPDKLTVGGSTRGGLIPTDKVNN TRAVSSVLISKRATI ISABERBRANDLTVGGSTRGTGGLIPTDKVNN TRAVSSVLISKRATI ISABERBRANDLTVG	"349	j '3	1430	
DEVVILTIEGGNIGHRINGERLITATPOVVVURUPTPRVQADSDIT VLRHLERMGCRIAMRPQAILINCVRKFWTPQRIAGHGVPLDDTFS YGGHENPARM IDRARVLEPFMVVRKFWTPQRIAGHGVPLDDTFS YGGHENPARM IDRARVLEPFMVVRKFRGRENKAVPLARDKHHLA DLSHLIRBAPYLPGKYVKESHGRDVRVIVVGGTDLL GERGROGGSCLGGVGGMGSLSGGGGGLATQVSNILGHDYGGTDLL MKDDGSFCVCRNNNVGPIAPDRACHLDVAGIIADVAASLLPSG GERGROGGSCLGGVGGMGSLSGGGGGATAQVSNILGHDYGGTDLL MKDDGSFCVCRNNNVGPIAPDRACHLDVAGIIADVAASLLPSG RLTRRMSLLSVVSTASHTGEBPBLGPPASTAVDNMSASSSSVDSD PBSTRRELUTKLPGGDLYNMNQDLABUKILDVD  6550 2293 922 FRVSRIGADGCJERMGLAMHRIGGSYARAGGSSGGWYYLRYPF LYSKLIGHLIIGHLWVGXNHVSLAGATERRASGLYSQ LLGLTASGSNLYKELNFTTRAKDAIMQMMINARRDLDRINASFR OCGGRVIYTMRQYMAAIILBERGCRODQROMINAGRGIYSQ LLGLTASGSNLYKELNFTTRAKDAIMQMMINARRDLDRINASFR OCGGRVIYTMRQYMAAIILBERGCRODQROMINAGIDARINASFR LDNLGTANJAPHGGSILASTRACDGHMSSSKVELBASGLAD IERVARRSDLORQKLERAQGELRASGCAKQKVEKBAQARRAKLQ ABGSROTGLABERRAVIRKERNILAKELEEKKRERAGGLRMELAT RNSALDTCIKTKSQPMPWSPRMGPWSPSSSKVELBASGLAD IERVARRSDDLORQKLEAQGGLRASGCAKQKVEKBAQARRAKLQ ABGSROTGLABERRAVIRKERNILAKELEEKKRERAGGLRMELAT RNSALDTCIKTKSQPMPWSPRMGPWOPP IDPASLEEPKRKI LBSGRPPAGIPVDASSG  6551 157 748 TQPPDPRNMTLAAYKEMKELPLVSLFCSCFLADPLINKSSYKYE ADTVOLINGCVISIBMEVIELIKKCTSGGSFEVILKPPSFDGVPERM ASLPRRDPSILBEIQKKLBABERRRYGRABLLAMLERLQ EKVICKALEENNDFIKMAKKLLAQNGESNKENRRAHLAAMLERLQ EKVICKALEENNDFIKMAKKLLAQNGESNKENRRAHLAAMLERLQ EKVICKALEENNDFIKMAKKLLAQNGESNKENRRAHLAAMLERLQ EKVICKALEENNDFIKMAKKLLAQNGESNKENRRAHLAAMLERLQ EKVICKALEENNDFIKMAKKLLAQNGESNKENRRAHLAAMLERLQ EKVICKALEENNDFIKMAKKLLAQNGESNKENRRAHLAAMLERLQ EKVICKALEENNDFIKMAKKLLAQNGESNKENRRAHLAAMLERLQ EKVICKALEENNDFIKMAKKLLAQNGESNKENRRAHLAAMLERLQ EKVICKALEENNDFIKMAKKLLAQNGESNKENRRAHLAAMLERLQ EKVICKALEENNDFIKMAKKLLAQNGESNKENRRAHLAAMLERLQ EKVICKALEENNDFIKMAKKLLAQNGESNKENRRAHAAMLERLQ EKVICKALEENNDFIKMAKKLLAQNGESNKENRRAHLAAMLERLQ EKVICKALEENNDFIKMAKKLAQNGESNKENRRAHLAAMLERLQ EKVICKALEENNDFIKMAKKLAQNGESNKENRRAHALAAMLERLQ EKVICKALEENNDFIKMAKKLAGGGGDNAMMINKRREPTC SQNSIFPVPOMILLLADENGGGGOLLAGFAKKACHLEDGTG SANAMT TYPV RPBLEIDDT ANGROGGONDFIRMAKKRICHAAR GREIDTN YNAGSVLSKAKKATITALBHADDVBB EKRAGLAR	1			
VLERLERMGCRI MRRPQALINCUNKEWPEQBLAGHGUPL.PDTPEE YGGRISPRAM IDRARVLEPPMVUNTTGRIRGKAVPILARDKHILA DLSHLIRHEAPYLFQKTVKESKGRDVRVITVGGRVUGTMLRCST DGRMQSNCSLGGVCMMCSLSBQGKQLATQWSNILADVGGTULGCST DGRMQSNCSLGGVCMMCSLSBQGKQLATQWSNILADVAGSLLFSG RLTRRMSLLSVVSTASSTSEPBIGPPASTAVDMRSASSSSVDSD PBSTERBLITKILPGGLYMMSQLLANBIKGLYMD 6550 2293 922 FRVSRDGAPDGSISMGLAMBIGGSYARAGGSSRGCWYYLRYPFP LFVSLLQPILIGLULEMVYGSWHYSTESSLQATERRABGLYSQ CQGDEVITYNNQRYMAATILEBKQCROQFKDHNKSCDALLFML NQKVKTLVEVLAKERTICTTRURSSVLINKRYAEBQLVECVKTRE LGHQERQLAKBQLGRVQALCLELDDKKFEDDKRENDLSSFRGCLYSY LDRIGSVNLTKKLRDGSNLTKKLINGTTARADATWAEBQLVECVKTRE LQHQERQLAKBQLGRVQALCLELDDKKFEDDKRENDLSFRSLAD TREVARENDLQROKLARGQGGRASGKVYKRAGRARALQ AECSROTOLALBERKAVLRKERDLGKFKFERARQLRMBLSITERS LDRIGSVNLTYLKTSQDMPWSRPMGPVPDPQPIDPASLBEFKKL LESQRPPAGIPVAPSSC 6551 157 748 IQPPDPRMNTLAAVKERMKELPLUSLFCSCFLADPLINKSSYKYE ASLPRRDPSLBETQKKLRAAKGREEPKKYORABLLAKHLARKREHBE EVIQKAIBENNPIHMAKEKLAGRESKKYUGBALLAKKREHBE EVIQKAIBENNPIHMAKEKLAGRMSSNKENRRAHLAAMLERLQ KRURHABEVRRINKELKERASR 6552 157 748 IQPPDPRNNTLAAVKERMKELPLUSLFCSCFLADPLINKSSYKYE ASLPRRDPSLBETQKKLRAAKGREKKYQGBBLLKHLAKKREHBE EVIQKAIBENNPIHMAKEKLAGRMSSNKENRRAHLAAMLERLQ KRURHABEVRRINKELKERASR 6553 2 1807 FVMSKMAARLSYGRWINIVLRERVGREDSHLIKHERKERHBE EVIQKAIBENNPIHMAKEKLAGRMSSNKENRRAHLAAMLERLQ KRUKHABEVRRINKELKERASR 6553 2 1807 FVMSKMAARLSYGRWINIVLRERVGREDFRADVINITFEFV RPILELMDITAENVLSEDRRGPTROPHILPVPRRSLLCEQRLKD LGVIGSFHIRBSYSLDLIPPODLLISHBSGRFKCYLEGGOTS SQNSIFPVFDNLLLLDENNDLLTPLATOILTYBGLLDETYGGON YVKLPPEKRAPKKGGGGROLPTRAKKLQUNSABELYAEIRDKN YNAVGSVLSKKAKTISAAFERRHAKTVGSLKQFVSQLPHQAA RGSLANHTSIABLIKDVTTSEDFPCKLTVGERRGGIDTDKVNN YIEDCLARQKHSLIKURLGVSCNGSLKQKVLDYYKREPLOT YGYEHLTLIHDLERKGPLGCGGRNYYPTIRKTERLMMDDVNB QNPTDISYVYSGYAPLSVRLAQLLSRYGGGRNYPPTIRKTERLMMDDVNB QNPTDISYVYSGYAPLSVRLAQLLSRYGGGRNYPPTIRKTERLMMDDVNB QNPTDISYVYGGYAPLSVRLAQLLSRYGGGTERELEEVLRILDGUN BRRQELPTGLQKKRQEGRNYVDLTFLGGGTTARKITARLMMDDVNB QNPTDISYVYSGYAPLSVRLAQLLSRYGGTERSLEEVLRILDEDGIL BRRQELPTGLQKKRQEGRNYVDLTFLGGGTTARLTALMMDDVNB	1	[		
VGGHZMPAKH IDRAKVLEPMVUNTTGJHGKAVFLARDKHHLA DLSHLIRHBAPYLPQKYVKESHGRDVYIVVGGRVVGTMLRCST DGMQSNCSLGGVGMMCSLSGQKQLLAIQVSNILGMDVCGIDLI, MKDDGSFCVCRNANVGFIAPDKACHLDVAGIIAPDKASLLPSG RLTRRRMSLLSVVSTASETGBERLQFSATAVINMSASSSVDSD PBSTERBLITKLPGGLYMMGLANBIKLIVD  6550 2293 922 FRVSRGAPDCSIEMMGLANBIGGSYARAGSSSRGCWYYLRYPP LFVSLLQFILIGLIVLFMVYCNVTPSSNLQATERRAEGLYSQ LLGITASQSNLTKELNFTTRAKDAIMMMINARROLDRINASFR QCCGDRVITYNNQRYMAAIILSBCDGFKDMKSCDALLFMLP NQKVKTLEVBIAREKTICTKDKBSVLINKRVABEQLYBCVKTRE LONIGSRUTYTNNQRYMAAIILSBCDGFKDMKSCDALLFML NQKVKTLEVBIAREKTICTKDKBSVLINKRVABEQLYBCVKTRE LONIGSRUTYNNQRYMAAIILSBCLAFSKRAD IERVARENSDLOKOKLBAQQGLRASQBAKOKVKBRAQARBAKLQ ABCSBOTOLALBEKAVLRKERIDLAKERBKKRERKKREAGLRBELAI RNSALDTCTKTKSQPMMPVSRPMGPVDNPQPIDPASLBEFFRKK LBSQRPPAGIPVAPSSG 157 748 1QPPDPRINTLANYKERMKBLPLVSLFCSCFLADPLNKSSYKYE ADTVOLNWCVISDMEVIBLNKCTSGQSPEVILKPPSPDGVPEPN ASSLPRRRPPSJBETQRKLBAABERRRYQGABLLKHLARKREHBR EVJQKAJBENNNYFIKMAKBLLARMERNLAMLERILQ EKOKHABEVRKNKELKBRASR 6552 157 748 1QPPDPRINTLANYKERKKELPLVSLFCSCFLADPLNKSSYKYE ADTVOLNWCVISDMEVIBLNKCTSGQSPEVILKPPSPDGVPEPN ASSLPRRRPPSJBEIGKLBBAABERRRYQGABLLKHLARKREHBR EVJQKAJBENNNYFIKMAKBLLARMFSNKANBRAHLARMLERILQ EKOKHABEVRKNKELKBRASR 6553 2 1807 FVMSKMAAHLSYGRVNLNVLREAVRRELEFFLDKCAGSKAIVWD EVJTGPFGLJAQYSLKEHEVBRWFTLKGNRLPAADVKNIIFF RPLIELMDIIARNVLSDDRRGPTRDPHILFPVBRSLLCEGRIKD LQULGSFIRRBYSIGLIPPDGDLLSMESSGAFRECYLEGDQTS VYNLPPEKRAPKKGEGGSKDLPTPAKKLQLNSABERLCEGRIKD SQNSIFPVBDLLLLDRNVDLLTPLATDLTYGGLIDEIYGIQNS VYLLPPEKRAPKKGEGGSKDLPTPAKKLQLNSABERLYRREITERMDDVBR RGSLANHTSIABLI KDVITTSEDPFDKLITVEGLIDEIYGIQNS VYLLPPEKRAPKKGEGGSKOLLPTBKKNN RSALARHTSIABLI KDVITTSEDPFDKLITVEGLIDEIYGIQNS VYLLPPEKRAPKKGEGGSKOLLPTBKKNN RSALARHTSIABLI KDVITTSEDPFDKLITVEGLIDEIYGIQNS VYLLPPEKRAPKKGEGGSKOLLPTBKKNN RSALARHTSIABLI KDVITTSEDPFDKLITVEGLIDEIYGINS VYLLPPEKRAPKKGEGGSKOLLPTBKKRILANARTHSGL RSALARHTSIABLI KDVITTSEDPFDKLITVEGENSGLKOLLDYKRENDRING PROTDISYVYSGYAPLSVRILRUCLQSVCRSGLKOVLDYVKREILDFIPGIPF RSRQPLPTGLKKRURGPCRNNVTLIFFLEGVFTFALIAALRFLSGL	1			
DLSHLIRHERPYLFOKYVKESHGEDVRVITVEGGRVCFMILRGST DGRMQSNCSLGGVGMNCSLSBQGKQLAIQVSNILGMDVCGIDLL MKDDGSFCVCRANANOFLAPUKACHLOVAGI IADYAASLLPSG RLTRINGLISJVVSTASETGEFLOPPASTAVINMSASSSSVDSD PSSTERRELITKLEGGLAPMINGLANE KLLVD PSSTERRELITKLEGGLAPMINGLANE KLLVD  6550  2293  922  FRVSRDGAPDCGLEGMGLAMEHGGSYARAGGSSRGCWYYLRYFF LFVSLLQFIJILIGLVLMVYCNVHVSTESHLQATERRAEGLYSQ LLGLTASQSNLTVEKKIPTTRAKADIMOMINARROLDRINASFR QCQGDRVIYTNINQRYMAAIILSBKQCRDQFKDMIKSCDALLFML NQKVKTLEVEILARERTICTKDRESVILINKRVABEQLVECVKTRE LDRIGGRQLAKEQLOXVQALCLFLDDKKYFEMDLRNLWRSIIPRS LDRIGGRQLAKEQLOXVQALCLFLDDKKYFEMDLRNLWRSIIPRS LDRIGGRQLAKEQLOXVQALCLFLDDKKYFEMDLRNLWRSIIPRS LDRIGGRQLAKEQLOXVQALCLFLDDKKYFEMDLRNLWRSIIPRS LDRIGGRQLAKEQLOXVQALCLFLDDKKYFEMDLRNLWRSIIPRS LDRIGGRQLAKEQLOXVQALCLFLDKKYFEMDLRNLWRSIIPRS LDRIGGRQLAKEQLOXVQALCLFLDKKYFEMDLRNLWRSIIPRS LDRIGGRQLAKEQLOXVQALCLFLDKKYFEMDLRNLWRSIIPRS LDRIGGRQLAKEQLOXVQALCLFLDKKYFEMDLRNLWRSIIPRS LDRIGGRQLAKEQLOXVQALCLFLDKKYFEMDLRNLKRSIIRAD TERVANERBODLORQKUARQQCLARSQCKVVEKFAQARRAKLQ AECSRQTQLALBERAVLRKERAGQGSREVTUKPSFTDGVPENN ASLERRRDPSLEELGKALBAQGGLARSQCKVLKPSFTDGVPENN ASLERRRDPSLEELGKALBAARERRYQGRAELLKRPSFDGVPENN ASLERRRDPSLEELGKALBAASERRYQGRAELLKEPSFDGVPENN ASLERRRDPSLEELGKALBAASERRYQGRAELLKHPSFDGVPENN ASLERRRDPSLEELGKALBAASERRRYQGRAELLKHPSFDGVPENN ASLERRRDPSLEELGKALBAASERRRYQGRAELLKHPSFDGVPENN ASLERRANGHISTGRAWMNUKBAASERRRYQGRAELLKHPSFDGVPENN ASLERRANGHISTGRAWMNUKBAARERRRYDGRAERLEKREBRE EVIQKAIEENNNFIKMKELLKBAASR  6552  1807  1807  FVINKMAAHLSTGRAWMNUKBAARERRRYDGRACKTLEGDGTS LYHAARGLMYLOALYGTIPQIFGKGCARQVANMIRMKREFTG SQNSIFFVYBGDFULLLLDRNVDLLTPLATQLTYBGLIDEIYGIQNS VYLLPPEKRAPKRGGGGGKULPTBAKKLQLNSABELYGETGGNS LYHAARGLMYLQALYGTIPQIFGKGCARQVANMIRMKREFTG SQNSIFFVYBGRAAHLSTGARGGGRULPTBAKKLQLNSABELYGREGTDTDKVNN YEBDELTAGRHSLIKVLELVCLOGVCNSGLKKYLDYYRFELLGT YGGELHTHBILBERGREFRENATVUGEIKGFVSQLPHMQAA RGSLANHTSIABLIKUTUTSEDFFDKLTVERGEFRINGTDTDKVNN YEBDELTAGRHSLIKVLELVCLOGVCNSGLKKYLDYYRFELLGT YGGELTAGRASLIKVLELVCLOGVCNSGLKKYLDYYRFELLGT YGGELTAGRASLIKVLELVCLOGVCNSGLKKYLDYYRFELLGT RGCANHTITLBRRAGGLKEPTGGRNYTTETRTHRUMDDVWE QN		ļ		
DGMMQSNCSLGGUGHMCSLSBQRQLAIQVSNILGMDVGGILL MKDDGSFCVCRANANVGPIAPDRACHLOVAGIIADYAASLLPSG RLTRRMSLLSVVSTASBTGBEBLJPPASTAVDNMSASSSVDSD PBSTERBLITKLPGGLYMMNQLLANBEKLLVVD  6550 2293 922 FRVSRGADDGGIEGMGLAMEGEGAPAGGGSSEGMYYLRYPF LFVSLIQFLIILGLVLFMVYCNVHVSTESNLQATERRABGLYSQ LLGITASQSNLTKKLNFTTRAKDAIMQMINARRDLDDEINASFR QCQGDRGVITTNNQRYMAAIILSBCDQFQFKDMNSCCALLFFUL NQKVKTLEVBIARBKTICTKDKBSVLLINKRVABEQLVECVKTRE LQHQERQLAKEQLQXVQALCLPLDKDKFEMDLRNLMRDSIIPRS LDNLGYNLHPHJGSSIASIRRACHPHSIMSSKVEBLARSIRRAD IBRVARENSDLOKQKLBAQQGLRASQBAKQKVEKBAQARBAKLQ ABCSGTOLALBERKAVLBKRERDISKLEEKKRRBGDLTMSLATI RNSSALDTCIKTKSQDMDVSPPMGPVPNPQPIDPASLBEPKRKI LBSQRPPAGIPVAPSG  6551 157 748 1QPPDPRNNTLABYKERNKELPLVSLFCSCFLADPLNKSSYKYE ADTVQLINWCVISDMSVIBLANKCTSGQSFSVILKPPSFDGVPEPN ASLPRRDPSLBEIQKKLBAABRRRKYQBAKLLHLAEKREHBR EVIQKALBENNNFIKMAKBKLAQKMESNKENBRAHLAAMLERLQ EKNKHABEVRKNKELKBRASR 1QPPDPRNNTLASYKERNKELDFLVSLFCSCFLADPLNKSSYKYE ADTVQLINWCVISDMSVIBLINKCTSGQSFSVILKPPSFDGVPEPN ASLPRRDPSLBEIQKLBABBRRKYQBAKLLKHLAEKREHBR EVIQKALBENNNFIKMAKBKLAQKMSSNKENBRAHLAAMLERLQ EKNKHABEVRKNKELKBRASR 1QPPDPRNNTLASYKENKELREASR 6552 157 748 1QPPDFSNNTLASYKENKELKBRASR 6553 2 1807 FVMSKMAAHLSYGRVNLDVLFEGSCFLADPLNKSSYKYE ADTVQLINWCVISDMSVIBLINKCTSGQSFSVILKPPSFDGVPEPN ASLPRRDPSLBEIQKLBABRRRKYQBRILKHLAEKREHBR EVIQKAJEENNNFIKMARBKLAQKMSSNKENBRAHLAAMLERLQ EKNKHABEVRINKELKBRASR 6553 2 1807 FVMSKMAAHLSYGRVNLDVLFEQUFTERSLLCEQRLKD LGVLSSFIRRBYSLDLIPFDGLISMBSBGAFKRYZUEGDQTS SQNSIFPVEDNILLLIDRINVDLLTPLATDLTVEGLIDEITYGIQNS VYKLPPEKRAPKKQBGGSKOLPFPRAKKLQUNSABELYABIRDKN FNAVGSVLEKKAKIISAAFBERNATVGEIKOPVSQLPHMQAA RGSLANHTSIABLIKDVTTSDDFFOKLTVEGEINDEIYGIQNS VYKLPPEKRAPKKQBGGSKOLPFPRAKKLQUNSABELYABIRDKN FNAVGSVLEKKAKIISAAFBERNATVTGEIKOFVSQLPHMQAA RGSLANHTSIABLIKDVTTSDDFFOKLTVEGERMSGIDTDKVNN FNAVGSVLEKKAKIISAAFBERNATTVGEIKOFVSQLPHMQAA RGSLANHTSIABLIKDVTLSDDFFOKLTVEGERMSGIDTOKVNN FNAVGSVLEKKAKIILARLKCHLAULLAGLLEEVERSIELEEVLRILLPGPHF BRQPLPTGLKKKRQPCGRNENTTLIFFLGGVFFASLIAALRFLSQL GNPTDISYVYSGYAPLSVKLAULLLCLGGVCNSGELKOTLDSVKREDIGFF				
MKDDGSPCVCRANANGPTAPDRACKIDVAGIIADYAASILPSG RLTRRMSLLSVVSTASBTSEPELGPASTAVDNMSASSSVDSD PBSTERRELITKLEGGLYMNINGLAMEIKILDUD  6550 2293 922 FRVSRDGAPDCGIEGMGLAMERIGGSVARRGSSRSCMYTLRYPP LFVSLIOPLIILGULFMYCRVIVVSTESNLQATERRAEGLYSQ LLGLTASQSNLTKKEMPTTRAKDATMQMINARRDLDRINASPR QCQGDRVITYNNQRYMAAIILEBRQCRDQFKDMMKSCDALLFYNL NGKVKTLEVBIARKRTICTKDRUILMRKRAEGLYSQCWKTRE LQHQERQLAKEQLQKVQALCLPLDKDKFEMDLRNLWRDSIIPRS LDRIGYNLMHPLGSBLASIRRRCDHMPSIMSKVEELARSLRAD IRRVARENSDLQKOKKLEAQQGRSQARQKVERRAGQARRAKLQ AECSBOTQLALBEKAVLRRERDNLAKELEBEKRRAGARRAKLQ AECSBOTQLALBEKAVLRRERDNLAKELEBEKRREAGDLRMELAI RNSALDTCIKTKSQPMMPVSRPMGPVPPDPDFDSLEBEKRKL ABCYDPAGIPVAPSSG 6551 157 748 1QPPDPRNMTLAAYKEKMKBLPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIBLINKCTSQGSPEVILKPPSPGVPEPN ASLPRRNDPSLBEIGKKLEAARBRRKYQBABLLKHLABKKEHER EVIQKAIERNNNFIKMAKEKLAQKMESKKRNRAHLAAMLERLQ EKKKHABEVYRKNELKERRASR ASLPRRNDPSLBEIGKKLEAABERRKYQBABLLKHLABKKEHER EVIQKAIERNNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKKKHABEVRKNELKERRASR 1QPFDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLIMUCVISDMEVIBLINKCTSQGSPVILKPPSPGUPERN ASLPRRNDPSLBEIGKKLEAABERRKYQBABLLKHLABKKEHER EVIQKAIERNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKKHABEVRKNKELKERRASR 1QPFDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLIMUCVISDMEVIBLINKCTSQGSPVILKPBFSDGVERFN EVIGKAIERNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKKHABEVRKNKELKERRASR 5553 2 1807 FVMSKWAAHLSYSKAVNLINVIRREAVEREIRBFLDKCAGSKAIVWD BYLTGPFGLIAQYSLLKEHEVSKMFTLKGNRLPAADVKNIIFFV RPRLEILIDIILARNVISEBORROPTROPHILTPVPRRSLLCEQRLKD SQMSIPPVPDNLLLLDRNVOLLTPLATQLIYEGILDESYGIQMS YVKLPPEKRAPKKQGGGGGDLPTERKKLQUINSARBIYABITDRN FNAVGSVLSKKAKIISABFERRNKTVGBIENGFYGENDEFNG LYHAARGLMTLQALYGTJERQFFKSCULDCYSLEPHMQAA RGSLANHTSIABLIKOVTTSBDFFVGLVILVPGEFMSGIDTDKVNN YIEDCLTAQKHSILKVILRUCLOSVCNSGLAQKVLDYYKRELLCT YGYEHILITLINLEKAGULKPQGGRNNYPTIRKTTALRIJMDDVMB QNPTDISYVYSGYAPLSVURAQLLSPPGWSIBEVURILDGIPGPHF BRRQPLPTGLQKKRQBGGRNDLPTRKKILLKBILLGDLRILGDRIKG GNEHILTHRINGENGSTEBEVIR BERGERINDDWB QNPTDISYVYSGYAPLSVURAQLLSPPGWSIBEVERILDFIPGPHF BRRQPLPTGLQKKRQBGRNAVULLITFREGGYFFAELAALRELSGL	i	ì		
RLTERMSLLSVYSTASSTSEPBLGPPASTAVDNMSASSSSVDSD  6550  2293  922  FRYSRDGAPDCGTEGMCLAMERIGSVARACGSSRSCWYYLRYPF LFYSLIQFLIILGLVILAWICHNIVDLANE ILLAUD  COCGDEVITINGRYMATULESCRECKPYTLRYPF OCGDEVITINGRYMATULESCRECKPYTLRYPF OCGDEVITINGRYMATULESCRECKPYTLRYPF OCGDEVITINGRYMATULESCRECKPYTURKSCHALLFYLL NQKVKTLEVBLAKEKTICTKDKESVILLNERVAERDLOVCVKTRE LQHOERQLAKEQLQKVQALCLPLDKKFEMDLRRILMDSIIPRS LDNLGYNLYHPLGSBLASIERACDEMPSLMSSKVEELARSLRAD IERVARRISDLOROKULBAQGGLRASGEAROKVEKKAQARRAKLQ AECSROTOLALEEKAVLRKERDNLAKELEEKKREAEQLRMELAI RNSALDTCIKTKSQPMPDVSRPMGVPPPQPIDPASLEEKKRK AECSROTOLALEEKAVLRKERDNLAKELEEKKREAEQLRMELAI RNSALDTCIKTKSQPMPDVSRPMGVPPPQPIDPASLEEKKRK LESQRPPAGIPVAPSSS  6551  157  748  IQPPDPRIMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVOLINGVISHMEVISHMKCTISQQSFEVILKPPSFDGVPERN ASLPRRDPSLEBIORKLEARASRRKYQBABLLAHLARKREHER EVIQKAIEENINPINAKKKLAQKMESNKENREAHLAAMLERLQ KENKHAEEVRINKELKERASR  6552  157  748  IQPPDPRIMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVOLINGVISHMEVISHMKCTISQQSFEVILKPPSPDGVPERN ASLPRRDPSLEBIOKKLEABASERRKYQBABLLKHLAEKREHER EVIQKAIEENINPINAKKKLAGRMESNKENREAHLAAMLERLQ EKOKHAEEVRINKELKERASR  6553  2  1807  FVMSKMAAHLSYGRVILNVLREAVRRELREFLDKCAGSKAIVWD EYLTGFFGLIAQYSLLKEHEVEKMFTLKGINFLPAADVKNTIFFV RPLLEHMDIIAKNULSBURGPUPHILPVPIRSLLCEDQRLKD LGVLGSFIHREBYSLDLIPFDGDLISHESBGAFKBCCLEGDQTS LYHAARGIMTLQALYSTIQIIFGKGECARQVANMMIEMRREFTG SQNSIFPVFDILLLDRINDLLTPLATQLITYBGLIDEIYGIQINS FNAVGSVLSKKKAKIISAAFERRHINAKTVGBIKDFVSGLDPHMQAA RGSLAMHTSIABLIKOVTTSRDFPDKLTVBOEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLOSVCNSGLKQKVLDYYKRELLQT YQCHILITHINLEKAGLLKPQTGGRNNYPTIRKTIRLRIMDDVBB QNFTISTYYSGYAPLSVELAQLITSPGGWRISTEEVLRILDGPHF BERQPLPTGLQKKRAGREGENDLTFRKKLQINSAEBLYREILDT YQCHILITHINLEKAGLLKPQTGGRNNYPTIRKTIRLIKMDDVBB QNFTISTYYSGYAPLSVELAGLFFFORSERIEEVLRILDGPHF BERQPLPTGLQKKRAPALSQULRPPGGRNNYPTIRKTIRLRIJMDDVBB QNFTISTYYSGYAPLSVELAGREFFERERERISTLEGUR LIDGPHF	1			
PRSTERELLTKLÞGGLFNMMQLLANE KKLUVD  FRVSRDGAPDUGIEQMGLANEHGGSYARAGGSSRGCWYYLRYPP LFVSLLQFLI ILGLULFMVZCNVHVSTESNLQATERRÆGLISQ LLGLTASQSNLTKKLNFTTRAKDAIMQMINARRDLDRINASPR QCQGRVIYTNNQRYMAAIILSEKQCRQPKDNNKSCDALLFML NQKVKTLEVSLIAKEKTICTKDKSSVLLNKRVAERQLJVCVKTRE LQHQERQLAKKQLQKVQALCLFLDKDKFEMDLRNLNKDSIIPRS LDMLGYMLYHPLGSBLASIRRACDHMSSLMSSKVEELARSLRAD IERVARENSDLQKQKLEAQQGLRRSQEAKKVEKRAQARBAKLQ AECSBOTQLALBEKAVLRKERDNLAKKLEKKKRABDLRHELAI RNSALDTCIKTKSQPMMPVSRPMGPVPNPQPIDPASLEBFKKL LESQRPPAGIPVAPSSG  157 748 IQPDDRNMTLANYKEMKBLPLVSLFCSCFLADPLNKSSYKVE ADTVOLNMCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPERN ASLPRRDDSLEEIQRKLEAABERRKYQBABLLKHLAEKREHBR EVIQRAIBENNNTIKMAKEKLAQKMESNKENNRBAHLAAMLERLQ EKDKHABEVKRNKELKERAS ASTLPRRDDSLEEIQKKLEAABERRKYQBABLLKHLAEKREHBR EVIQKAIBENNNTIKMAKEKLAQKMESNKENNRBAHLAAMLERLQ EKDKHABEVKRNKELKERASS ASTLPRRDDSLEEIQKKLEAABERRKYQBABLLKHLAEKREHBR EVIQKAIBENNNTIKMAKEKLAQKMESNKENNRBAHLAAMLERLQ EKDKHABEVKRNKELKERASS ASTLPRRDDSLEEIQKKLEAABERRKYQBABLLKHLAEKREHBR EVIQKAIBENNNTIKMAKERLAQKMESNKENNRBAHLAAMLBRLQ EKDKHABEVKRNKELKERASS  6553 2 1807 FVWSKMAHLSYGRVENINVLÆRAWRELEBFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLDAADVKNIIFPV RPRLEIMDIIARNVLSEBRRGPTRDPHILFVPRRSLLCEQRKED LGVIGSFIHREBYSLDLIPPDGDLLSMESGGFRECYLEGDQTS LYHAAKGIMTIQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIPPVPDNLLLLDRNVDLIPPLATQLTYBGLIDEIYGIGNS YVKLPPEKFAPKKQGGGGKDLPTEAKKLQUNSABBLYABIRDKN FNAVGSVLSKKAIISAAPERRNARTVGEIKGFVSQLPHMQAA RGSLANHTSIARLIKUVTTSEDPFDKLTVEQEFRMSGIDTDKVNN YIEDCIAQKHSLIKVLELUCLQSVCNSGLKQKULDYYKREILGT YGYEHILTLIHNLEKAGLLKPQTGGRNNYPTIRKTLRIMMDDVNB UNPTDISYVYSGYAPLSVRAUGLISRPGWSIEEVLRILPGPHIP BRRQPLPTGLQKKRQFGGRNVTLIFFLGGVTFABLIAALRFLSQL	ļ			
FRVSRDGAPDCGIEGMGLAMEHGGSYARACGSSRGCWYYLRYFF   LFVSLIQFLIILGIULFMVYCNVHUYSTESALQATERRAEGLYSQ   LLGITAGGSNITKKLNFTTRAKDATMGMINTARRADLDR INASFR   QCQGDRVIYTNINQRYMAAIILSEKQCRDQFKDMNKSCDALLFML   NQKVKTLEVEIJAKEKTICTKDKESVILINREVAEEQLVECVUKTRE   LOHIGYNLYPHIGSBLASIRRACDHMPSLMSSKVEELARSLRAD   IRRVARENSDLQRCKLEAQGGLRRSGEKQKVEKRAQARRAKLQ   AECSBOTQLALBERAVIRKERREDNIAKELEEKKREABGLRMELAI   RNSALDTCIKTKSQPMHDVSRPMGPVPNPQPIDPASLEEFKKI   LESQRPPAGIPVADPSG   157				
LFVSLIQFLIILGLVLFMVYGNVHVSTESNIQATERRARGLYSQ LLGITASQSNITKKLINFITRANDAIMMINARRDLDRINASFR QCQGDRVIYTMNQRYMAS ILSBEQCROPFKDMKSCDALLFML NQKVKTLEVEIAKEKTICTKDKBSVLLNKRVAEBQLVECVKTRE LQHQERQLAKKQLQKVQALCLPLDKDKFEMDLRNINKDSIIPRS LDNLGYMLYHPLGSBLASIRRACDHMPSLMSSKVEELARSLARAD IERVARENSDLQKQKLEAQQGLRRSQGRAKVSKKBQARBAKLQ AECSBOTQLALBEKAVLRKBRDNLAKKLEKKKRABQLRMELAT RNSALDTCIKTKSQPMMPVSRPMGVPDPPQPIDPASLEBFKKI LBSQRPPAGIPVAPSSG ADTVOLNWCVISDMEVIRLNKCTSQGSFEVILKPPSFDGVPEFN ASSLPRRRDPSLEEIQKKLBABARBRRKVQRABLLKHLAKREHER EVIQKAIEENNNTIKMAKBKLAQKMESNKENRBAHLAAMLERLQ KKDKHABEVYRKNKELKBRASR  6552 157 748 IQPDPRNMTLAAYKEMKELPLVSLFCSCFLADPLNKSSYKVE ADTVOLNWCVISDMEVIBLNKCTSGQSFEVILKPPSFDGVPEFN ASILPRRDPSLEEIQKRLBABERRKVQRABLLKHLAEKREHER EVIQKAIEENNNTIKMAKBKLAQKMESNKENRBAHLAAMLERLQ EKDKHABEVRKNKELKBRASR  6553 2 1807 FVWSKMABHLSYGRVNINVIRRAWRELREPLDKCAGSKAIVWD EKDKHAEVRKNKELKEBASR 6553 2 1807 FVWSKMABHLSYGRVNINVIRRAWRELREPLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLBEMDILBENDALTARBVLSEDRRGPTRDHILLFVPRRSLLCEQRLKD LGYLGSFIHRBYSLOLIFPGGLLSMESBGAFKECTLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKBCARQVAMMIRKKEFTG SQNSIFPVFNNLLLDRNUDLTPLATOLTYBGLIDEIYGIGNS YVKLPPEKFAPKKQGJGGKOLPTBAKKLQLNSABBLYARIRDKN 7:NAVGSVLSKKAIISABAFERRINTOGEIKQFVSQLPHMQAA RGSLANHTSIRABLIKDVTTSEDFFDKLTTVGBFMSGLDTDKVAN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLIHNLEKAGLLKPQTGGRNNYPTIRKTLRIMMDDVNB BRQPLPTGLQKKRQLEKPCTLIFLGGHF BBRQPLPTGLQKKRQPGERKVTLIFFILGGVTFABLAALARFLSQL	6550	2203	922	
LIGITAGOSNITKEINPTTRAKDAIMOMMINARRDIDRINASFR QCQGDRVIYTMORYMAAIILESEKGCROOFKDMINKSCDAILFFIL NQKVKTIEVBIAKERIICTROKESVILINKRVABEQI/VECVKTRE LQHQERQIAKEQIQXVQALCI-PIDKOKFEMDIRNIMRDSIIPRS LDNIGYMIYHPIGEBIASIRRACDHIPSIMSSKVEEIARSIRAD IERVARRINSDI-QKOKIBAQOGILRASQEARGVVEKEAQARRAKIQ AECSROTQI-ALBEKAVIRKERDNIAKELEEKKREAEQIRMELAI RNSAIDTCIKTKSQPMBVSRPMGPVPNPQPIDPASI-BEFKRKI LESGRPPAGITVAPSSG ADTVOLINWCVISDMEVIBINKCTISQSFRVIIKPPSFDGVPERN ASIPRRDPSIBEIQKILBABERRRYQBRBLIAHILABKREHER EVIQKAIBENNNFIKMAKEKLAQKMESNKENRRAHLAAMLERIQ EKNKHABEVKRNKELKERASR ADTVOLINWCVISDMEVIBINKCTISQSFRVIIKPPSFDGVPERN ASIPRRDPSIBEIQKKLEAASERRRYQBRBLIAKHIABKREHER EVIQKAIBENNNFIKMAKEKLAQKMESNKENRRAHLAAMLERIQ EKNKHABEVKRNKELKERASR ADTVOLINWCVISDMEVIBINKCTISQSFRVIIKPPSFDGVPERN ASIPRRDPSIBEIQKKLEAASERRRYQBRBLIKHIABKREHER EVIQKAIBENNNFIKMAKEKLAQKMESNKENRBAHLAAMLERIQ EKNKHABEVKRNKELKERASR  6553 2 1807 FVMSKMAHLSYGRVNIMVLRRAVERELEFIDKCAGSKAIVWD EYLIGPFGLIAQYSILKEHEVEKMFTLKGNRLPAADVKNIIFFV RPPLIBLMDIIABNULSBORROPTROFHIIFVPRRSILCEQRIKD LGVIGSFIHRENSIJDLIPPTODILISMESGGAFRECYLEGDQTS LYHAAKGIMTIQAIYOTIPQIFGKGECARQVANMIRMRREFTG SQNSIFPVPNNILLILDRNVLLSBORROPTROFHIIFVEGLIDEITGIGNS YVKLPPEKFAPKKQGDGGKDLPTRAKKIQINSAEBLYAEIRDKN 73NVGSVISKKAKIISAAFERRHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIABLIKOVTEDFPOKITUPGENMEGITOTKVMN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILITIINIBRRGILKPQTGGRNNYPTIRKTIRLIMHDDUNB QNPTDISYVYSGYAPLSVRRUVLGGVFRONTPTIRKTIRLIMHDDUNB QNPTDISYVYSGYAPLSVRRUVLIGGVFFABLTAALRFILGQI BERQPLPTGLQKKRQPEGRNVTDITFIGGSFFEVIRIPGPIPF	0550	2293	922	
QCQGRTIYTMNQRYMAAIILSBKQCRDQFKDMNKSCDALLFMI NQKVKTLEVBIAKEKTICTKDKBSVILMKRVABEQLVECVKTRE LQHQERQLAKKQLQKVQALCLFLDKDKFEMDIRNIMRDSIIPRS LDNLGYNLYHPLGSKLASIRRACDHMPSLMSSKVEELARSLRAD IRRVARENSDLQRQKJRAQQGLRASQBARQKVEKRAQARRAKLQ AECSROTQLALBERVAVKRERDNLAKELBEKKREAQCRMELAI RNSALDTCIKTKSQFMMPVSRPMGPVPNPQPIDPASLBEKKRLAI RNSALDTCIKTKSQFMMPVSRPMGPVPNPQPIDPASLBEKKRLAI RNSALDTCIKTKSQFMMPVSRPMGPVPNPQPIDPASLBEKKRLAI RNSALDTCIKTKSQFMMPVSRPMGPVPNPQPIDPASLBEKKRLAI BESQRPPAGIIVAPSSG  157 748 IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKVE ADTVDLIMVCVISDMEVIBLINKCTSQQSFEVILKPPSFDGVPERN ASLPRRDPSLBEIQKULBAABERRRYQBABLLKHLABKREHBR EVIQKAIEENNNFIKMAKEKLAQKMESNKRNRBAHLAAMLERLQ EKNKHABEVKRNKELKBRASR  6552 157 748 IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKVE ADTVDLIMVCVISDMEVIBLINKCTSQQSFEVILKPPSFDGVPERN ASLPRRDPSLBEIQKULBAABERRKYQBABLLKHLABKREHBR EVIQKAIEENNNFIKMAKEKLAQKMESNKRNRBAHLAAMLBRLQ EKNKHABEVKRNKBLKBBASR  6553 2 1807 FVWSKMAAHLSYGRVULNVLREAVRRELREFLDKCAGSKAIVWD EKNKHABEVKRNKBLKBBASR FVUSKMAHLSYGRVULNVLREAVRRELREFLDKCAGSKAIVWD EVILGPFBLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFF RPLELMDIIABKULSQKRESNKRNRBAHLAAMLBRLQ EKNKHABEVKRNLKBLKBEASR FVLGVIGSFIHRBYSLDLIPPFOBLISMBESGAFRBCYLEGDOTS TYTTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFF RPLELMDIIABKLGTTQQIFGKBCAQVANMMIRMKREFTG SQNSIPPVFDNLLLLDRNVDLLTPLATQLITYBGLIDETYGIQNS YVKLPPEKFAPKKGGDGGKDLPTRKKKLQLNSABELYABIRDKN YVKLPPEKFAPKKGGDGGKDLPTRKKKLQLNSABELYABIRDKN YNAVGSVLSKKAKIISAAFERHNAKTVGEIKQFVSQLPHMQAA RGSLAHHTSLABLIKDVTTSBDFPDKLTVTEGDFMSGIDTDKVNN YIEDCIAQKHSLIKVTGLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILITLENLBKAGGLLKPQTGGRNNYFTIRKTLRLMMDDVNB QNPTDISYVYSGYAPLSQLLKPQTGGRNNYFTIRKTLRLMMDDVNB QNPTDISYVYSGYAPLSQLLKPQTGGRNNYFTIRKTLRLMMDDVNB GNPTDISYVYSGYAPLSQLLKPQTGGRNNYFTIRKTLRLMMDDVNB BRRQPLPTGLQKKRQPGENRVTLIFFGGYFFABLAALRFTLSQL	i			
NQKVKTLEVE LAKERTICTKDKESVILINKRVABEQI-VECVKTRE LQHICERQLAKEQI-QKVQALCLI-DKDKFEMDI-RNI-MRDSII PRS LDHILGYNI-HYPLIGSBI-ASI RRACDHMPSI-MSSK-VEELARSLRAD IERVARENSDL-QROKLEAQQGI-RRSQERKQKVEKRAQAREAKLQ AECSROTQI-ALBERHAVI-RRERDNI-AKBI-EEKKREARQLREMKL-A RNSALDTCI-KTKSQPMPDVSEPMGPVPNPQPIDPASI-EEFFRKI LBSQRPPAGI PVAPSSG  157 748 1QPPDPRNMTLAAYKEKMKBL-PLVSLFCSCFLADPLINKSSYKYE ADTVOLI-MVCV I SDMEVI BLINKCTSQ-GS-FEVIL-KPPS-PDGVPEPN ASI-PRRRDPSI-BEI QKKLEAAERRRY-QREAKLL-KHL-ARKREHER EVIQKA I BENNNFI KMAKEKL-AQKMESNKENRRAHL-AAML-ERLQ EKNKHABEVRINKEL-KERRASR  157 748 1QPPDPRNMTLAAYKEKMKEL-PLVSLFCSCFLADPLINKSSYKYE ADTVOLI-MVCV I SDMEVI BLINKCTSQ-GS-FEVIL-KPPS-PDGVPEFN ASI-PRRDPSI-BEI QKKLEAAERRKY-QEARLL-KHL-AEKREHER EVIQKA I BENNNFI KMAKEKL-AQKMESNKENRRAHL-AAML-BRLQ EKNKHABEVRINKEL-KERRASR  6553 2 1807 FVWSKMAHL-SYGRVINI-NI-REAVRREL-REFI-DKCAGSKAI-VWD EYLTGPFG-LIAQY-SIL-KEHEVEKMFTL-KGNRL-PAADV-KNI I PFV RPLIBLI-MDI I ABNVL-SEDRRGPTRDPHIL-EVPRRS-LI-CEQRL-KD LGVI-GS-PI-HREBYSI-DLI-PDG-DLI-SMES-BGAFKECY-LEGDQT-S LYHAAKGL-MTI-QAL-YGTI-PQI-PGKGECARQ-VANMMIR-MKREFT-G SQNSI PPVFDNL-LL-LDRNVDL-LTPL-ATQL-TYBG-LI-DEI YGI-QNS YVKL-PEKK-PAFKKQG-GG-GKD-LPT-BKKL-QL-MSABEL-YAB-I-RDKN YVKL-PEKK-PAFKKQG-GG-GKD-LPT-BKKL-QUI-DEN-MQA-A RGSLANHTSI ABL-I KOVTTSED-FPDKL-TV-SQL-PHMQA-A RGSLANHTSI ABL-I KOVTTSED-FPDKL-TV-SQL-PHMQA-A RGSLANHTSI ABL-I KOVTTSED-FPDKL-TV-SQL-PHMQA-A RGSLANHTSI ABL-I KOVTTSED-FPDKL-TV-SQL-PHMQA-A YSPL-SKKA-KI I SAA-FEERINAKTV-GEI KQFV-SQL-PHMQA-A RGSLANHTSI ABL-I KOVTTSED-FPDKL-TV-SQL-PHMQA-A RGSLANHTSI ABL-I KOVTTSED-FPDKL-TV-SQL-PHMQA-A YEBC-LAQKHSL-I KV-LR-LV-CL-QSV-CNSGL-KQKV-LD-YYR-EL-QT YGYEH LT-L-IN-LE-KAGLL-KQ-T-GGRNN-YFI-TKT-LR-LM-MDDON-B QNFTDIS-YVY-SGYAP-LS-V-R-L-Q-LL-SRP-GWS-I BEVLR-TL-PG-HF BRQ-PL-PTG-LQK-KR-Q-P-G-RN-YT-TI-KT-LR-LM-MDDON-B GNFTDIS-YVY-SGYAP-LS-V-R-L-Q-LL-SRP-GWS-I BEVLR-TL-PG-HF BRQ-PL-PTG-LQK-KR-Q-P-G-RN-YT-L-I-L-PG-HF BRQ-PL-PTG-LQK-KR-Q-P-G-RN-YT-L-I-L-PG-HF BRQ-PL-PTG-LQK-KR-Q-P-G-RN-YT-L-I-L-PG-HF BRQ-PL-PTG-LQK-KR-Q-P-G-RN-YT-L-I-L-PG-HF BRQ-PL-PTG-LQK-KR-Q-P-G-RN-YT-L-I-L-PG-HF BRQ-PL-	1			
LQHGERQLAKEQLQKWQALCLPLDKDKFEMDLRNLMRDSIIPRS LDNLGYNLYHPIGSELASIRAGLHMPSIMSKVEELAASIRAD IERVARRNSDLQRQKLEAQQGIARAGCARKGVEKERQAGRAKICQ AECSRQTQLALEEKAVLRKERDNLAKELEEKKREAQQRRAKICQ AECSRQTQLALEEKAVLRKERDNLAKELEEKKREAQQRRAKICA RNSALDTCIKTTSQPMMPVSRPMGPVPNPQPIDPASLBEPKRKI LESQRPPAGIPVAPSSG  157 748 IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLMVCVISDMEVIBLNKCTSGQSFEVILKPPSFDGVPEPN ASLPRRDPSISEIQRKLEAABERRKYQEARLLKHLAKKREHER EVYQKAIBENNNPIKMAKKLAQRMESNKRNREALLAHLAMLERLQ KKDKHAEEVRKNKELKERASR  6552 157 748 IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLMVCVISDMEVIBLNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRDPSISEIQRKLEAABERRKYQEARLLKHLAEKREHER EVIQKAIBENNNPIKMAKEKLAQKMESNKRNRAHLAAMLERLQ EKDKHAEEVRKNKELKERASR  6553 2 1807 FVWSKMAAHLSYGRVUNVIREAVRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGRRLPAADVKNIIFFV RPRLBLMDIIARVLSGDRRGPTRDPHILFVPRRSLLCCQRLKD LGVLGSFIHRBYSLDLIPPDGDLLSMESGAFKECYLEGDQTS LYHAAKGLMTIQALYGTIPQIPEKGECARQVANMMIRMKREFTG SQNSIPPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGGGGRDLPPEAKKLQINSAEBLYABIRDRN PNAVGSVLSKKAKIISAAPERHNAKTVGEIKQFVSQLPHMQAA RGSLAHHTSIABLIKULRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLINLEKAGLLKPQTGGRNNYPITIKTTLRLMMDDVNE QNPTDISYVYSGYAPLSKLAQLLSRPGWRSIEEVLRILPGHF BRQPLPTGLQKKRQPGENRVTIJIFFLGGVTFAELAARFISQL				
LDNLGYNLYHPLGSELASIRRACDHMPSIMSSKVEELARSLRAD IRRVARRASDLOROKLEAQOGIRASQEAROKVEKAQAREAKLQ AECSROTQLALEEKURKERDNLAKELEEKKREAEQLRMELAI RNSALDTCIKTESOPMMPVSEPMGPVPNPCPPIDPASLEEFKRKI LESGRPPAGIPVAPSSG  157 748 IQPPDPRNMTLANYKEKMKELPLVSLFCSCFLADPINKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSPDGVPEFN ASLPRRDPSLEEIQKKLEAABERRRYQEABLLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKERASR  6552 157 748 IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPINKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN ASILPRRDPSLEEIQKKLEAABERRRYQEABLLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKERASR  6553 2 1807 FVWSKMAAHLSYGRVNINVLREAVRRELREFLDKCAGSKAIVWD EYLIGBFGLIAQYSLLKEHEVEKMETLKGURLPADVKNIIFFV RPRLELMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRKKD LGYLGSFIHRENSYLDLIPFDGDLISMESBGAFKECYLEGDOTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKRETTG SQNSIFPVFDNLLLLDRNVDLITPLATDLTYEGLIDEIYGIONS YVKLPPEKKFAPKKQGGGGKDLPTBAKKLQLINSAEBLYAEIRDKN FNAVGSVLSKKAKI IGAAFERRHNKTVGEIKGFVSQLPHMQAA RGSLANHTSIAELIKDVITSEDPFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLKLUCJOVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKGGLLKPQTGGRNNYPTIRKTLRLWMDDDVNB QNFTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGBHF BRQPLPTGLQKKRQPGENRVTLIFFEGGVTFAEIAALRFISQL	Į į			
IERVARENSDLQRQKLEAQQGLRASQEAKQKVEKEAQAREAKLQ AECSRQTQLALEEKAVLAKREIDNIAKBILEEKKREABQLRMELAI RNSALDTCIKTKSQPMMPVSRPMGPVPNPQPIDPASLEEPKRKI LBSQRPPAGIPVAPSSG  157 748 IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLANGCUISDMEVIBLINKCTSQQSFEVILKPPSFDGVPEFN ASLPRRDPSLEEIQKKLEAAEBERRKYQEABLLKHLAEKREHER BYQQKAIBENNNPIKMAEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKERASR  6552 157 748 IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIBLIKCTSQGSFEVILKPPSFDGVPEFN ASLPRRDPSLEEIQKKLEAAEBERRKYQEABLLKHLAEKREHER EVIQKAIEENNNPIKMAKEKLAQKMESNKRNRBAHLAAMLERLQ EKDKHAEEVRKNKELKEBASR  6553 2 1807 FVWSKMAAHLSYGRVNINVLREAVREIREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLBLMDIIARAVLSKDRRGPTRDPHILFVPRRSLLCEQRIKD LGVLGSFIHREBYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGILDEIYGIQNS YVKLPPEKFAPKKGGDGGKDLPTRAKKLQLNSAEBLYAEIRDEN FNAVGSVLSKKAKIISAAFERERNNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIABLIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGILKPQTGGRNNYPTIRKTLRLWMDDVNB QNFTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF BBRQPLPTGLQKKKQPGENRVTLIFFIGGVTFAKIAALRFISQL	1	'		
AECSRQTQLALBEKAVLRKERDNLAKELEKKRREAGLRMELAI RNSALDTCIKTKSQPMBDVSRPMGPVPNPQPIDPASLEBPKRKI LESQRPPAGIPVAPSSG  157 748 IQPPDPRNMTLAAYKEKMKELPLUSLFCSCFLADPLAKSSYKYE ADTVDLNWCVISDMEVIBLNKCTSGQSPEVILKPPSPDGVPEFN ASLPRRRDPSLBEIQKKLEABERRRKYQBABLLKHLABKREHER EVIQKAIBENNNPIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKBRASR  6552 157 748 IQPPDPRNMTLAAYKEKMKELPLUSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIBLINKCTSGQSFEVILKPPSFDGVPEFN ASLPRRRDPSLBEIQKKLEABERRKYQBABLLKHLAEKREHER EVIQKAIBENNNPIKMAKEKLAQKMESNKENRBAHLAAMLBRLQ EKDKHAEEVRKNKELKEBASR  6553 2 1807 FVWSKMAAHLSYGRVNLWVLREAVREELREFLDKCAGSKAIVWD EYLIGPFELIAQVSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPHLBLMDIIABNVLSEDRRGPTRDPHILFVPRSLLCEQRLKD LGVIGSFIHRBEYSLDLIPFOGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFFVFDNLLLLDRNVDLLTPLATQLITYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTBAKKLQLNSAEBLYABIRDKN FNAVGSVLSKKAKIISAAFEERRINAKTVGEIKQFVSQLPHMQAA RGSLANHTSIABLIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLGLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKGALLKPQTGGRNNYPTIRKTLRLWMDDVNB QNFTDISYVYSGYAPLSVRLAQLLSRFGWRSIEEVLRILPGFHF BBRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAELAALRFLSQL	1			
RNSALDTCIKTKSQPMMPVSRPMGPVPNPQPIDPASLEBPKRKI LESQRPPAGIPVAPSG  1QPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNMCVISDMRVIELINKCTSGQSFEVILKPPSFDGVPEFN ASLPRRDPSLEBIQKKLEAAEKRRYQEKELLKHLAEKREHER EVIQKAIBENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKERASR  157 748 1QPPDPRNMTLAAYKEKMELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNMCVISDMEVIBLINKCTSGQSFEVILKPPSFDGVPEFN ASLPRRDPSLEBIQKKLEAAERRKYQEABLLKHLAEKREHER EVIQKAIBENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKERASR  6553 2 1807 FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EKUKHAEEVRKNKELKERASR  6553 1807 FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EKUKHAEBVRKNKELKERASR  6554 EVIGKAIBENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKERASR  6555 EVIGKAIBENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKERASR  6556 EVIGKAIBENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKERASR  6557 EVISKAMAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EKULTGPFGLIAQYSLLKEHEVEKMFILGGNELPEADVKNIIFFV RPRLELMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD LGVIGSFIHREBYSLDLIPPGGLLSMESEGAFRECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFFGKECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVUDLLTPLATQLTYBGLIDEIYGIQNS EVICKIPPEKFAPKRQGJEGGRUDPTERKKLQUNSAEELYABIRDKN PNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIABLIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLELVUCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLERAGILKPQTGGRNNYPTIRKTLRLWMDDVNB QNPTDISTVYSGYAPLSVELAQLLSGRPGWESIEEVLRILDEGHF BERQPLPTGLQKKRQPGENRVTDIFFLGGVTFAKIAALRFLSQL				
LESQRPPAGIPVAPSSG  157  748  1QPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVOLNMCVISDMEVIRLINKCTSGQSFEVILKPPSFDGVPEFN ASLPRRDPSLBEIQKKLEAAERRRKYQEAELLKHLAEKREHER EVYQKAIBENNNFIKWAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKERASR  1QPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVOLNWCVISDMEVIBLINKCTSGQSFEVILKPPSFDGVPEFN ASLPRRDPSLBEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIBENNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKERASR  6553  2 1807  FVWSKMAAHLSYGRVNLNVLREAVRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLBLMDIIARNVLSEDRRGPTRDFHILFVPRRSLLCEQRIKD LGVLGSFIHREBYSLDLIPFDGDLLSMESGAFKECYLEGDOTS LVHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTC SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGTQNS YVKLPPEKFAPKKQGDGGKDLPTBAKKLQLNSAEBLYABIRDKN FNAVGSVLSKKAKIISAAFERRNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKOVTTSEDFFDKLTVEQERMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLINLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISTVYSGYAPLSVRLAQLLSRFGWRSIEEVLRILPGPFF BRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAELAALRFLSQL	<b>!</b>			
157 748 1QPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVOLNWCVISDMEVIBLNKCTSGQSPEVILKPPSFDGVPEFN ASSPRRNDPSLBEIQKKLBAABERRKYQBABLLKHLABKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKOKHAEEVYRKKELKBRASR 6552 157 748 1QPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVOLNWCVISDMEVIBLNKCTSGQSPEVILKPPSFDGVPEFN ASSPRRNDPSLBEIQKKLBAABERRKYQBABLLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENRHAHLAAMLERLQ EKOKHAEEVYRKKELKEBASR 6553 2 1807 FWSKMAAHLSYGRVNINVLREAVRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLBLMDIIAENVLSEDRRGPTRDFHILPVPRRSLLCEQRLKD LGVIGSFIHREBYSLDLIPFDGULSMESBGAFKECYLEGDQTS LYHAAKGLMTIQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNILLLDRNVOLLTPLATQLTYEGIDDEIYGIONS YVKLPPEKFAPKKQGDGGKOLPTEAKKLQLNSAEBLYABIRDKN PNAVGSVLSKKAKIISAAFERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIABLIKOVTTSBDFFOKLTVEQBEMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLINLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISTVYSGYAPLSVRLAQLLSRFGWRSIEEVLRILPGPHF BBRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSQL	1 :			
ADTYDLNWCYISDMEYIELNKCTSGQSFEVILKPPSFDGYPEFN ASLPRRDPSLEEIQRKLEAABERRKYQEABLLKHLAEKREHER EVIQKAIBENNNPIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKERASR  10PPDPRINTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTYDLNWCVISDMEVIBLNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRDPSLBEIQKKLBAASERRKYQBABLLKHLAEKREHER EVIQKAIBENNNPIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEBASR  6553 2 1807 FVWSKMAAHLSYGRVBLINVLREAVRELREFLDKCAGSKAIVWD EYLIGPFGLIAQYSLLKEHEVEKMFILKGNRLPAADVKNIIFFV RPRLBLMDIIAENVLSEDRRGPTRDPHILFVPRRSLLCEQRLKD LGYLGSFIHREBYSLDLIPFDGDLLSMESBGAFKECYLEGDQTS LYHAAKGLMTIQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYBGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTBAKKLQLNSAEBLYABIRDKN FNAVGSVLSKKKAKIISAAFERHNAKTYGEIKOFVSQLPHMQAA RGSLANHTSIABLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEBVLRILPGFPFF BBRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAKIAALRFLSQL	6553	157	740	
ASLPRRDPSLBEIQKKLEAABERRKYQEABLLKHLABKREHER EVIQKAIBENNNPIKMAKBKLAQKMESNKENREAHLAAMLERLQ BKDKHABEVRKNKELKBRASR  10PPDPRWTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIBLNKCTSGQSPEVILKPPSPDGVPBEN ASLPRRDPSLBEIQKKLBAASERRKYQBABLLKHLAEKREHER EVIQKAIBENNNPIKMAKEKLAQKMESNKENRBAHLAAMLBRLQ EKDKHABEVRKNKELKBEASR  6553 2 1807 FVWSKMAAHLSYGRVBLNVLREAVRELREFLDKCAGSKAIVWD EYLITGPFGLIAQYSLLKEHEVEKMFILKENRLPAADVKNIIFFV RPRLBLMDIIAENVLSEDRRGPTRDPHILFVPRRSLLCEQRIKD LGVLGSFIHREBYSLDLIPFDGDLLSMESBGAFKBCYLEGDQTS LYHAAKGLMTIQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYBGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTBAKKLQLNSAEBLYABIRDKN FNAVGSVLSKKAKIISAAFERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIABLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGFHF BBRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAKIAALRFLSQL			, 40	
EVIQRAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKBRASR  1QPPDPRINTLAAYKEKKKELPLVSLFCSCFLADPLINKSSYKYE ADTVULNWCVISDMEVIBLINKCTSGQSPEVILKPPSFDGVPEFN ASI.PRRPDESLBEIQKKLEAAEERRKYQEABLLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEEASR  6553 2 1807 FVWSKMAAHLSYGRVNLINVLREAVRRELREFLDKCAGSKAIVWD BYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLELMDIIAENVLSEDRRGPTROFHILFVPRRSLLCEQRIKD LGVLGSFIHREBYSLDLIPFDGDLLSMESBGAFKECYLEGDQTS LYHAAKGLMTIQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVPDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTBAKKLQLNSAEBLYABIRDKN FNAVGSVLSKKAKIISAAFERRINAKTVGEIKOFVSQLPHMQAA RGSLANHTSIAELIKVUTTSEDFFDKLTVEQERMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLINLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRFGWRSIEEVLRILPGFFFF BRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAKIAALRFLSQL	[	]		
EKDKHAEEVRKNKELKBRASR  1QPPDPRNMTTAAYKEKMKELPLVSLFCSCPLADPLNKSSYKYE ADTVUDLNWCVISDMEVIBLINKCTSGQSFEVILKPPSFDGVPEFN ASLPRRDPSLBEIQKKLBAAEERRKYQEABLLKHLAEKREHER EVTQKAIEENNNFIKMAKEKLAQKMESNKENRBAHLAAMLBRLQ EKDKHAEEVRKNKELKEBASR  2 1807 FVWSKMAAHLSYGRVNLNVLREAVRELREFLDKCAGSKAIVWD BYLTGPFGLTAQYSLLKEHEVBKMFTLKGNRLPAADVKNIIFFV RPRLBLMDILAENVLSEDRRGPTRDFHTLFVPRRSLLCEGRIKD LGVLGSFIHREBYSLDLIPFDGDLLSMESGAPKECYLEGDGTS LVHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNILLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTBAKKLQLNSAEBLYABIRDKN FNAVGSVLSKKAKIISAAFERRINAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKVVTTSEDFFDKLTVEQERMSGIDTDKVNN YIEDCLAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLINLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNB QNPTDISTVYSGYAPLSVRLAQLLSRFGWRSIEBVLRIDFGPFF BBRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAKIAALRFLSQL	1	İ		
157 748 1QPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIBLNKCTSGQSPEVILKPPSFDGVPEFN ASI.PRRDPSLBEIQKKLBAASERRKYQBABLLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKKRREAHLAAMLBRLQ EKOKHAEEVKRKKELKEBASR 6553 2 1807 FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLELMDIIARVLSEDRRGPTROPHILFVPRRSLLCEQRLKD LGVIGSFIHREBYSLDLIPFDGDLISMESGAFKECYLEGDQTS LYHAAKGLMTIQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVENNILLLDRNVDLLTPLATQLTYEGLIDEIYGIONS YVKLPPEKFAPKKQGDGGKDLPTBAKKLQLNSAEBLYABIRDKN FNAVGSVLSKKAKIISAAFERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIABLIKOVITSBDFFDKLTVEQBEMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNB QNPTDISTVYSGYAPLSVRLAQLLSRFGWRSIEBVLRIDFGPFF BBRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSQL				
ADTVOLINGCVISOMEVIBLIKCTSGQSFRVILKPSFPGVPEFN ASLPRRDPSLBEIQKKLBAABERRKYQBABLLKHLAEKREHER EVIQKAIBENNNFIKMAKEKLAQKMESNKENRBAHLAAMLBRLQ EKOKHAEBVRKNKBLKBEASR  6553 2 1807 FVWSKMAAHLSYGRVNINVLREAVRRELREFLDKCAGSKAIVWD BYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLBLMDIIABNVLSEDRRGPTRDFHILPVPRRSLLCEQQTS LYHAAKGLMTLQALYGTIPQIPGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYBGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTBAKKLQLNSAEBLYABIRDKN FNAVGSVLSKKAKIISAAFBERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIABLIKDVTTSBDFFDKLTVBQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLBKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNB QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGPHF BBRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAKIAALRFLSQL	6552	157	749	
ASIPRRDPSLEEIQKKLKAAEERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEASR  6553 2 1807 FVWSKMAAHLSYGRVNINVLREAVRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLELMDIIAENVLSEDRGPTROPHILPVPRRSLLCEQRLKD LGVIGSPIHREBYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIPGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYBGLIDEIYGIQNS YVKLPPEKFAPKKQGGSGKDLPTEAKKLQLNSAEBLYABIRDKN PNAVGSVLSKKAKIISAAFERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIABLIKDVTTSBDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGPHF BBRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAKIAALRFLSQL			, 20	
EVIQKAIEENNNFIKMAKEKLAQKMESNKKNREAHLAAMLERLQ EKDKHAEEVRKNKELKEEASR  6553 2 1807 FVWSKMAAHLSYGRVMINVLREAVRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLBLMDIIAENVLSEDRRGPTRDPHILPVPRRSLLCEQQRTS LGVIGSFIHREEYSLDLIPFDGDLISMESGAPKECYLEGDQTS LYHAAKGLMTIQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTBAKKLQLNSAEBLYARIRDKN FYAVGSVLSKKAKIISAAFERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIABLIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF BBRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAKIAALRFLSQL	]			
EKDKHAEEVRKNKELKEBASR  6553  2 1807  FVWSKMAAHLSYGRVNUNVLREAVRRELREFLDKCAGSKAIVWD  BYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV  RPRLELMDIIAENVLSEDRRGPTROPHILFVPRRSLLCEQRIKD  LGVLGSFIHREBYSLDLIPFDGDLLSMESBGAFKECYLEGDQTS  LYHAAKGLMTIQALYGTIPQIFGKGECARQVANMMIRMKREFTG  SQNSIFPVPDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS  YVKLPPEKFAPKKQGDGGKDLPTBAKKLQLNSAEBLYABIRDKN  FYAVGSVLSKKAKIISAAFBERHNAKTVGEIKQFVSQLPHMQAA  RGSLANHTSIAELIKVVTTSEDFFDKLTVEQEFMSGIDTDKVNN  YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT  YGYEHILTLINNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE  QNPTDISYVYSGYAPLSVRLAQLLSRFGWRSIEBVLRIDFGPFF  BBRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAKIAALRFLSQL	[ ]			
6553 2 1807 FVWSKMAAHLSYGRVNINVLREAVRREIREFLDKCAGSKAIVWD BYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLELMDITAENVLSEDRRGPTROPHILFVPRRSLLCEGORLKD LGVIGSFIHREBYSLDLIPFDGDLISMESEGAFKECYLEGDOTS LYHAAKGLMTIQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQMSIFPVFDNILLLDRNVDLLTPLATQLTYEGLIDEIYGIONS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEELYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIABLIKOVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLINLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISTVYSGYAPLSVRLAQLLSRFGWRSIEBVLRIDFGPFF BERQPLPTGLQKKRQPGENRVTLFFLGGVTFAEIAALRFLSQL	!!			
BYLTGPFGLTAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLELMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEGRLKD LGVLGSFIHREBYSLDLIPFDGDLLSMESEGAFKECYLEGDOTS LYHAAKGLMTIQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYBGLIDEIYGIQNS YVKLPPEKFAPKKQGDGKDLPTBAKKLQLNSAEBLYABIRDKN PNAVGSVLSKKAKIISAAFBERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIABLIKDVTTSBDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLBKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNB QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGPHF BBRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAKIAALRFLSQL	6553	<del></del>	1807	1 - 1
RPRLELMDI IAENVLSEDRRGPTRDFHILFVPRRSLLCEQRIKD LGVIGSFIHREBYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTIQALYGTIPQI FGKGECARQVANMMIRMKREFTG SQNSI FPVFDNILLLDRNVDLLTPLATQLTYEGLIDEI YGIQNS YVKLPPEKFAPKKQGDGKDLFTRAKKIQLNSAEBLYABIRDKN PNAVGSVLSKKAKI ISAAFEERHNAKTVGEI KQFVSQLPHMQAA RGSLANHTSIABLI KDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YTEDCIAQKHSLIKVLKLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLR ILPGPHF BBRQPLPTGLQKKRQPGENRVTLJFFLGGVTFAKIAALRFLSQL			1007	
LGVLGSFIHREBYSLDLIPFDGDLLSMESEGAFKECYLEGDOTS LYHAAKGLMTIQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYBGLIDEIYGIQNS YVKLPPEKFAPKKQGJGGKDLPTEAKKLQLINSAEBLYABIRDKN ?NAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIABLIKDVTTSBDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLBKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNB QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGPHF BBRQPLPTGLQKKRQPGENRVTLJFFLGGVTFAKIAALRFLSQL				
LYHAAKGLMTIQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQMSIFPVFDNLLLLDRNVDLLTPLATQLTYBGLIDEIYGIQNS VVKLPPEKFAPKKQGGGKDLPTRAKKLQLNSAEBLYABIRDKN ?NAVGSVLSKKAKIISAAFBEHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIABLIKDVITSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLKLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLBKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNB QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGPHF BBRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAKIAALRFLSQL				
SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYBGLIDEIYGIQNS YVKLPPEKFAPKKQGGGKDLPTBAKKLQLNSAEBLYABIRDKN FYAVGSVLSKKAKIISAAFEERHNAKTVGEIKOFVSQLPHMQAA RGSLANHTSIABLIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNB QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF BBRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAKIAALRFLSQL	1			
. YVKLPPEKFAPKKQGDGGKDLPTBAKKLQLINSAEBLYABIRDKN F:NAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIABLIKOVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLINLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNB QNPTDISTVYSGYAPLSVRLAQLLSRPGWRSIEBVLRILPGPHF BBRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAKIAALRFLSQL				
PNAVGSVLSKKAKI ISAAFEERHNAKTVGEI KQFVSQLPHMQAA RGSLANHTSIAELI KDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLI KVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLR ILPGPHF BBRQPLPTGLQKKRQPGENRVTLIFFLGGVTFAKIAALRFLSQL	]			
RGSLANHTSIAELIKDVITSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTIHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQDLSRPGWRSIEEVLRILPGPHF BBRQPLPTGLQKKRQPGENRVTDIFFLGGVTFAKIAALRFLSQL	•		•	
YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTIHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQDLSRPGWRSIEEVLRILPGPHF BBRQPLPTGLQKKRQPGENRVTDIFFLGGVTFAKIAALRFLSQL				
YGYEHILTIHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQDLSRPGWRSIBEVLRILPGPHF BBRQPLPTGLQKKRQPGENRVTDIFFLGGVTFAKIAALRFLSQL	j			
QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGPHF BBRQPLPTGLQKKRQPGENRVTLJFFLGGVTFAKIAALRFLSQL		Ì		
BERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAELAALRFLSQL			İ	
KDGGTBYVIATTKLMNGTSWIRALMEKPF		t		
	Ll			KDGGIKYVIATIKLMNGISWIRALMEKPF

			Secretaria de la companya de la companya de la companya de la companya de la companya de la companya de la comp
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
į.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
CET A	sequence	1044	\=possible nucleotide insertion)
6554	119	1244	FEMGSQVSVESGALHVVIVGGGFGGIAAASQLQALNVPFMLVDM
1	1		KDSFHHNVAALRASVETGFAKKTFISYSVTFKDNFRQGLVVGID
ĺ			LKNOMVLLQGGRALPFSHLILATGSTGPFPGKFNEVSSQQAAIQ
	<b> </b>		AYEDMVRQVQRSRFIVVVGGGSAGVEMAARIKTEYPRKEVTLIH
1	1		SQVALADKELLPSVRQEVKEILLRKGVQLLLSERVSNLEELPLN
,	ł		EYREYIKVQTDKGTEVATNLVILCTGIKINSSAYRKAFESRLAS
1			SGALRVNEHLQVEGHSNVYAIGDCADVRTPKMAYLAGLHANIAV
1			ANIVNSVKQRPLQAYKPGALTFLLSMGRNDGVGQISGFYVGRLM
6555	1552	498	VRLTKSRDLFVSTSWKTMRQSPP
0333	1334	470	THMALLRKINQVLLFLLTVTLCVILYKKVHKGTVPKNDADDESE
i			TPEKLEREIPVVICAAAGRMGATMAAINSIYSNTDANILFYVVG
			LRNTLTRIRKWIKHSKLRBINFKIVEFNPMGLKGKIRPDSSRPR
1			LLQPLNFVRFYLPILIHQHEKVIYLDDDVIVQGDIQELYDTTLA
1		l	LGHAAAPSDDCDLPSAQDINRLVGLQNTYMGYLDYRKKAIKDLG ISPSTCSFNPGVIVANMTEWKHQRITKQLEKWMQKNVEENLYSS
			SIGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFL
ł			QEAKLLHNNGRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS
6556	241	1449	ASLCKGCFFVTHVLVIILPSLQSPPTFGFLLDIDGVLVRGHRVI
1			PAALKAFRRLVNSQCQLRVPVVFVTNACNILQHSKAQELSALLG
1			CEVDADQVILSHSPMKLFSEYHBKRMLVSGQGPVMENAQGLGFR
			NVVTVDBLRMAPPLLDMVDLERRLKTTPLPRNDFPRIEGVLLLG
			BPVRWETSLQLIMDVLLSNGSPGAGLATPPYPHLPVLASNMDLL
			WMAEAKMPRFGHGTFLLCLETIYQKVTGKELRYEGLMGKPSILT
			YOYAEDLIRRQAERRGWAAPIRKLYAVGDNPMSDVYGANLFHQY
1			LQKATHDGAPELGAGGTRQQQPSASQSCISILVCTGVYNPRNPQ
			STEPVLGGGEPDFHGHRDLCFSPGLMEASHVVNDVNEAVQLVFR
			KEGWALE
6557	2590	1534	RMCGRTSCHLPRDVLTRACAYQDRRGQQRLPEWRDPDKYCPSYN
			K9PQSN9PVLLSRLHFEKDADSSERI LAPMRWGLVPSWFKESDP
1			SKLQFNTTNCRSDTVMBKRSFKVPLGKGRRCVVLADGFYRWQRC
]			QGINQRQPYFIYFPQIKIBKSGSIGAADSPENWEKVWDNWRLLT
] .			MAGIFDCWEPPEGGDVLYSYTIITVDSCKGLSDIHHRMPAILDG
			BEAVSKWLDFGEVSTQEALKLIHPTENITFHAVSSVVNNSRNNT
			PECLAPVOLVVKKELRASGSSQRMLQWLATKSPKKEDSKTPQKE
			ESDVPQWSSQFLQKSPLPTKRGTAGLLEQWLKRRKEBEPVAKRP
6558		1220	YSQ
1 0000	21	1138	FHGRRRGGRKMELGSCLEGGREAAREEGEPEVKKRRLLCVEFAS
	1		VASCDAAVAQCFLAKNDWEMERALNSYFEPPVRESALERRPETI
j	ł		SEPKTYVDLTNEKTTDSTTSKISPSEDTQQENGSMFSLITWNID
	Į		GLDINNLSERARGVCSYLALYSPDVIFLQBVIPPYYSYLKKRSS
	ļ		NYBIITGHEEGYPTAIMLKKSRVKLKSQBIIPFPSTKMMRNLLC
	. 1		VHVNVSGNBLCLMTSHLESTRGHAAERMNQLKMVLKKMQEAPES ATVIFAGDTNLRDREVTRCGGLPNNIVDVWEPLGKPKHCQYTWD
	1		TOMNSNLGITAACKLRFDRIFFRAAAEBGHIIPRSLDLLGLEKI,
] [	f		DCGRPPSDHWGLLCNLDIIL
6559	3	364	GPBLSGLPTRPKKLKANOTPIAMDCCASRSCSVPTGPATTICSS
	Ĭ	J01	DKSCRCGVCLPSTCPHTVWLLEPTCCDNCPPPCHIPQPCVPTCF
	j		LINSCOPTPGLETINLTTFTQPCCEPCLPRGC
6560	3	1435	
"""	,	7433	TATSGGIWLRRKWRCHWPRPLPQSCVGTEGGLQVRDTSSRIAKG
	· .	i	GVDHTKMSLHGASGGHERSRDRRRSSDRSRDSSHERTESQLTPC
	i		IRNVTSPTRQHHVEREKDHSSSRPSSPRPQKASPNGSISSAGNS
	ļ	. 1	SRNSSQSSSDGSCKTAGEMVFVYENAKEGARNIRTSBRVTLIVD
[		l	NTRFVVDPSIFTAQPNTMLGRMFGSGREHNFTRPNEKGEYEVAB
		. 1	GIGSTVFRAILDYYKTGIIRCPDGISIPELREACDYLCISFEYS
	İ	j	TIKCRDLSALMHELSNDGARRQFEFYLEEMILPLMVASAQSGER
			ECHIVVLTDDDVVDWDBKYPPQMGEBYSQ11Y3TKLYRFFKY1E

C13/	Predicted	I handleted and	Taming agid gormont contributed
SEQ	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
NO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
]	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ľ	sequence		\=possible nucleotide insertion)
<del> </del>			NRDVAKSVLKERGLKKIRLGIEGYPTYKEKVKKRPGGRPEVIYN
į	l		YVQRPFIRMSWEKEEGKSRHVDFQCVKSKSITNLAAAADIPQD
1	j		QLVVMHPTPQVDELDILPIHPPSGNSDLDPDAQNPML
6561	3	1086	PGRRFRRKESSSSRWFPADCLLGLRGPASSLLSPEPSPSWPSHS
1	_		PCPMAALTDLSFMYRWFKNCNLVGNLSEKYVFITGCDSGFGNLL
1	ļ		AKQLVDRGMQVLAACFTEEGSQKLQRDTSYRLQTTLLDVTKSES
1		i	IKAAAQWVRDKVGEQGLWALVMNAGVGLPSGPNEWLTKDDFVKV
i	}		INVNLVGLIEVTLHMLPMVKRARGRVVNMSSSGGRVAVIGGGYC
l	}		VSKPGVEAPSDSIRRELYYFGVKVCIIEPGNYRTAILGKENLES
1	[	İ	RMRKLWERLPQETRDSYGEDYFRIYTDKLKNIMQVARPRVRDVI
			nsmehaivsrspriryn <b>p</b> gldakllyiplaklptpvtdfilsry
	1		LPRPADSV
6562	1	1562	MSTLYDIRAHKAQLLRFFASSDSNKALBQRRTLHTPKLEHLDRV
ļ			LYEWFLGKRSEGVFVSGPMLIBKAKDFYEQMQLTBPCVFSGGWL
l	i ·		wrfkarhgikkldassekqsadhqaabqfcaffrslaabhglsa
] .	Į		EQVYNADETGLFWRCLPNPTPEGGAVPGPKQGKDRLTVLMCANA
1			TGSHRLKPLAIGKCSGPRAFKGIQHLPVAYKAQGNAWVDKBIFS
			DWFHHIPVPSVREHFRTIGLPEDSKAVLLLDSSRAHDQEAELVS
į ,	Į,		SNVFTIFLPASVASLVQPMEQGIRRDFMRNFINPPVPLQGPHAR
i			YNMNDAIFSVACAWNAVPSHVFRAWRKLWPSVAFAEGSSSERE
			LEAECFPVKPHNKSFAHILELVKEGSSCPGQLRQRQAASWGVAG REAEGGRPPAATSPAEVVWSSEKTPKADQDGRGDPGEGEEVAWE
			QAAVAFDAVLRFAEROPCFSAQEVGQLRALRAVFRSOOOVRRRR
			GALGAVVKVEALQEGPGGCGATAQSPLPCSSTAGDN
6563	1319	2694	LARPAQPVLLREPEGAGPPVPAGHLVHHLQGGHLRERAHPDLEA
			HEHPLPCDOMFWROMGGHLRMVEANSRGVVWGIGYDHTAWVYTG
1			GYGGGCPQGLASSTSNIYTQSDVKCVHIYENQRWNPVTGYTSRG
		•	LPTDRYMWSDASGLQECTKAGTKPPSLQWAWVSDWFVDFSVPGG
	·		TDQEGWQYASDFPASYHGSKTMKDFVRRRCWARKCKLVTSGPWL
!			EVPPIALRDVSIIPESPGAEGSGHSIALWAVSDKGDVLCRLGVS
1			BLNPAGSSWLHVGTDQPFASISIGACYQVWAVARDGSAFYRGSV
			YPSQPAGDCWYHIPSPPRQRLKQVSAGQTSVYALDKNGNLWYRQ
			GITPSYPQGSSWEHVSNNVCRVSVGPLDQVWVIANKVQGSHSLS
			RGTVCHRTGVQPHEPKGHGWDYGIGGGWDHISVRANATRAPRSS
			SQEQEPSAPPEAHGPVCC
6564	1	975	APGSCALWSYCGRGWSRAMRGCQLLGLRSSWPGDLLSARLLSQE
			KRAABTHFGPETVSEERKGGKVYQVFESVAKKYDVMNDMMSLGI
			HRVWKDILLWKMHPLPGTQLLDVAGGTGDIAFRFINYVQSQHQR
			KQKRQLRAQQNLSWEEIAKEYQNEBDSLGGSRVVVCDINKEMLK
			VGKQKALAQGYRAGLAWVLGDAEELPFDDDKFDIYTIAFGIRNV THIDOALORAHRVLKPGGRFLCLBFSOVNNPLISRLYDLYSFOV
			IPVLGEVIAGDWKSYQYLVESIRRPPSQEEFKDMIEDAGFHKVT
			YESLTSGIVAIHSGFKL
6565	1464	999	RSAVANGLTKRRMGLKLNGRYISLILAVQIAYLVQAVRAAGKCD
			AVPKGPSDCLLKLGDSMANYPQGLDDKTNIKTVCTYWEDPHSCT
			VTALTDCOEGAKDMWDKLRKESKNLNIOGSLFELCGSGNGAAGS
			LLPAFPVILVSLSAALATWLSF
6566	3	1385	KYESAQPGGTQPEPGLGARMATHKALVMCLGLPLFLPPGAWAQG
		··- <del></del>	HVPPGCSQGLNPLYYNLCDRSGAWGIVLEAVAGAGIVTTFVLTI
			ILVASLPFVODTKKRSLLGTOVFFLLGTLGLFCLVFACVEKPDF
			STCASRRFLFGVLFAICFSCLAAHVFALNFLARKNHGPRGWVIF
			TVALLLTEVEVIINTEWLIITLVRGSGEGGPQGNSSAGNAVASP
	]		CATANMDFVMALIYVMILLILGAFLGAWPALCGRYKRWRKHGVFV
	·		LLTTATSVAIWVVWIVMYTYGNKOHNSPTWDDPTLAIALAANAW
		i	APVLFYVIPEVSQVTKSSPEQSYQGDMYPTRGVGYETILKEQKG
			QSMFVKNKAPSMDEPVAAKRPVSPYSGYNGQLLTSVYQPTBMAL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1 !	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1 1	sequence		\=possible nucleotide insertion)
<b></b>			MHKVPSEGAYDIILPRATANSQVMGSANSTLRAEDMYSAOSHQA
1 1			ATPPKDGKNSOVFRNPYVWD
6567	125	863	TKRSNLKAYACSIHHIRTMSYVFVNDSSQTNVPLLQACIDGDFN
1		1	YSKRLLESGFDPNIRDSRGRTGLHLAAARGNVDICQLLHKFGAD
i i			LLATDYQGNTALHLCGHVDTIQFLVENGLKIDICNHQGATPLVL
1 1			AKRRGVNKDVIRLLESLBEQEVKGFNRGTHSKLETMOTAESRSA
i I			MESHSLINPNLQQGEGVLSSFRTTWQEFVEDLGFWRVLLLIFVI
1			ALLSLGIAYYVSGVLPFVENQPBLVH
6568	3	1183	HASDRLLVLPDNYSHFSQASANLQGPSRTTRLFHPTLASISSPM
1			LEGAELYFNVDHGYLEGLVRGCKASLLTQQDYINLVQCETLEDL
1			KIHLOTTDYGNFLANHTNPLTVSKIDTEMRKRLCGBFBYFRNHS
1			LEPLSTFLTYMTCSYMIDNVILLMNGALQKKSVKBILGKCHPLG
]		l	RFTEMEAVNIABTPSDLFNAILIBTPLAPFFODCMSENALDELN
1 1			IELLRNKLYKSYLEAFYKFCKNHGDVTAEVMCPILEFEADRRAF
			IITLNSFGTELSKEDRETLYPTFGKLYPEGLRLLAQAEDFDQMK
1 1			NVADHYGVYKPLFEAVGGSGGKTLEDVFYEREVQMNVLAFNRQF
1			HYGVFYAYVKLKEQEIRNIVWIAECISQRHRTKINSYIPIL
6569	205	1532	RRRGPORLGHGRPTPLLCRWRTAGPSHWRKQARAFQGLRPVDPR
!			RMSWLFPLTKSASSSAAGSPGGLTSLQQQKQRLIESLRNSHSSI
1 1			AEIQKDVEYRLPFTINNLTININILLPPQFPQEKPVISVYPPIR
1			HHLMDKQGVYVTSPLVNNFTMHSDLGKIIQSLLDEFWKNPPVLA
i - I			PTSTAFPYLYSNPSGMSPYASQGFPFLPPYPPQRANRSITSLSV
1 1			ADTVSSSTTSHTTAKPAAPSFGVLSNLPLPIPTVDASIPTSONG
l			FGYKMPDVPDAFPELSELSVSQLTDMNEQEEVLLEQFLTLPQLK
] [			QIITDKDDLVKSIEKLARKNLLLBPSLBAKRQTVLDKYELLTQM
i I			KSTFEKKMQRQHELSESCSASALQARLKVAAHEAEEESDNIAED
			FLEGKMEIDDYLSSFMEKRTICHCRRAKEEKLQQAIAMHSQFHA
<u>i</u>			PL
6570	330	1304	ARLPRITFIREGFLYVILLSHWVFVGAPRPPASDSWKKGLVPSAP
1 1			PASRKMGSKALPAPIPLHPSLQLTNYSFLQAVNTFPATVDHLQG
			LYGLSAVQTMHMNHWTLGYPNVHEITRSTITEMAAAQGLVDAR?
1 1			PFPALPFTHLFHPKQGAIAHVLPALHKDRPRFDFANLAVAATQ
i i			EDPPKMGDLSKLSPGLGSPISGLSKLTPDRKPSRGRLPSKTKKE
j l			FICKPCGRHFTKSYNLLIHERTHTDERPYTCDICHKAFRRQDHL
1 !			RDHRYIHSKEKPFKCQRCGKGFCQSRTLAVHKTLHMQTSSPTAA
L			SSAAKCSGETVICGGT
6571	169	656	APDMNRKKLQKLIDTLIKNCKHLFRGFDKONDGCVNVLEWIHGL
			SLFLRGSLEBKMKYCFEVFDLNGDGFISKEEMFHMLKNSLLKQP
			SEEDPDEGIKDLVEITLKKMDHDHDGKLSFADYRLAVREETLLL
J-25			EAFGPCLPDPKSQMEFEAQVFKDPNEFNDM
6572	49	1646	TPERAQPGALLGAAGCCVCGGRWWPRSHERGYPSSAKMGSKRRN
1 1			LSCSERHQKLVDRNYCKKLHVQALKNVNSQIRNQMVQNENDNRV
1 I			QRKQFLRLLQNEQFELDMEBAIQKAEENKRLKELQLKQEEKLAM
j 1			BLAKI-KHESI-KDEKMRQQVRENSIELRELEKKI-KAAYMNKERAA
			QIAEKDAIKYEOMKRDABIAKTMMBEHKRIIKEBNAAEDKRNKA
( I			KAQYYLDLEKQLERQEKKKQRAYEQLLKEKLMIDEIVRKIYEED
į l			QLEKQQKLEKMNAMRRYIREFQKEQALWRKKKREEMEEENRKII
		!	BFANMQQQREEDRMAKVQKNBEKRLQLQNALTQKLBEMLRQRKD
1		•	I DOLLARD MANDAL THURSDAY WITH THE TOTAL THE PARTY WAS A CONTRACT OF THE PARTY OF T
			LEQVRQELYQEEQAETYKSKLKEEAEKKLRKQKEMKQDFEEQMA
			LKBLVLQAAKEBEENFRKTMLAKFAEDDRIELMNAQKQRMKQLE
			LKBLVLQAAKEBEENFRKTMLAKFAEDDRIELMNAGKQRMKQLE HRRAVBKLIEERRQQFLADKQRELBEWQLQQRRQGFINAIIEBE
			LKBLVLQAAKEBEBNFRKTMLAKFAEDDRIELMNAQKQRMKQLB HRRAVEKLIEBRRQQFLADKQRELBEWQLQQRRQGFINAIIEBE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSBI
			LKBLVLQAAKEBEBNFRKTMLAKFAEDDRIELMNAQKQRMKQLB HRRAVEKLIEERRQQFLADKQRELBEWQLQQRRQGFINAIIEBE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSBI CEEK
6573	767	275	LKBLVLQAAKEBEBNFRKTMLAKFAEDDRIELMNAQKQRMKQLB HRRAVEKLIEERRQQFLADKQRELBEWQLQQRRQGFINAIIEBE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSBI CEBK GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMYQGGYDMVQK
6573	767	275	LKBLVLQAAKEBEBNFRKTMLAKFAEDDRIELMNAQKQRMKQLB HRRAVEKLIEERRQQFLADKQRELBEWQLQQRRQGFINAIIEBE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSBI CEEK

SEO	Predicted	Predicted end	Amino agid committee
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
""	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
J	sequence		\=possible nucleotide insertion)
ļ	<del>  •</del>		LTAADKVSRGECWRVGGRTVCWVSLGSPLGSV
6574	204	1159	LESSVPVSVGVFWACGVSWTGAAGLQDGALSDTMARNAEKAMTA
J			LARFROAQLEBGKVKERRPFLASECTBLPKAEKWRRQIIGRISK
1	f		KVAQIQNAGLGEFRIRDLNDEINKLLREKGHWEVRIKELGGPDY
			GKVGPKMLDHEGKEVPGNRGYKYFGAAKDLPGVRELFEKEPLPP
į.	i		PRKTRAELMKAIDPRYYGYLDEDDGVIVPLEQEYEKKLRAELVE
			KWKABREARLARGEKEEBEBEEBEINIYAVTEEBSDEEGSQEKG
			GDDSQQKFIAHVPVPSQQBIBBALVRRKKMBLLQKYASETLQAQ
	}		SEEARRLIGY
6575	117	820	SPALASQSGGITERKMLEPQENGVIDLPDYEHVEDETFPPFPPPP
			ASPERQDGEGTEPDEESGNGAPVPVPPKRTVKRNIPKLDAQRLI
			SERGLPALRHVFDKAKFKGKGHEAEDLKMLIRHMEHWAHRLFPK
1	į .	ı	LQFEDFIDRVEYLGSKKEVQTCLKRIRLDLPILHEDFVSNNDEV
ı			AENNEHDVTSTELDPFLTNLSESEMFASELSISLTBEQQQRIER
			NKQLALERRQAKLP
6576	1	1060	PEPQALVGQKRGALRLLVARLVLTVSAPAEVRRRVLRPVLSWMD
Į.			RETRALADSHFRGLGVDVPGVGQAPGRVAFVSEPGAFSYADFVR
1			GFLLPNLPCVFSSAFTQGWGSRRRWVTPAGRPDFDHLLRTYGDV
i		-	VVPVANCGVQEYNSNPKEHMTLRDYITYWKEYIQAGYSSPRGCL
1			YLKDWHLCRDFPVBDVFTLPVYFSSDWLNEFWDALDVDDYRFVY
1			AGPAGSWSPFHADIPRSFSWSVNVCGRKKWLLFPPGQBEALRDR
1			HGNLPYDVTSPALCDTHLHPRNQLAGPPLEITQEAGEMVFVPSG
1			WHHQVHNLVMCCFSCPLSGAFLQEDGSTTSPLSQPELGWNGVAH   G
6577	2271	987	SDRMASDDFDIVIEAMLEAPYKKEEDEQQRKEVKKDYPSNTTSS
		30.	TSNSGNETSGSSTIGETSNRSRDRDRYRRRNSRSRSPGRQCRHR
1 1			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF
1			REKSPVREPVDNLSPBERDARTVPCMQLAARIRPRDLEDFFSAV
1			GKVRDVRIISDRNSRRSKGIAYVEPCEIQSVPLAIGLTGQRLLG
i i			VPIIVQASQABKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED
			MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL
1 1			EQLNGFRLAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG
			RFQLMAKLAEGAGIQLPSTAAAAAAAAAAAAQAAALQLNGAVPLGA
L			LNPAALTALSPALNLASQCLQLSSLFTPQTM
6578	377	1489	PSSSATMNRAPLKRATILHMALTGASDPSABAEANGEKPYLLRA
			LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL
			VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG
			MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA
			LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI
}	}		YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLIGBLQALRDF AQLGSAHFWGMMTLGGLPGPAIGYVTGLQIKFTSPLTHNVSGTA
	ŀ		KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK
] • [			KTPREPSPKDSEKSAMGV
6579	2	711	RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT
	i	<del></del>	IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI
1 1	•		EDIPKEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM
1	ļ		DVGQIGFHRQKDVKIVTVBKKVNBILNRLEKTKVERFPDLAAEK
j ł	İ	1	BCRDREERNEKKAQIQEMKKREKEEMKKKREMDELRSYSSLMKV
L	j		ENMSSNQDGNDSDBFM
6580	62	1571	LVALKNWKPKGTNIPAPQSPVFGRAVSGVYMMTKVLGMAPVLGP
	ľ		RPPQEQVGPLMVKVEEKEEKGKYLPSLEMFRQRFRQFGYHDTPG
	[	ļ	PREALSQLRVLCCEWLRPBIHTKEQILELLVLBQFLTII.PQBLQ
[	1		AWVQEHCPESAEEAVTILLEDLERELDEPGHQVSTPPNEQKPVWE
[		ļ	KISSSGTAKESPSSMOPOPLETSHKYESWGPLYIQESGEEQBPA
	İ		QDPRKVRDCRLSTQHRBSADEQKG9EAEGLKGDIISVIIANKPE
L			ASLERQCVNLENBKGTKPPLQEAGSKKGRESVPTKPTPGERRYI

<u> </u>	Drodi ot - 3	I manage at a discourse	
SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ī	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Deguario	\=possible nucleotide insertion)
<b> </b>	bequence		CAECGKAFSNSSNLTKHRRTHTGEKPYVCTKCGKAFSHSSNLTL
l	ł		HYRTHLVDRPYDCKCGKAFGOSSDLLKHORMITERAPYOCKDCG
1			KAFSGKGSLIRHYRIHTGEKPYQCNECGKSFSQHAGLSSHORLH
ļ	[	İ	TGEKPYKCKECGKAPNHSSNFNKHHRIHTGEKPYWCHHCGKTFC
	1		SKSNLSKHORVHTGEGEAP
6581	228	476	RVFLKDLSSTPMASNNTASIAQARKLVEQLKMEANIDRIKVSKA
		1	AADLMAYCEAHAKEDPLLTPVPASENPFREKKFFCAIL
6582	1428	718	CFTTKTHCSPVSVPYLSPLVLRKELESLLENEGDQVIHTSSFIN
			QHP11FWTLVWYFRRLDLPSNLPGLILTSEHCNEGVQLPLSSLS
		1	QDSKLVYIQLLWDNINLHQEPREPLYVSWRNFNSEKKSSLLSRE
!		1	QQETSTLVETIRQSIQHNNVLKPINLLSQQMKPGMKRQRSLYRB
		1	ILFLSLVSLGRENIDIEAFDNEYGIAYNSLSSEILERLQKIDAP
			PSASVEWCRKCFGAPLI
6583	487	41	RIFSMTSGRLRWRCTWRPATALWSASLRIGTSSMHPSPRSISLP
		]	LSMMLSPLPSNTRGLSPTALFRSPDSEHATSCPRLHLWRCRAPL
	i		RSPSPLGRLQVLPRSPLHVHTHNSGKEVLGLQVQRSRSGTGPAC
	Ĭ	!	SQAGSGAVQGGNWCIP
6584	189	1750	PLPMAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFAT
	1	j	WNQARLERDLENKKIYQEEEMPESGAGSBFNRKLRBRARRKKYG
		1	IVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQ
			CPDGAFEAFPVHNNYNFTPLARHRTLTABBABBEBWBRRNKVLNH
			FSIMQQRRLKDQDQDEDEEEKEKRGRRKASELRIHDLRDDLEMS
	l	1	SDASDASGEEGGRVPKAKKKAPLAKGGRKKKKKKGSDDEAFEDS
	,		DDGDFBGQEVDYMSDGSSSSQEEPESKAKAPQQEEGPKGVDEQS
		}	DSSRESERRKPPBEDKEREEERKAPTPQBKKRRKDSSRESDSSR
		ļ	ESDIDSEASSAFFMAKKKTPPKRERKPSGGSSRGNSRPGTPSAE
	l	ì	GGSTSSTLRAAASKLEQGKRVSEMPAAKRLRLDTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK
	1	}	TGLSSEQTVNVLAQILKRLNPERKMINDKMHFSLKE
6585	: 3	1678	GPIRNSRIDDFVGGDPRAKASCSVLHSKPHAMADSRDPASDOMO
0505	1 . 3	10/8	HWKEQRAAQKADVI:TTGAGNPVGDKLNVITVGPRGPLLVQDVVF
			TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE
	ł	ł	HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL
		1	VGNNTPIFPIRDPILPPSFIHSOKRNPOTHLKDPDMVWDFWSLR
	1	Į	PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGRAVYCK
	1	Į	PHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW
	,		TFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRN
,	1		PVNYFAEVEQIAFDPSNMPPGIKASPDKMLQGRLFAYPDTHRHR
	}		LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF
	1	1	GAPEQQPSALEHSIQYSGEVRRENTANDDNVTQVRAFYVNVLNE
	1		EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL
	[		DKYNAEKPKNAIHTFVQSGSHLAAREKANL
6586	32	804	PLPEQPARSTSTMPVSGTPAPNKKRKSSKLIMBLTGGGQBSSGL
	1		NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP
	ĺ		DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG
			SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGR
			TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA
			ygakarlpkyksfnrtampyggybkaskrmtfqmpkv
6587	75	1117	RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY
			HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF
			PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA
			LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH
			LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD
	1		INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT
			PLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS
			RTASLTSASSVDGSRPQACTHSRSSEGLGQVNHTMEVSC
	I	L	WINDTONDANDAY AUCTIOD DO DO MAINTING AC

			The said appears with a solution	- RAMBARA (PS)
SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide	
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,	
1	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,	
	corresponding	to first	Talougine Manthiania N America	
	to first	amino acid	Labeucine, Mamethionine, NaAsparagine,	
1		ľ	P=Proline, Q=Glutamine, R=Arginine,	
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,	
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop	
1	amino acid	sequence	Codon, /=possible nucleotide deletion,	
	sequence		\=possible mucleotide insertion)	
6588	137	501	LGLQAQLLELRINNYQLSDELRKNGVELTSLRQKVAYLDKEFSK	
1			AQKALSKSKKAQEVEVLLSENEMLQAKLHSQEEDFRLQNSTLMA	
1			BFSKLCSQMEQLEQRNQQLKRGAAGAGVAQAGP	
6589	2	1405	RPNGSAMATFSRØEFFQQLLQGCLLPTAQQGLDQIWLLLAICLA	
1	1	<b>{</b>	CRILWRLGLPSYLKHASTVAGGFPSLYHPPOLHMVWVVILLSLLC	
1			YLVLFLCRHSSHRGVFLSVTILIYLIMGEMHMVDTVTWHKMRGA	
1			QMIVAMKAVSLGFDLDRGEVGTVPSPVEFMGYLYFVGTIVFGPW	
1	[	Í		
1	1		ISPHSYLQAVQGRPLSCRWLQKVARSLALALLCLVLSTCVGPYL	
ì	1	Į.	FPYFIPLNGDRLLRNKKRKARGTMVRWLRAYESAVSFHFSNYFV	
	I		GFLSEATATLAGAGFTEKKDHLEWDLTVSKPLNVELPRSMVEVV	•
I	I		TSWNLPMSYWLNNYVFKNALRLGTFSAVLVTYAASALLHGFSPH	
i	ſ	I	LAAVLLSLAFITYVEHVLRKRLARILSACVLSKRCPPDCSHQHR	
1			LGLGVRALNLLFGALAIFHLAYLGSLFDVDVDDTTEEQGYGMAY	
j	}		TVHKWSELSWASHWVTFGCWIFYRLIG	
6590	2177	656	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR	
1			GSLSLDDFRNTQKRGRSFGISRIGSKIKGVFKSTTMEGAMLPNY	
j			GVAEGEDDFIEEGIVVMKDDSPVEAVSTPNTPRNLAAWKISIPY	
1	J	}	VDFFEDPSSERKEKKERIPVFCIDVERNDRRAVGHEPEHWSVYR	
	ļ	Í	RYLEFYVLESKLTRFHGAFPDAOLPSKRIIGPKNYEFLKSKREE	
1				
1		ŀ	PQEYLQKLLQHPELSNSQLLADFLSPNGGBTQFLDKILPDVNLG	
			KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL	• •
1 ' '			SPTSENNKKLFNDLFKNNANRAENTERKQNQNYFMEVMTVEGVY	
		,	DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLQCKL	
1		·	EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM	
]		+	MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI	
			VIQELFPELNKVQKEVTSVTSWM	
6591	2177	656	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR	
1 1		i	GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTTMEGAMLPNY	
			GVAEGEDDFIEEGIVVMEDDSPVRAVSTPNTPRNLAAWKISIPY	
1 1			VDFFEDPSSERKEKKERIPVFCIDVERNDRRAVGHEPEHWSVYR	
i I		ľ	RYLEFYVLESKLTEFHGAFPDAQLPSKRIIGPKNYEFLKSKREE	
1 1		ł	FQEYLQKLLQHPELSNSQLLADFLSPNGGRTQFLDKILPDVNLG	
1 1			KIIKSVPGKLMKEKGQHLEPPIMNFINSCHSPKPKPSRPELTIL	
l i		•		
1 1			SPTSENNKKLPNDLPKNMANRAENTERKQNQNYFMBVMTVEGVY	
			DYLMYVGRVVPQVPDWLHHLLMGTRILFKNTLEMYTDYYLQCKL	
1 1			EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM	
į į			MNYIPDLLVKCIGEBTKYESIRLLFDGLQQPVLNKQLTYVLLDI	
L			VIQRLPPELNKVQKEVTSVTSWM	
6592	3	1861	APEFLGSTISSGSMIDANLKLLQRABQRLKAIVAEKFALATKEG	
į i			DLPQVERFFKIPPLLGLHEEGLRKFSEYLCKQVASKAEENLLMV	
			LGTDMSDRRAAVIFADTLTLLFEGIARIVETHOPIVETYYGPGR	
ļ			LYTLIKYLQVECDRQVEKVVDKFIKQRDYHQQFRHVQNNLMRNS	
;			TTEKIEPRELDPILTEVTLMNARSELYLRFLKKRISSDFEVGDS	
]·			MASEBVKQEHQKCLDKLLNNCLLSCTMQELIGLYVTMEBYFMRB	
; I				
1 1			TVNKAVALDTYEKGQLTSSMVDDVFYIVKKCIGRALSSSSIDCL	
			CAMINLATTELESDFRDVLCNKLRMGFPATTFQDIQRGVTSAVN	
}			IMHSSLQQGKFDTKGIBSTDEAKMSFLVTLNNVEVCSENISTLK	
l			KTLESDCTKLFSQGIGGEQAQAKFDSCLSDLAAVSNKFRDLLQB	
			GLTELNSTAIKPQVQPWINSFFSVSHNIEEEEFNDYBANDPWVQ	
[			QFILNLEQQMAEFKASLSPVIYDSLTGLMTSLVAVELEKVVLKS	
	İ		TFNRLGGLQFDKELRSLIAYLTTVTTWTIRDKFARLSQMATILN	
1			LERVTEILDYWGPNSGPLTWRLTPAEVRQVLALRIDFRSEDIKR	
l	_		LRL	
6593	3	1837	EAFSAGSRRRGLALORGVLGGLGGYCPCCCRRGRLLVLLLLVR	
*****	·	1031		
			RGGEGGGRGRGDKRRRRQARRQRRRPRPAKARGGKMADVLSVL	
			RQYNIQKKEIVVKGDEVIFGEFSWPKNVKTNYVVWGTGKEGQPR	

Degiming   location				
Docation   Corresponding to first   Service	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cortain   Corresponding to first   Endewine, X-Eysine, Lequelie, M-Methioloine, N-Apparagine, veridue of amino acid amino acid sequence   Peroline, Q-Glutamine, R-Arginine, Sequence   S				
corresponding to first amino acid amino acid residue of amino acid residue of amino acid sequence sequ	NO:			
amino acid medio acid				
### amino acid				
mein acid sequence    Martyplopham, Y=Tyrosine, K=Dhknown, *=Stop   Coden, /=possible nucleotide deletion    Coden, /=possible nucleotide deletion    Coden, /=possible nucleotide deletion    EYYTLDELIJLIAMVHASSPYVARAKERPIDENDAGE   EYYTLDELIJLIAMVHASSPYVARAKERPIDENDAGE   EYYTLDELIJLIAMVHASSPYVARAKERPIDENDAGE   EYRTLDELIJLIAMVHASSPYVARAKERPIDENDAGE   EYRTLDELIJLIAMVHASSPYVARAKERPIDENDAGE   EVANT		•		
### sequence   Codom, /=possible mucloctide deletion,				
Sequence				
### STYTLDS LIFILIAMYHLSHPVVRRAATRIN TPVRREPIRROLD TINGKRASTRASI TIRSARLISIGIQUSTOVRAADRIJARAKKERI HERROLDKERLAARIKERI VOTBOLSSIKRIMSVEKTAR LIKAKIMAKKESI TETULDUDI TALKORSE YUNAKUTUDI TUSER RIVAKIMAKKESI TETULDUDI TALKORSE YUNAKUTUDI TUSER RIVAKIMAKKESI TETULDUDI TALKORSE YUNAKUTUDI TUSER RIVAKIMAKKESI TETULDUDI TALKORSE YUNAKUTUDI TUSER RIVAKUTURI TITI TANATTSILTIMINKULQDI KEVESEBIKKKOG QURRINTI I TIRAATTSILTIMINKULQDI KEVESEBIKKKOG QURRINTI I TIRAATTSILTIMINKULQDI KEVESEBIKKKOG QURRINTI I TIRAATTSILTIMINKULQDI KEVESEBIKKKOG QURRINTI I TIRAATTSILTIMINKULLQDI KEVESEBIKKKOG QURRINTI I TIRAATTSILTIMINKULLQDI KEVESEBIKKKOG QURRINTI I QURRINOM MONTULELS YIKKEHLDER VELKUMENTULDE YUNGKUSHIT TIRAATTSILTIMINKULLQDI KEVESEBIKKKOG QURRINTI I TIRAATTSILTIMINKULLQDI KEVESEBIKKKOG QURRINTI KERABITI KANATURI KENESEPEN KOMA DI SITTOTIMI TIRIAH KOMA TUSER KENESOKI KANATURI KENESEPEN KOMA TIRAATEKA TUSEK KANATURI KENESEPEN KOMA TIRAATI KENESEPEN KOMA TIRAATI KENESEPEN KOMA TIRAATI KENESEPEN KOMA TIRAATI KENESEPEN KOMA TIRAATI KENESEPEN KANATURI KENESEPEN KANA			sequence	
TIANGHASTSAIIDSAPLEIGIGOSTOVKRAADEVIJABRAKYETÄÄ  EDERCYELDKERIADITAHARIKKESTI KYDIJDIDITALKORSFYVDAKUDVTEDITSKER  RVERTITILGSTONDISKII FALLGSVEAREERAPEORRAE  AAPUDPTIRTKOR TIANILGSVEAREERAPEORRAE  AAPUDPTIRTKOR TAAINITAHARISTI TATULDIDITALKORSFYVDAKUDVTEDITSKER  RVERTITIKORTOKUSKII FALLGSVEAREERAPEORRAE  AAPUDPTIRTKOR TAAINITAHORICICALUKSVEAREERAPEORRAE  TIITAAATSLITHIINAKULLOJUKEVYSBEKKKOGOKRINSTI  IQRRKOONG-GOTALSVITYYKVUODPILLIHPODAGRVADTYTT  IQRRKOONG-GOTALSVITYYKVUODPILLIHPODAGRVADVIVOKO  GPANOG-GOTALSVITYYKVUODPILLIHPODAGRVADVIVOKO  GPANOG-GOTALSVITYYKVUODPILLIHPODAGRVADVIVOKO  GPANOG-GOTALSVITYYKVUODPILLIHPODAGRVADVIVOKO  GPANOG-GOTALSVITYYKVUODPILLIHPODAGRVADVIVOKO  GPANOG-GOTALSVITYYKVUODPILLIHPODAGRVADVIVOKO  GPANOG-GOTALSVITYYKVUODPILLIHPODAGRVADVIVOKO  GPANOG-GOTALSVITYYKVUODPILLIHPODAGRVADVIVOKO  GPANOG-GOTALSVITYYKVUODPILLIHPODAGRVADVIVOKO  GPANOG-GOTALSVITYYKVUODPILLIHPODAGRVADVIVOKO  AVIALITATIOKVURENOSSII KARCHARIADVILLIHPONGALKEE  ARKHEBEPRROKLORKETULINALEN KORCHARIADVILLIHPONGALEE  ARKHEBEPRROKLORKETULINALEN KORCHARIADVILLIHPONGALEE  AVIALITATIOKVURENOSSII KARCHARIADVILLIHPONGALEE  AVIALITATIOKVURENOSSII KARCHARIADVILLIHPONGALEE  AVIALITATIOKVURENOSSII KARCHARIADVILLIHPONGALEE  AVIALITATIOKVURENOSSII KARCHARIADVILLIHPONGALEE  AVIALITATIOKVURENOSSII KARCHARIADVILLIHPONGALEE  AVIALITATIOKVURENOSSII KARCHARIADVILLIHPONGALEE  AVIALITATIOKVURENOSSII KARCHARIADVILLIHPONGALEE  AVIALITATIOKVURENOSSII KARCHARIADVILLIHPONGALEE  AVIALITATIOKVURENOSSII KARCHARIADVILLIHPONGALEE  AVIALITATIOKVURENOSSII KARCHARIADVILLIHPONGALEE  AVIALITATIOKVURENOSSII KARCHARIADVILLIHPONGALEE  TURKAVENSOORIANAPARATORIA PERGEBANATI YARCHARIADVILLIHPONGALEE  AVIALITATIOKVURENOSSII KARCHARIADATI TORGATI TAATIOKATA  PUPUNAMPIKARIA KARCHARIADVILLIHPONGAL		sequence	<u></u>	1 · ·
IDBRICUPIDIKEHARAHIRESI VUTUGILSIKANNAVEKTI		<u> </u>	Ì	
TKAKIMAKKSTITUIDIDITALKQRSFVDAKVDVTDIVZS   PVPRTTTTILGTKONSKNIT PALLGSVARAREGRAPDGPRAPN   AD PUPTITATROP I PALYINY DOGREFKUKETSERS PLOPARY   AD PUPTITATROP I PALYINY DOGREFKUKETSERS LOTVATSTY   GMTLKSVTEGAGREKTGTEARPY GPRAPOKKSTYT   ITII PALTISLITMINARDLLQDLKFVPSDEKKKQGOPENETL   IQRKUQMQ-RGSTALSVTVYTEVVOQELLIMPQDKORVANTY   GERKOQMQ-RGSTALSVTVYTEVVOQELIMPQDKORVANTY   GERKOQMQ-RGSTALSVTVYTEVVOQELIMPQDKORVANTY   GERKOQMQ-RGSTALSVTVYTEVVOQELIMPQDKORVANTY   GERKOQMQ-RGSTALSVTVYTEVVOQELIMPQDKORVANTY   GERKOQMQ-RGSTALSVTVYTEVVOQELIMPQDKORVANTY   GERKOQMQ-RGSTALSVTVYTEVVOQELIMPQDKORVANTY   GERKOCKGRATELSSYVOLLANGER   GERKOGERGE   GERKOGERG				
RYMETETTILGSTIGNIPSKHITPALIGGUERREGGEREGPENDEN ADVODTITERTEQ IPADANIN LODGEREKKEETEGEKLOTMGTTIL GMTLKSVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRTP IIIIRAATISLITMIANADLLQDLGVPSDEKKKGGGGRENTL IQRKOQMQ29GATLSVTVSTEVVOQELAIMEQDEKEVVADVEVO GPANQRKOMPHLEPDGSEVUJIPAKIKAFHLKYDEVULDBUNQKM DVTVLELSYMKREHLDROPPIRKVVOQELAIMEQDEKEVVADVEVO GPANQRKOMPHLEPDGSEVUJIPAKIKAFHLKYDEVULDBUNQKM DVTVLELSYMKEHLDROPPIRKVVOTELAIMENDEVKUSHVUND GPANQRKOMPHLEPDGSEVUJIPAKIKAFHLKYDEVULDBUNQKM DVTVLELSYMKEHLDROPPIRKVESTLERIMENDEVKOMPUNA BEFORRERKOSQASPLCARCOPALLBADTRAAMTRSLEKKGMVSA ALKHESPERKOKLQAKTERLINDAHIKMGSLEKE ARKMESPERKOKLQAKTERLINDAHIKMGSLEKETANATERSKYKOLLI NLSSKKUPCGQSEINTIKRALEVVKQQUUNVAQCHIQLAGSLEE ARKMESPERKOKLQAKTERLINDAHIKMGSLEKETANATERSDEK AYMLHIGTILDEVKRSMQSEHLINDAHIKMGSLERITNTPRINAIMI HVNQLSQQCVTSDENTEQVRKSLEMCSIQNDIKYVATOSDEK AYMLHIGTILDEVKRSMGSEHLINDAHIKMGSLERINTPRINAIMI HVNQLSQQCVTSDENTEQVRKSLEMCSIQNDIKYVATOSDEK AYMLHIGTILDEVKRSMGSEHLINDAHIKMGSERINDERSSVKILERDMIXIH HVNQLSQQCVTSDENTEQVRKSLEMCSIQNIBERSVKILLEDDMIXIH RYNAYSSIGKIKLLSGQOTNISVLQICINNPINARRELLEDDMIXIH RYNAYSSIGKIKLLSGQOTNISVLQICINNPINARRELLEDDMIXIH RYNAYSSIGKIKLLSGQOTNISVLQICINNPINARRELLEDDMIXIH RYNAYSSIGKIKLLSGQOTNISVLQICINNPINARRELLEDDMIXIH RYNAYSSIGKIKLLSGQOTNISVLQICINNPINARRELLEDDMIXIH RYNAYSSIGKIKLLSGQOTNISVLQICINNPINARRELLEDDMIXIHL RYNAYSSIGKIKLLSGQOTNISVLQICINNVILAVANIVALSICH GERRICUTDDCAKTFTDISVLQICINNININARRELLEDDMIXIHL RYNAYSSIGKERPAPPPREGRILSSYKULAVANIVALSICHANIVALSURANIVAL GERRICUTDDCAKTFTDISVLQICINNPINARRELLIDAHANIY HIVOLANDAMIKEQBRADLSSNEDHSSYKULAVANIVALSKIRD PITYOLANDAMIKEQBRADLSSNEDHSSYKULAVANIVALSKIRD PITYOLANDAMIKEQBRADLSSNEDHSSYKULAVANIVALSKIRD PITYOLANDAMIKEQBRADLSSNEDHVENGOGLILAPORSSYKLLD FDISETTETEVEVERLEPIDIGIP TITARRSTQAHLAPVVCPKOV KMILSHLENKVANIVAVSKRROSHRIGHTANATAY VLIQKSQMTERGEDDVKKTEBERDVECGDDLILAPQPSSSYKLLD FDISETTETEVEVERLEPIDIGIP TITARRSTQAHLAPVVCPKOV KMILSHLENKVANIVAVSVENGVGGLILEGBERGENGONSV PITYALTMERGENGANGRADLANDENGRADLATIANIVANIVA  BERNOCUTODCAKTFTOR BODGRETATIANIVARROLLIPHOR VLIPKORTATA  GERRCUTODCAKTFTOR BODGRETATIANIVARROLLIPHOR VLIP				
APPUDPTILITROP IP JAANNEY DOER PRIKKETERGEK LOTTATYTT  GINTLKSVTEGASARKTYOTER AND VOR PVEN OARDEP PROKKESSTEY  III I PAATTSLITMINAKOLLODISUUT PAKKAFILLOE POOK VAN VARVO  GERANOEKSUFMULE POOS VOLT PAKKAFILLOE POOK VARVOEVO  GERANOEKSUFMULE POOS VOLT PAKKAFILLOE POOK VARVOEVO  GERANOEKSUFMULE POOS VOLT PAKKAFILLOE PAKKAFILLOE POOK VARVOEVO  DVTULELSYHKREILOER PVELKEWASTIANTSLEKKOHEWSA  DILSTIGYDNI I GILMINGERINGER PEKKAFILER PAKKAFILLOEN PVEKKEN  BILSTIGYDNI I GILMINGERINGER PEKKAFILER PAKKAFILLOLAOS LEERE  ARKHERSPRINGKI QIRKTISLIMDA I HEKKASI OPEKTYDDAKARIYE  GROED BARADAYS SAALI VAN PROQUESTIAN PEKKAFIYA DESANO  AYMLHIGTIDKVREWQSEHI KACEAPBAQECER IN PERNALINI.  HVANDLSQOCYTSOBNI TROVESCI GIRDIE PERVIKITEROLI IL  HVANDLSQOCYTSOBNI TROVESCI GIRDIE PERVIKITEROLI IL  PERPA INTENTY SSQUKAAV PAGAKATOPIN LARREFLEP DIR SSEPDOD  NYSLVIDUSILLYO  FELTYMSSOBLISCO PILSTAGER SIGNOL PERVIKITE SSEPDOD  NYSLVIDUSILLYO  GERONOFTI SERGGIASIDVALI PERSSEPSELVAPAPATIVILISLE  GERONOFTI SERGGIASIDVALI PERSSEPSELVAPAPATIVILISLE  VOMINISCO PERLEPENDER PER PERSOBLES SKILLI VENGLARAEMIKLOK  GERONOTIDICAN PERSSEPSELVAPAPATIVILISLE  GERROCI DIOCASI FEITE SDD LIDD PROTILLOPHEN PER PER PER PER PER PERSOBLES SKILLI LINQUES SVILLOPHEN PER PER PER PERSOBLES SKILLOPES SVILLOPHEN PER PER PER PER PER PERSOBLES SKILLOPES SVILLOPHEN PER PER PER PER PERSOBLES SKILLOPES SVILLOPHEN PER PER PER PER PERSOBLES PER PER PER PER PER PER PER PER PER PER				
GMTLKSVTEGASARKTOJPAAGD VERPVSGARPPENGKESSTP  II I I I I I I PAATTSI JETMIAMADLLODLKEV PSDEKKIGGOPENISTI  I I I I I GRRIDOMQPGGTALSVTVPYRVUOQPLKILMPQDKDRVVAVFVO  GPANQPKOMPHILEPOSS VID I PAKTIKHFILK YDEVRLOPWIJON  DVTVLELSYMKRILDEN PVETKARTEN KRIKERFE  6594  1 1096  E PPORRFRIGSGASPLCATGEPALLEADTRAAMTRSLEKKEMFSA  BLISTIGTINI I I GHLIMNGRIKK GEREP DILERRAT BERKYOKULL  NLSKKEPCOGEINTIKRALEVEKOQUNNACHIOLAGIERE  ARKMESPIRISKI, JOHNACH HOK MINGSKORT JOHNACHIOLAGIERE  ARKMESPIRISKI, JOHNACH HOK MINGSKORT JOHNACHIOLAGIERE  ARKMESPIRISKI, JOHNACH HOK MINGSKORT JOHNACH JOHNACH JOHNACH  HVANGLSQOCTUS BONTROUKESIERECS JOHNACH STEVENORICUS JI  PPAP I HYRRIPYSSGKIAN PAGKATGENILARREGILD I FEVSIORICUS JI  PPAP I HYRRIPYSSGKIAN PAGKATGENILARREGILD I FEVSIORICUS JI  RYNAYSSGKIKLISLGOOTINISKIERI JOHNACH JOHNACH JOHNACH  GKOPNOPTI SRIGGKASDVALPRGSSPEVLANSVERPTINI JILL KRAK  GERRICUIDOCAKI JECUT SEDDIJOK KRIKERINLEKS JOHNACH JOHNACH  GERRICUIDOCAKI JECUT SEDDIJOK KRIKERINLEKS JOHNACH JOH		}		1
1111PARTISLITMINARDILLODLKFVPSDEKKKGGCQRRNTTL 1QRRKDQMGGTAT 15VTPV VOOPELINGERVEVAVVVQ GPAMQPKGGPMLPDGSPVD1PAKTKAFHLKYDEVRLDPNVQXW DVTVLELSTHKRRILDRFVPTKVWBTITLERTWYGKRISHBIFF 5594 1 1096 EPPGRFRFKSGSSPICATCGPALLEAPTRAAMTRSLFKGRFWSA DILSTIGYDNITQHLMNGRKNCKEPEDPLERRAATBERYGKDLL MLSRKBCGGSESITNITRABLEAVFKQCUDINAGKHSHBIFF QKCRDDRARGAVSRAALLVAWKQOKLUPKLATSKITAVESDEK KARMBERPRKQKLQRKXTBLIMDAIHKQKSLQFKKTMDAKNYE QKCRDDRARGAVSRAALLVAWKQOKLUPKLATSKITAVESDEK ARMBERPRKQKLQRKXTBLIMDAIHKQKSLQFKKTMDAKNYE QKCRDDRARGAVSRAALLVAWKQOKLUPKLATSKITAVESDEK AYMLHIGTIDKVERRBQSHITKACRAPKAQGECRINFPRALMIN HVNOLSQCCYTSDBMYEDVYKSKGEMCSTGORD FRYVNORKTGGI PPAP IMYENPYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDD NYSLVDDISLING GKDPNOFTISRGKGKASUVALDRGSSFEVLLAVDOKTYGL GKDNOFTISRGKGKASUVALDRGSSFEVLAVPOSTITLITAREA GKPONOFTISRGKGKASUVALDRGSSFEVLAVPOSTITLITAREA GSPTGGLWTTP PFPTPEDGKDFSSFEVLAVPOSTITLITAREA GSPTGGLWTTP PFPTPEDGKDFSSFEVLAVPOSTITLITAREA GSPTGGLWTTP PFPTPEDGKDFSSFEVLAVPOSTITLITAREA GSPTGGLWTTP PFPTPEDGKDFSSFEVLAVPOSTITLITAREA GSPTGGLWTTP PFPTPEDGKDFSSFEVLAVPOSTITLITAREA GSPTGLWTTP PFPTPEDGKDFSSFEVLAVPOSTITLITAREA GSPTGLWTTP PFPTPEDGKDFSSFEVLAVPOSTITLITAREA GSPTGLWTTP PFPTPEDGKFSSFEVLAVPOSTITLITAREA GSPTGLWTTP PFPTPEDGKFSSFEVLAVPOSTITLITAREA GSPTGLWTTP PFPTPEDGKFSSFEVLAVPOSTITLITAREA GSPTGLWTTP PFPTPEDGKFSSFEVLAVPOSTITLITAREA GSPTGLWTTP PFPTPEDGKFSSFEVLAVPOSTOV VLICKSQWTEREGDVKKTESEBEVSCBDILLLAQPESSVKALD FDISETRTEVEVERLEP DIMGTBITTORSSFCOAHLAVVCROV KWILSKLENKKLASATHTITYARITYCEXCOLDITLACQPESSVKALD FDISETRTEVEVERLEP DIMGTBITTORSSFCOAHLAVVCROV KWILSKLENKKLASATHTITYARITYCEXCOLDITLACQPESSVKALD FDISETRTEVEVERLEP DIMGTBITTORSSFCOAHLAVVCROV KWILSKLENKKLASATHTITYARITYCEXCOLDITLACQPESSVKALD FDISETRTSVEVERLEP DIMGTBITTORSSFCOAHLAVVCROV KWILSKLENKKLASATHTITYARITYCEXCOLDITLACQPESSVKALD FDISETRTSVEVERLEP DIMGTBITTORSSFCOAHLAVVCROV KWILSKLENKKLASATHTYAYARITYCERKOPTICKKGLAANATY LUVENSTYTNSBESSKALGKNKKVKKKKKRKHRH LUVENSTYTNSBESSKALGKNKKVKKKKKKKHRH LUVENSTYTNSBESSKALGKNKKVKKKKKKKHRH LUVENSTYTNSBESSKALGKNKVKKKKKKKTH LUVENSTYTNSBESSKALGKNKKVKKKKKKKKTH LUVENSTYNSBESSKAL		ĺ		
I ORRKIDOMO-GESTAL SYTTYPYRVUODPLIKIMPODRIVANSWO GPANOPKRIMPHILLDES PUD I FARTIKAFIEN KURDRIVADNUKM DVTVLKLSYHKRHLDRPVFLRVMETLLXTBURLDRVUKM DVTVLKLSYHKRHLDRPVFLRVMETLDRYMVKHKSHLRP  5594  1 1096  EFPERRERGSQASPLCATCGEALLRAPTRAAMITESPEKGNEWAS DUISTIGUNTI TOHLBANGERKOKEPFEDPLERRAATIBERVGKULDL NLSRKKPCGOSEINTIKRALBVFRQOVDMVAQCHIQLAGSLEBE ARKMEBFREKKOKLGKKKELLIMDAIHKGHERAATIBERVGKULDL NLSRKKPCGOSEINTIKRALBVFRQOVDMVAQCHIQLAGSLEBE ARKMEBFREKKOKLGKKELLIMDAIHKGHERAATIBERVGKULDL NLSRKKPCGOSEINTYKRALBVFRQOVDMVAQCHIQLAGSLEBE ARKMEBFREKKOKLGKKELLIMDAIHKGHERATISTAVECSDK AYMLHIGTIDLIVERBUGSBIT KACEBAPEGKEINFRALMIL HVWQLSQQCVTSDEMYSQVRKSLEMCSIQRDI EYFVNQRKTGQI PPAP IMYRHYTSSQRBAVPACKATGENIARREDI-PI FYSS PUDD WYSLVDUSYSLLINQ  FPAP IMYRHYTSSQRBAVPACKATGENIARREDI-PI FYSS PUDD PPAP IMYRHYTSSQRBAVPACKATGENIARREDI-PI FYSS PUDD PPAP IMYRHYTSSGRBAVPACKATGENIARREDI-PI FYSS PUDD PPAP IMYRHYTSSGRBAVPACKATGENIARREDI-PI FYSS PUDD PPAP IMYRHYTSSGRBAVPACKATGENIARREDI-PI FYSS PUDD PPAP IMYRHYTSSGRBAVPACKATGENIARREDI-PI FYSS PUDD PPAP IMYRHYTSSGRBAVPACKATGENIARREDI-PI FYSS PUDD PRASILING GKDPADI-RAVUS GKDPADI-RAVUS AGNORESI FANAPATY GKDPADI-RAVUS AGNORESI FANAPATY GKDPADI-RAVUS KURD PPAP IMYRHYTSSGRBAVA PROGRESI FANAPATY PI YQIAMPHILAGORENDI-RASILBEI YI QNIGESI LYLWWEKIRD PI STERTERVEVELEP PI DHGI PI TITARE PADI-RAVUS FANAPAT PI YQIAMPHILAGORENDI-RASILBEI YI QNIGESI LYLWWEKIRD PI STERTERVEVELP PI DHGI PI TITARE PATHA ANGARILMEN			1	· · · · · · · · · · · · · · · · · · ·
GPANQEKGMPHLLEDGSPUD FRATKAFHLKYDEVILDAWUKM  DVTVIKLSYHKRHIDBRSPFLRWBTLDRYWKHKSHLERP  6594  1 1096  EFPERRIPKESGASPLCATGSPALLRAPTRAMITESLPKGNEWSA DILSTIGYDNIIGHLINGGRKCKEFEDPILRRAPTRAMITESLPKGNEWSA NLSKRKPGCOSENITIKERALEWFRQCUDWAQCHIQLAGSLEEE ARMBEBPRKOKLGRKKTELIMDALHHQKSLGPKKTMDAKNIYE QRCHDKURBAGDAUSRSANLAWPKQOGELKHATSKTAVEGSDK AYMLHIGTLDRVREBWGSEHIKACKAPERAGECERIPFFRNALMIL HVROLSQCCYTSDBMTGVYRKSLEMCSIGNIIBTPVNQRKTCQI PPAPINYRHYTSSGKAUSPACKATGGMIARREPLIPIBKSSDDD NYSLVDDVSLLVQ PPAPINYRHYTSSGKAUSPACKATGGMIARREPLIPIBKSSDDD NYSLVDDVSLLVQ FULGMENTYSSGKAUSPACKATGGMIARREPLIPIBKSSDDD NYSLVDDVSLLVQ GKDPNOFTISRGGKASDUALPRGSSEPILLEDMIRKT GKDPNOFTISRGGKASDUALPRGSSEPILLEDMIRKT GKDPNOFTISRGGKASDUALPRGSSEPILLEDMIRKT GKDPNOFTISRGGKASDUALPRGSSEPILLEDMIRKT GKDPNOFTISRGGKASDUALPRGSSEPILLEDMIRKT GKDPNOFTISRGGKASDUALPRGSSEPILLEDMIRKT GSPTGGLINNTPPPTPEGDKKENSSFÇLLUKVALGRABEMILGK COPPSLIFLARTPIPLEVSRIPQ  6596  2 1026  PRIDVERYRHGRRSTGGRSGGMARGDAGSDQROMEBIRAMANIY VILOKSGMTEPGPDVKKKTEBDVECEDDLILLACQPESSVKALD FDISBTRTEVEVERLEPIDHGIPITORRSTCPAHLAPVUCKQV KMVLSKLYBNYINSPERSSKALGKNKKVRIKKRBEH  FRIDVERYRYTSPERSKALGKNKKVRIKKRBEH  6597  2 1026  PRIDVERYREREREDVECEDDLILLACQPESSVKALD FDISBTRTEVEVERLEPIDHGIPITORRSTCPAHLAPVUCKQV KMVLSKLYBNKKLASATINITAKRITCENKGTFLQOMEDGETA AGGRILHTMELTAWNKWYVVSRNYGGILLGPDEPKRHINNCARN ILVEKNYTINSPERSSKALGKNKKVRIKKRBEH  VILOKSGWTERGPDVKKKTEBEDVECEDDLILACQPESSVKALD FDISBTRTEVEVERLEPIDHGIPITORRSTCQALLAPVUCKQV KMVLSKLYBNKKLASATINITAKRITCHKOKTPILQVECKOV KMVLSKLYBNKKLASATINITAKRITCHKOKTPILQVECKOV KMVLSKLYBNKKLASATINITAKRITCHKOKTPILQVECKOV KMVLSKLYBNKKLASATINITAKRITCHKOKTPILQVECKOV KMVLSKLYBNKKLASATINITAKRITCHKOKTPILQVECKOV KMVLSKLYBNKKLASATINITAKRITCHKOKTPILLOCEDDGETA AGGRILHTMELTAWNKWYVVSRNYGGILLGPDEPKRHINCARN ILVEKNYTNSPERSSKALGKNKKVRIKKRBEH  FRIENTEFREVEVERLEPIDHGIPITORRSTCQALLAGAGSTL VLSPGCTANGKKKATRIKARRITTAKRITCHKOKTPILLOCEDGETA AGGRILHTMELTAWNKWYTORYSGGILLGPDEPKRHINCARN ILVEKNYTNSPERSSKALGKNKKVRIKKARRITTAKRITCHCOKTPILOCEDGETA AGGRILHTMELTAWNKWYTORYSGGILLGPDEPKRHINCARN ILVEKNYTNSPERSSKALGKKKRORKREBH FRIENTERPTEVERS				· · · · · · · · · · · · · · · · · · ·
Dytylkisyhrehidrylkykritorywykrishirp   1			ĺ	
1 1096 BFPGRRPRGSQASPICATGGPALLRAPTRAMTRSLPKGNPWSA DILSTIGYDNIIQHLMNGRKNCKEPRDFIRRAAIBERYGKDLI MLSRKIPGGGSEINTLKRALEVPFQQVDNVAQGIIQLAGSLEBE ARMBERRKQKLQRKKTELIMDALHKQKSLQPKKMDAKRIYE QKCRDKDRABQAVSRSANLAVPRQQEELFYKLATSKTAVEOSDK AYMLHIGTIDLKVRSENGSEHIKACKEAPERQECERINFFRRAIML HVRQLSQQCVSTSBMTEGOVRSLEMCISTEVVLQRKTGQI PPAPIMYENFYSQKNAVPAGKATGPNLARRGPLPIPKSSPDDP NYSLVDDYSLLNQ FLOTMSDSDLSEDEGILSLAGKKKRRGNLPKESVKLLRDWLYLH RYNAYPSRQRKISLGGYTNLSVLQICNWFINARRKLLPDMLRKG GKDPNOFTISRGGKASDUALPRGSSEPLAVPGSTLILLTRAEA GSPTGGLFNTPPPTPPPQDKRGPSSPQLIVEVALQRAEMELQK GKDPNOFTISRGGKASDUALPRGSSEPLAVPGSTLILLTRAEA GSPTGGLFNTPPPTPPPPQDKRGPSSPQLIVEVALQRAEMELQK QQDPSLPLHRTPIPLVSENPQ 6596 2 1026 PRLPVRRYBGRRIJGGRSGGMARGDASDQGQREEIRAMAAIY VLIQKSQMTRBGDPVKKRYBEEDWCRGDULLACQPSSVKALD FDISETRTEVEVERLPPIDHGIPITDRRSTPQAHLAPVVCPKQV KMVLSKLYBNKLLSATINNITARRIJCEDRGTFLJQCDEDGETA AGGRLHLMERLBAVNKWVVVSRNYGGILLGPDRFFKHINNCARN ILVEKNYTNSPERSSKALGKNKKVRKRREH PTYQLMAPWLKQGERADLSNSLBEIYIQNIGSSILYLWVEKTRD VLIQKSQMTERGDDVKKKYREBEDWCRGDUFGDDGETA AGGRLHLMERLBAVKNWVVVSRNYGGILLGPDRFFKHINNCARN ILVEKNYTNSPERSSKALGKNKKVRKRREH PTYQLMAPWLKQGERADLSNSLBEIYIQNIGSSILYLWVEKTRD VLIQKSQMTERGDDVKKKYREBEDDUCTORT-QOCEDDGETA AGGRLHHMERLBAVKNWVVVSRNYGGILLGPDRFKHINNCARN ILVEKNYTNSPERSSKALGKNKKVRKRREH PTSTETRTEVEVERLPPIDHGIPITDRRSTPQABLAPVVCPKQV KMVLSKLYRNKKLASATINITARRIJAKTGLAPFLQDCEDDGETA AGGRLHHMERLBAVKNWVVVSRNYGGILLGPDRFKHINNCARN ILVEKNYTNSPERSSKALGKNKKVRKREH PTSTETRTEVEVERLPPIDHGIPITDRRSTPQABLAPVVCPKQV KMVLSKLYRNKKLASATINITARRIJAKTGLAPFLQDCEDDGETA AGGRLHHMERLBAVKNWVVVSRNYGGILLGPDRFKHINNCARN ILVEKNYTNSPERSSKALGKNKKVRKKREH PRVRANTRANGFRENGERSGSGRIDAGDGAPFRGFKRINTCARN ILVEKNYTNSPERSSKALGKNKKVRKREH FRIKKGBLEBRIJAKTARVATIVAKYVGVSSCSONNSV FTLYBILTNGEDTEDBEFHGLDEATLLRALQQLGHKARSITTVS DGRPRGVVLLARGTCLAPTGCBFFENSKLQUGDFFFTLVRBGGERSGSGRIDB DFRKVVLLARGTCRGEFFFTDVRBGGERSGSGRIDB DFRKVVLLARGTCRGEFFTDVRBGGERSGSGRIDB DFRKVVLGGGSVERANTALARALGALLQGERKRGETER MREVNAADVKQLGGSVELVDIGKQKLPOSETPLPFILLGRIGG DPRKVVLLDGGSVELVDIGKGKETCLEGRESSGSGGLDB LIFARDTFFFKDVDVVCISONVALDGRIFTLIFBHKDTLHBIG VESNANDHERSGR			•	· -
DILSTIGYDNI I GHLMMGRINCKEPEDPLIKRRAALHERYGKOLLA NLSRKKPCQSSEINTLKRALEVPKQVODNVAQCHIQLAQSLREE ARKMEEPRKQKLQRKKTELIMDALHKRQSLQPKKTMDAKKNYE QKCRDKOBAEQAVSRSANLWNPKQQEKLPYKLINSTKIVAEDSD AYMLHIGTILDKVRERWIGSBEII KACEAPRAGECRIMPFERNALML HVNQLSQQCYTSDENYRQVRKSLEMCSIQRDI BYFVNQRKTSQI PPAP IMYENTYSSQKNAVPAGKATGPNLARRGLPI PKSSPDDD NYSLVUDIYSLLYQ  6595 57 781 PLOTMSDSDLGEDEGLLSLAGKRRREGHLPRESVKLIERDWLYLH RYNNYPSSQKKLSUSGYNLSVJQI CNMP IMARRILLIPDMLRKD GKDPNQFTISRRGGKASDVALPRGSSPSVLAVSVPAPTHVILSLS VCSMPIHSQGGEKPAAPPPRGBLES SKDLAVSVPAPTHVILSLS VCSMPIHSQGGEKPAAPPPRGBLES SKDLAVSVPAPTHVILSLS VCSMPIHSQGGEKPAAPPPRGBLES SKDLAVSVPAPTHVILSLS VCSMPIHSQGGEKPAAPPPRGBLES SKDLAVSVPAPTHVILSLS VCSMPIHSQGGEKPAAPPPRGBLES SKDLAVSVPAPTHVILSLS VCSMPIHSQGGEKPAAPPPRGBLES KDLAVSVPAPTHVILSLS VCSMPIHSQGGEKPAAPPPRGBLES KDLAVSVPAPTHVILSLS VCSMPIHSQGGEKPAAPPPRGBLES KDLAVSVPAPTHVILSLS VCSMPIHSQGGEKPAAPPPRGBLES KDLAVSVPAPTHVILSLS VCSMPIHSQGGEKPAAPPPRGBLES KDLAVSVPAPTHVILSLS VCSMPIHSQGGEKPAAPPPRGBLES KDLAVSVPAPTHVILSLS VCSMPIHSQGGEKPAAPPPRGBLES KDLAVSVPAPTHVILSLS VCSMPIHSQGGEKPAAPPPRGBLES KDLAVSVPAPTHVILSLS VCSMPIHSQGGEKPAAPPPRGBLES KDLAVSVPAPTHVILSLS VCSMPIHSTERPPTTPEQOKREPSTFQLALMAVIV GERKCVIDDCAKIFCI ISDDLDDPKWTILCLQWULPNETYGAAP PIYQLAMPHIKQGERADLANSLESSI IT VCDRGTFLQCDEGTA AGGRILHIMBILNVRNVWVVVSRWGGILLISPDRFHIINNCARN LUVEKSYTYTISSPESSKALGKNKKVRKRKRBH  6597 2 1026 PREPVRRYHSGRRILQGRSGGBAGEGDAGSQGROBES EAMAAIY VLIQKSQMTEPSPDVKKRTEBEDVECEDDLILACQPESSVKALD PDISTTETTEVEVELB PIDEG PITTORSTFQABLAPVVCPKQV KMVLSKLYRNKILASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRILHIMEILNVRNWVVVSRWGGILLISPDFHTHINNCARN LUVEKSYTTHSPESSKALGKNKKVRKRRBH  6598 1099 419 PROVENATTHSPESSKALGKNKKVRKRKRBH LUKRKGRILBWARGESPLFANGADSLAVKLORKFURSTFHUNCARN LUVEKSYTTYSPESSKALGKNKKVRKRKRBH LRKGGLBWALGAGSPLFANGADSLAVKLORKFURSTFHUNCARN VLSKLYRNKLASATHNIYARIYCEDKGRANGAGILGTVFIR SKGLQS  DPCKTVCTYGHLDVQPAALEBDMDSRFFTUNGCALHGRGS DPCKTVCTYGHLDVQPAALEBDMDSRFFTUNGCKLIGRGS DPCKTVCTYGHLDVQPAALEBDMDSRFFTUNGCKLIGRGS DPCKTVCTYGHLDVQPAALEBDMDSRFFTUNGCKLIGRGS DPCKTVCTYGHLDVQRAGGSLIGHGER MEVAADVKGCGSFVGGSVHRAMTOLLILKM	- FF0.4		1000	I
MLSRKKPCGOSETNTIKRALRYPKQQVDNVAQCHIQLAGSIREE ARKMEBPREKQKLQRKKTELIMDAIHKQKSLQFKKTMDAKKNYE QKCRDKDRAEQAVSRSANLVNPKQQEKLFVKLATSKTAVEDSDK AYMLHGTLDKVRERGGSBHI KACEAPBAQGCERIMFFRINALMI. HVRQLSQCCYTSDEMYROVPKSLEMKSTQRDI BYFVVQKRTGLI PPAP IMYENFYSSQKNAVPAGKATGPNLARRGPLPI PKSSPDDP MYSLVDYSLLIVQ  6595 57 781 PLOTMESDLGEDEGLISLAGKRKRRGMLPKESVKILRDWLYLH RYNNYPSBQEKLSLSGYTNLSVLQI COMPINARRILIPDMLPKD GKDPNOPTI STRRGGKRSDWALPRGSPUAVSVPAPTHVILGS VCSMPILHSQGGKPAAPPPRGBLES-YKPLVTPGSTLTLLTRAEA GSPTGGLEMTPPPTPPEQDKEDFSSFQLLDVEALQRAARMELQK QODPSLPLHTTI PLLVESMPQ  6596 2 1026 PRLDVRRYHGRRRILGGRSGEMBAEGDAGSDQRONBESIRMANL FOLSKAPWLKGQRRADLSNSLEETYIQNIGESILVIMVEKIRD VLIQKSQMTERGPDVKKKTEEBDVECEDDLILAGPESVKALK FOLSKAPWLKGQRRADLSNSLEETYIQNIGESILVIMVEKIRD VLIQKSQMTERGPDVKKKTEEBDVECEDDLILAGPESVKALK AGGRLLHHMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSFERSSKALGKNKKVRKKKREH  6597 2 1026 PRLDVRRYHGRRRILQGRSGCHBAEGDAGSDQRONBEIRAMAAIY VLIQKSQMTERGPDVKKKTEBEDVECEDDLILAGPDRFKHINNCARN ILVEKNYTNSFERSSKALGKNKKVRKKRENE  6597 2 1026 PRLDVRRYHGRRRILGGRSGEHBAEGDAGSDQRONBEIRAMAAIY VLIQKSQMTERGPDVKKKTEBEDVECEDDLILAGPDRFKHINNCARN ILVEKNYTHSFERSSKALGKNKKVRKNKREH  6598 1099 419 PRVQLNAPBEGGBRADLSNSLERIYIQMIGBSILVIMVEKIRD VLIQKSQMTERGPDVKKKTEBEDVECEDDLILLGPDEFKHINNCARN ILVEKNYTNSPEBSSKALGKNKKVRKKKKHH  GSPRCVULLBGTLAGHLAGNATVARTYCEDKGTPLQCEDDGGETA AGGRLLHMEILNVKNVWVVSGNVGLLLGPDEFKHINNCARN ILVEKNYTNSPEBSSKALGKNKKVRKKKKHHILLGPDEFKHINNCARN ILVEKNYTNSPEBSSKALGKNKKVRKKKKHHILLGPDEFKHINNCARN ILVEKNYTNSPEBSSKALGKNKKVRKKKKHHILLGPDEFKHINNCARN ILVEKNYTNSPEBSSKALGKNKKVRKKKKHHILLGPDEFKHINNCARN ILVEKNYTNSPEBSSKALGKNKKVRKKKKHHILLGPDEFKHINNCARN ILVEKNYTNSPEBSSKALGKNKKVRKKKKHHILLGPDEFKHINNCARN ILVEKNYTNSPEBSSKALGKNKKVRKKKKHHINLARVATIGSUGNAMCSIL LRKKGRLEBHLDKSKISSLIMMRRPEEMGKLIYGWSRGGONGSV FTILYBLITNGGDTEDEEFHGLDEATILLALAGLQCHKKREITTVS DGRRRCVLLAFGCLUBGGSVELVDIGGSVELVDIGGRALITVS DGRRCVULLAFTCLEHLUNDRATURGLKKRETTURGKLEGRSGSGGLGDE DPQKKTVCTYCHLDVQPAALEDGMDSEPFTLVERGOKHINGKSS DDKGPVAGANINALBAYQKTGGGEIPVNYRFCLEGMEESGSGGGLGDE LIFARNDTFFKUDTUTCLSGNYTHGCKKKRPCLTYGLGEGLEGGSGGGDE LIF	0374	1 1	ودورد	
ARKMEBFREKORLORKATELLIMDALHIKOKSLÖPKKTMDÄRKNYE QKCRDICDEARGAVSRSANLVMPKQGEKLYVKLATSKTAVEDSDK AYMLHIGTIDKVRERMOSBHI KACEAPBAGECSRIMFERNALMI. HVNGLSQGCYTSDEMYSQVEKSLEMCSTQRDI SEFVINQRKTGGI PPAPI HYKRYFYSGGKANVPAGKATGGILARRGPLPI PKSSPDDP MYSLVDDYSLLVO  6595 57 481 PLGTMSDŠDLGSDEGILISLAGKRKRRGNLPKESVKILRDMLYLH RYMAYPSEGBKLSISGGTNILSVLQI COMP IMARRILLEPDMIRKD GKDPNOFTI SRRGGKASDVALPRGSSPSVLAVSVPAPTHVILSLS VCSMPLHSGOGEKPARPPRGBILGSSVLAVSVPAPTHVILSLS VCSMPLHSGOGEKPARPPRGBILGSSVLAVSVPAPTHVILSLS VCSMPLHSGOGEKPARPPRGBILGSSVLAVSVPAPTHVILSLS VCSMPLHSGOGEKPARPPRGBILGSSVLAVSVPAPTHVILSLS VCSMPLHSGOGEKPARPPRGBILGSVLAVSVPAPTHVILSLS VCSMPLHSGOGEKPARPPRGBILGSVLAVSVPAPTHVILSLS VCSMPLHSGOGEKPARPPRGBILGSVLAVSVPAPTHVILSLS VCSMPLHSGOGEKPARPPRGBILGSVLAVSVPAPTHVILSLS VCSMPLHSGOGEKPARPPRGBILGSVLAVSVPAPTHVILSLS GSPTGGLAFHTPPTPPEDDOKRDFSSFQLLVEVALGRAREMELQK QQDPSLPLLHTPIPLVSENPO  6596 2 1026 PREPVRRYBGRRIGGESGEBVAREGDAGSDQROMEEIRAMAATY VLIQKSQMTEROPDVKKKTEEBDVSCCBDLILAQPESSVKALD FDISETTREVEVENELPPIDHGIPITORRSTFQAHLAPVVCPKQV KMVLSKLYENKKLASATHNIVANRIYCEDKKNEMH  6597 2 1026 PREPVRRYBGRRILQGRSGEBMAEGDAGSDQROMEEIRAMAATY CERMCVIDDCAKIPCINISDDIDPKWTLCLQFUSNYEHTANAAY VLIQKSQMTEROPDVKKKTEBBUVSCEDDLILAQPESSVKALD FDISETTREVEVENELPPIDHGIPITORRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIVANRIYCEDKGTPIQDCEDDGETA AGGRILHIMBILNVKNWVVVSRWYGGILLISPDRFKHINNCARN VLIQKSQMTEROPDVKKKTEBBUVSCEDDLILAQPESSVKALD FDISETTREVEVENELPPIDHGIPITORRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIVANRIYCEDKGTPIQDCEDDGETA AGGRILHIMBILNVKNWVVVSRWYGGILLISPDRFKHINNCARN ILVEKMYTTSVENESSESKALGKNKKVKKKKRENEH  ERKKGNLEWLDKSKSSFLIMWRPEEWGKLIYQWVSRSGQNNSV FTLYBITNGEDTEDEEFHGLDBATLIKRAGLQGHAAGSL LRKKGNLEWLDKSKSSFLIMWRPEEWGKLIYQKUSRYPTPD SKGIQS  DPQKKTVCIYGHLDVQPAALEBDGMDSRFPTILVSCOCYPTPTD SKGIQGS  DPQKTVCIYGHUDVQCSVELVDICKQKIPDGSRIPLPPILLGRIGG DPQKTVCIYGHUDVQCSVELVDICKQKIPDGSRIPLPPILLGRIGG DPQKTVCIYGHUDVQCSVELVDICKQKIPDGSRIPLPPILLGRIGG DPQKTVCIYGHUDVQCSVELVDICKGKREPCITGGEBELGSEGEIDB LIPARDTFFROVDYVCISDNYHLCKKKPCITGGREGGEIGLB LEVARDTFFROVDYVCISDNYHLCKKKPCITGGREGGEIGLB LEVARDTFFROVDYVCISDNYHLCKKKPCLILLIS		1	[	
QKCRDKORARQAVSRSANLWAPKQQEKLFVKLATSKTAVESDK AYMLHIGTLDKVREBUQSBHI KACKAPRAQECERINFFRNALMI HYNQLSQQCYTSDRMYRQVRKSLEMCSIQRDI BYFVNQRKTSQI PPAP IMYRMYTSSQKNAVPAGKATGPNIARRGPLPI PKSSPDDP NYSLVDDYSLLVQ  6595 57 V81 PLGTMSDSDLGEDGGLLSLAGKRKRRCNLPKESVKLLRDWLYLH RYNAYPSEQEKLSLSGQTNLSVLQI CMNHARRGLLPDMLRKD GKDNDQFTISRRGGKASDVALPRGSSPSVLAVSVPAPTNVLSLS VCSMPLHSQGGKCPAPPPRGELESPKPLVTPGSTLTLLTRAEA GSPTGGLFMTPPPTPPPPDGPKEDSPKPLVTPGSTLTLLTRAEA GSPTGGLFMTPPPTPPPPDGDKEDSPKPLVVVALQRAAEMBLQK QQDPSLPLLHTPIPLVSENPQ 6596 2 1026 PRLPVRRYEGRRRILGGRSRGIMARGDAGSDQRORESIERAMAAIY GERKCVLDDCANI FCHIR SDDIDDPKWTLCLQVMLPNBYPGTAP PIVQLANAPMLKGQBRADLSNSLBEIYIQNIGBSILYLWVRLKD VLQKSQMTEPGPDVKKKTEEBDVBCCADLILACQPESSVKALD FD15ETRTRVEVEELPPIDHSIPLTDRRSTFQAHLAPVVCPRQV KMVLSKLYENKKLASATHNIVAKRIYCEDKQTFLQDCSDDCGTA AGGRLIGHMSILNVKNVWVVVSRNGLGLIGPDRRFHINNCARN ILVEKNYTNSPESSKALGKNKKVRKDKKRNRH 6597 2 1026 PRLPVRRYHSGRRRICGRSRGHMAEGDAGSLQQNEESIERAMAAIY GERRCVUDCALI PCIR ISDDIDDPKWTLCLQVMLPNBYPGTAP PIVQLANPHLKGGBRADLSNSLBBIYIQNIGBSILYLWVBKIRD VLQKSQMTEPGPDVKRKTEBEDVECDDLLLACQPESSVKALD FD15ETRTSVBVEBLPPIDHGIPITDRRSTFQAHLAFVVCPKQV KMVLSKLYENKRLASATHNIVAKRIYCEDKQTFLQDCSDUCATA AGGRLIGHMSILNVKNVVVVSRGUBLLGSDDRFKHINNCARN ILVEKNYTNSPBESSKALGKNKKVRKDKRNRH 6598 1099 419 PRVRMATTMAMSFEWFRQYGFPPFFTLQPWDTRQKQLAAWGSL LIKKGNLBWLDKSSSFLIMMRPEBKRGKLIYQWVSRSGONNSV PTLYBLITUGBDTEDBEFHGLDBATLLLALQALQQBHKABITTVS GGPRRQVLLAGTCLPPLLITSBLEDRAFKRRQTCCPPKTGSVTPPD SKGLQS  MAGALTTLEKYIDERMQDRYIKKLAKWAIQSVSAWPEKRGBIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSETPLPPILLGRLGS DPGKYTVCIYGHLDVQPAALEDGWDGRFFTLUKRGGKLHGRGST DDKGPVAGMINALLARQKGCGEIPKRCLGSGSGSGEDB LIFARKOTPFROUDYCLSDNYHLGKKKPCLTYHGLRGICYFFIE VKSNKOLLHSGVVGGSVVHEAMTDLILLURGSLUKKRGICTFFIE URSNKOLLHSGVVGGSVVHEAMTDLILLURGSLUKKRGICTFFIE VKSNKOLLHSGLUSVGSVVHEAMTDLILLURGSLUKKRGILLIFGIN EAVAAVTKEEHLLVDDIDFIIERFAKOVGQILLHSHKKDILHH EAVAAVTKEEHLLVDDIDFIIERFAKOVGQILLHSHKKDILHUR EAVAAVTKEEHLLVDDIDFIIERFAKOVGQILLHSHKKDILHUR		1	l	
AYMLHICTLDKVREEMQSEMIKACKAPEAGECRINFFRALWIL HVWQLSQCCYTDRMYRQVRKSLEMCSIQRDIBYFVNDRKTQQI PPAP IMYEMYTSSQLEMAYPACKATGEMILARRGPLEY PKSSPDDD NYSLVDDYSLLYQ  PLGTMSDSDLGBEGILSLAGKKKRRCNLPKESVKILRDWLYLH RYMAYPSEGEKLSLGGYTNLSVLQICNWFINARRKLLEDMIRKD GKDPNOFTISRRGGKASDVALPRGSSESVLAUSVPAPTINVISLS VCSMPHISGOGSKEPAAPPPRGELES PKPLLVEVALQRAEMBLQK QOPSLPLLHTIPLVSENPQ  6596 2 1026 PRIPVRYHGNRSLGGERGHMAGDAGSDQRQNEEIEAMAAIY GREWCVIDDCAKIFCIRISDDIDDPKWILCLQWMLPNSYPGTAP PIYQLMAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLQKSQMTEPGPDVKKKTBEEDVBCGDDLILLACQPESSVKALD FDISETRTBVEVEELPPIDHSIPITDRRSTFQAHLAPVVCPRQV MVLSKLYENKKLASATINIVAVRICDBOOTSTAAA AGGRILHIMBILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTHSPESSKALGKNKKVRDKKRNER  6597 2 1026 PRIPVRYHSRRBLQGRSRGHMAGDAGSDQRQNEEIEAMAAIY GERWCVIDDCAKIFCIRISDDIDDPKWILCLQVMLPNSYPGTAP PIYQLNAPMLKGQRRADLSNSLEEIYIQDEGSILYLWVEKIRD VLQKSQMTEPGPDVKKKTBEBDVBCCBDDLILLACQPESSVKALD FDISETRTBVEVELDPIDHSIPITDRRSTFCAHLAPVVCPRQV KMVLSKLYENKKLASATINIVAYRIYCBDKOTPILQDCBDGGETA AGGRILHHMEILNVKNWWVVVSRWYGGILLGDDFKHINNCARN ILVEKNYTHSPESSKALGKNKKVRDKKRNER  6598 1099 419 PRIVMATTAMASSERBWOQYRPPPFTLQPNOTRGKQLAAWGSL LKKKGNLBWLDKSKSSTLIMRRPEEMGKITYQWVSRSGQNNSV FTLYBILTNGEDTDEBEFHGLDBATTLARALQALQQEKARBITVSC DGPRRQVLLAGTCLPLLTSHLSRAPKRRQTOCPPKTGSVTPPD SKGLQS  WAALATTLEKYIDREDDEBEFHGLDBATTLARALQALQQEKARBITVSC DGPRRQVLLAGTCLPLLTSHLSRAPKRRQTOCPPKTGSVTPPD SKGLQS  WAALATTLEKYIDREDDEBEFHGLDBATTLARALQALQQEKARBITVSC DDRKGYVAGNINALRAPVKTCYGYGGVEHDAWTGLEGMESSSEGLDB LIFARKOTPFROUDYVCISONYMIGKKKPCITYGERGKIHGRGST DDRKGYVAGNINALRAPVKTCYGYGGVEHDAWTDLILUGSLUVKREGSGT DDRKGYVAGNINALRAPVKTCYGYGGVEHDAWTDLILUGSLUVKREGSITR MBEVAAADUWGLGGSVELVDIGKQKLPDGSTFLIPPTILLGRIGS DDRKGYVAGNINALRAPVKTCYGTPTRWRCTLEEGMESSSSEGLDB LIFARKOTFFROUDYVCISONYMIGKKKPCITYGERGCFTFIE VBCSNKCLHSGKVYGGSVHEAMTDLILUGSLUVKRGGICTFFTE VBCSNKCLHSGEVYGGSVHEAMTDLILUGSLUVKRGCILLIFGKG TDRKGYVAGNINALRAPVKTCYGGTCTPTRWOTCLEGMESSSSECLDB LIFARKOTFFROUDYVCISONYMIGKKKPCITYTGLRGTCTPFTE VBCSNKCLHSHCKVOTGDTDFILEFFRAUVCAQILLESHKKKDILHE				
HVNQLSQQCYTSDEMYEQVRKSLEMCSIQRDI BYFVNQRKTGQI PPAPIMYENPYSSQKNAVPAGKATGPHARRGPLPIPKSSPDDD NYSLVDDYSLLVQ  19LGTMSDSDLGEGGLLSLAGKRKRRGNLEKSVKILKDWLYLH RYNAVPSGOKLISLGGYNLSVLQICNMFINARRRILPDMLRKD GKDPNQFTISRRGGKABDVALPRGSSPSVLAVSVPAPTNVLSLS VCSMPLHSQGGKKPARPPRGELESSREULTPOSITLITLITREA GSPTGGGFMTPPPTPPPPRGERESSPFQLLVEVALQRAAEMBLQK QQDPSLPLLHTIPLVSENPQ  6596 2 1026 PREVVRTYHGRRZLQGRSRGHMAEGDAGSDQRQNEBIBAMAAIY ULQKSCMTPEGPDVKKTEEBDVBCGDULLLGAUPENSVFADH PIYQLMAPMIKGGBRADLSNSLBEIYIQNIGSSILYLWVBKIRD VLQKSCMTPEGPDVKKTEBEBVGCBDLILAGDPESSVKALD FDISETRTBVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMYLSKLYENKKLASATHNIVAKRIYCEBKGTFLQDCSBDCGHA AGGRLEHMBILNVKNOWVVSKRYGELLGPDRFKHINNCARN ILVEKNYTNSPESSSKALGKNKKVRKDKKRNBR  6597 2 1026 PREVVRTHGRRRLQGRSRGHMAEGDAGSDQRQNEBIBAMAAIY GERMCVIDDCARIFCIRISDDIDDPKWTLCLQVMLENBYPGTAP PIYQLMAPMIKGGBRADLSNSLBEIYIQNIGBSILYLWVBKIRD VLQKSCMTPGPDVKKKTEBBUVGCBDLILAGDCSDCGHA AGGRLEHMBILNVKNAVVVSKYDKYCFLDQCDSSUKALD FDISETRTBVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMYLSKLYENKKLASATHNIVAKRIYCEBKGTFLQDCGSDCKALA AGGRLEHMBILNVKNAVVVSKYDKYCFLDQCDSSUKALD FDISETRTBVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMYLSKLYENKKLASATHNIVAKRIYCEBKGTFLQDCGSDCKATA AGGRLEHMBILNVKNAVVVSKYDKYGCDLLLGDDFKHTHINCARN ILVEKNYTNSPBESSKALGKNKKVKRKDKKRNBH  6598 1099 419 PRVRMATTMAMSFEWFWQYRFPPFFTLQPWDTRQKQLAAWCSL ULGKRYTHSPBESSKALGKNKKVRKDKKRNBH  FRUKKGILBBLDKSSSFLIMMRPEEMGKLIYQWVSRSGQNNSV PTLYBITUNGBCTEBEBFHGLDBATLQALQQBKRKBITTVS DGPRRQVLLAGTCLPLLTSLLSARAKRRQTQCPPKTGSVTPPD SKGLQS  MEVAAADVKGLGGSVELVDIGKQKLPDGSBIPLPPILLGRLGS DPKGKTVCIYGHLDVQPAALEDGWDGSPFTLUERDGKLHGRGST MBEVAAADVKQLGGSVELVDIGKQKLPDGSBIPLPLPPILLGRLGS DPKGKTVCIYGHLDVQPAALEDGWDGSPFTLUERGGKLHGRGST MBEVAAADVKQLGGSVELVDIGKQKLPDGSBIPLPPILLGRLGS DPKGKTVCIYGHLDVQPAALEDGWDGSPFTLUERGGKLHGRGST MBEVAAADVKQLGGSVELVDIGKQKLPDGSUCLUERGGCTCYFFIE VECNIKOLLHSGVVGGSVVHEAMTDLILLURGSLUZKRGGICYFFIE VECNIKOLLHSGVVGGSVVHEAMTDLILLURGSLUZKRGCICYFFIE VECNIKOLLHSGVVGGSVVHEAMTDLILLURGSLUZKRGCICYFFIE VECNIKOLLHSGVVGGSVVHEAMTDLILLURGSLUZKRGCICYFFIE VECNIKOLLHSGVCGSVHEAMTDLILLURGSLUZKRGCICHFIE				
PPAP INTERPYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDP NYSLVUDIYSLLYQ PLGTMSDSDLGEDEGILSLAGKRKRRGNLPKESVKLLRDWLYLH RYNAVPSBQBKLGLSGGTNLSVLQI CNMP INARRELLEDMLRKD GKDPNQFTISRRGGKASDVALPRGSSPSVLAVSVPAPTNVLSLS GKDPNQFTISRRGGKASDVALPRGSSPSVLAVSVPAPTNVLSLS GSPTGGLFNTPPPTPPEQDKRDFSSSGLLVEVALQRAAEMELQK QQDPSLPLLHTP LPUSENPQ QQDPSLPLLHTP LPUSENPQ PI YQLNAPMLKGGGRADLSDLGETYIQNIGESILYLMVBKIRD PI YQLNAPMLKGGRRADLSDLEETYIQNIGESILYLMVBKIRD VLIQKSQMTEPGPDVKKKTBEEDVBCRDDLILACQPESSVKALD FDISETRTBVEVSELPP IDHGIP ITDRSTPQAHLAPVUCKQV MVLSKLYENKKLASATHNILYARYIYCEDKQTPTQDCKDDGSTA AGGRLLHIMBILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYINSPERSSKALGKNKKVRDKKRNEH GEBRCVIDDCAKIFCIR ISDDLDDPKWTLTQVMLPNSTYPGTAP PI YQLNAPMLKGGBRADLSNGLEBIYIQNIGESILYLMVBKIRD VLIQKSQMTEPGPDVKKKTBEEDVBCDDLILACQPESSVKALD FDISETRTBVEVEELPP IDHGIP ITDRSTPQAHLAPVUCKQV KWLLSKLYRNKKLASATHNILYARIYLGDKGTPFLQDCKDDGSTA AGGRLLHIMBILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN VLIQKSQMTEPGPDVKKKTBEEDVBCEDDLILACQPESSVKALD FDISETRTBVEVEELPP IDHGIP ITDRSTPQAHLAPVUCKQV KWLLSKLYRNKKLASATHNILYARIYLGBKGTPFLQDCKDDGSTA AGGRLLHIMBILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTINSPRESSKALGKNKKVNKDKKRNEH GSPLSHIMBILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTINSPRESSKALGKNKKVNKDKKRNEH KWLANATMAMSESPWWQVXFPDPPFTLQDCKDDGSTA AGGRLLHIMBILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVERNYTINSPRESSKALGKNKKVNKDKKRNEH KRKGRLBWLDKSKSSFIJMWRRPEBWGKLIYQWVSREGGNNSV VLSPCRLHKQSSMTVMEAQBSPLPNNVKLQRKLPVESIQIVLKE LRKKGRLBWLDKSKSSFIJMWRRPEBWGLIYQFVSTEGGNNSV VLSPCRLHKQSSMTVMEAQBSPLPNNVKLQRKLPVESIQIVLKE LRKKGRLBWLDKSKSSFIJMWRRPEBWGLIYQFVSTEGGNNSV DGPRRQVLLAGTCLPLLLTSHLSRAFKRQTQCPPKTGSVTPPD SKELQS KMAPALTTLFKYIDBNQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MBEVAAADVRDLGGSVELVDICKQKLPDGSRFPLPFILLGRIGGS DDKKFVVGYGGVHGABILDGWBSPPTLVERGGKLHGRGST DDKKFVVGYGGVHGABILDGWBSPPTLVERGGKLHGRGST DDKKFVVGYGGVHGABILDGKGCTVFFIR VGCSNKOLHSGVGGSVHEANTDLILLHGSLVDKRGTILLIGGI EAVAAVTEEBKLJYDDIDPILEFFKDVGAQILLHSHKKDLILHG		i	İ	
NYSLVDDYSILYQ				1
PIGTMSDSDLGEDEGILSLAGKRKRRGNDEGSVKILRDWLYLH   RYMNYPSBGEKLSLGGTMLSVLQICNWFIBARKRILLDMLRKD    GKDPMOPTISRGGKABDVALPGSSPSVLAVSVPAPTMVISLS    VCSMPLHSGGEKPAAPPRGRISES-KPLLVSVPAPTMVISLS    VCSMPLHSGGEKPAAPPRGRISES-KPLLVSVAAPTMVISLS    VCSMPLHSGGEKPAAPPRGRISES-KPLLVSVAAPTMVISLS    VCSMPLHSGGEKPAAPPRGRISES-KPLLVSVAAPTMVISLS    VCSMPLHSGGEKPAAPPRGRISES-KPLLVSVAAPTMVISLS    GEBWCVIDDCAKIFTIPPTPPDEQDKEDFSSFGLLVEVALQRAAEMBLQK    GEBWCVIDDCAKIFTIRDDIDDPKWTLCLQVMLPNSYPGTAP    VLIQKSGMTEPGPDVKKKTSEEDVECRODLILACQPESSVKALD    FDISETTRTSVEVSELPPIDHGIPITMRSTFGAHLAPVVCPKQV    KMVLSKLYENKKLASATHNIYAYRIYCEDKQTFLQDCEDDGSTA    AGGRLIHHMSILMVKNVMVVVSRWYGGILLGPDRFKHINNCARN    LLVEKMYTNSPESSKALGKNKKVRKDKKRKEH    FINGLANPHLKGGERADLSDLEBITYIONIGGSILYLMVERIRD    VLIQKSGMTEPGPDVKKKTSERDVKCEDDLILACQPESSVKALD    FOLSETTRTSVEVEELPPIDHGIPITTGRSTFGAHLAFVVCPKQV    KMVLSKLYENKKLASATHNIYAYRIYCEDKQTFLQDCEDCETA    AGGRLIHHMSILMVKNVMVVSRWYGGILLGPDRFKHINNCARN    LVEKNYTNSPRESSKALGKNKKKVRKKKKKRKHILAFUNCARN    LVEKNYTNSPRESSKALGKNKKKVRKKKKKRHILAFUNCARN    LVEKNYTNSPRESSKALGKNKKKVRKKKKKRHILAFUNCARN    LVEKNYTNSPRESSKALGKNKKVRKDKKRNEH    G598		İ		1
RYNAYPSBQEKLSLSGQTNLSVLQICNWFINARRRLLPDMLRKD GKDPNQFTISRRGKASDVALPRGSSEPVLAVSVPAPTNYLSL VCSMPLHSGGGEKPAPFPFRGBLESPKLLVTPGSTLTLITAREA GSPTGGLFNTPPPTPPEQDKRDFSSFQLLVEVALQRAAEMELQK QQDPSLPLLHTPIPLVSENPO  6596 2 1026 PRLPVRRYHGRRRIJGGRSGCHMARGDAGSDQRONEEIRAMAAIY GREWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPMLKGQERADLSNSLEEITYLONIGESILTMVEKIRD VLIQKSQMTERGPDVKKKTEREDVGCBDLILACQPESSVVALD FDISETRTEVEVERLPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMYLSKLYENKKLASATHNIYAXRIYCEDKQTFLQCEDDGSTA AGGRLLHIMBILMVKNUMVVSKNYGGILLGPDRFKHINNCARN ILVEKNYTINSPESSSKALGKNKKWRKDKKRNEH  6597 2 1026 PRLPVRRYHGRRRLQGRRGKGMKKWRKDKKRNEH  6597 CERKCVIDDCAKIFCIRISDDIDDPKWTLCLQVWLPNEYPGTAP PIYQLNAPWLKGQERADLSNSLEBIYIQNIGGSLQRONEBIRAMAAIY CERKCVIDCAKIFCIRISDDIDDPKWTLCLQVWLPNEYPGTAP PIYQLNAPWLKGQERADLSNSLEBIYIQNIGGSLQRONEBIRAMAAIY VLIQKSGMTERGEDVKKKTERBDVECEDDLILACQPESSVKALD FDISETRTEWEVERELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKLASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHMBILMVKNWVVVSKNYGGILLGPDEFKHINNCARN ILVEKNYTINSPERSSKALGKNKKVRKDKKRNEH  6598 1099 419 PRVWAATTMAMSFEWFWQYRFPPFFTLQPWVDTRQKQLAAWCGL LEKKKNILBELDKSKRSSFLIWRPEBEGKALIYVOWSESGONNSV PTLYBLTNGEDTEDEEFHGLDEATLLRALQALQQEHKABIITVS DGPRRQVLLAGTCLPILLITSHLSRAFKKRQTCCPPKTGSVTPPD SKGLQS  6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAQSSAMPEKRGBIRR MMEVAAADVKQLGGSVELVDIGKQKLPUSSGSPLIPLPFTLLGRIGS DPQKKTVCIYGHLDVQPAALEDGWDGRFPTLYRRDGKLHGRGST DDKKFVAGWINALKAYQKTCQBIPVNVFCLEGMEESGSEGLDE LIFARKDTFFRODDYVCISDNYMIGKKKPCITYGLRGICTFFIE VBCSNKDLHSGVYGGSVHEAMTOLILLHGBLILMGRILIPGIN VBCSNKDLHSGVYGGSVHEAMTOLILLHGRILLHGBLI VBCSNKDLHSGVYGGSVHEAMTOLILLHGBLIKKGILLHGI	6595	57	781	
GKDPNQFTISRGGKASDVALPRGSSPSVLAVSVPAPTNVISLS VCSMPLHISGGEKPARPFPRGRIESS_PKILVIPGSTLTLLITAREA GSPTGGLFNTPPPTPPERDKREFSSFQLLVEVALQRAAEMKLQK QQDPSLPLLHTPIPLVSENPQ  6596 2 1026 PRLFVRFYHGRRIQGRSGGHMAEGDASDGROMEEIAMAATY PIYQLNAPMLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSGMTERGEDVKKKTEEEDVEGDDLILACQPESSVKALD FDISETRTEVEVERLPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMYLSKLYENKKLASATHNIYAVRIYGEDKGTFLQDCEDDGSTA AGGRILHIMBILMVKNVMVVVSRNYGGILLGPDRFKHINNCARN ILVEKNYTNSPESSKALGKNKKVRKDKKKNRBH PRIFVRHYHGRRIQGRADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSGMTERGPDVKKKTEREDVGCDDLILACQPESSVKALD PRIFVRHYHGRRIQGRADLSNSLEEIYIQNIGESILYLWVEKIRD VLYQKSGMTERGPDVKKKTEREDVGCDDLILACQPESSVKALD PRIFVRHYHGRRIQGRADLSNSLEEIYIQNIGESILYLWVEKIRD VLYQKSGMTERGPDVKKKTEREDVGCDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYRNKKLASATHNIYAKRIYCEDKQTFLQCEDDGSTA AGGRILHIMILINVKNVMVVVSRNYGGILLGPDRFKHINNCARN ILVEKNYTNSPEBSSKALGKNKKVRKDKKRNEH PRIVMATTHAVRNIYVSKRYGGILLGPDRFKHINNCARN ILVEKNYTNSPEBSSKALGKNKKVRKDKKRNEH PRIVMATTMAMSFEWEWQYKFDPFFTLQPWUTTRQKQLAAWGSL LRKKGRLEHLMEILNVKNVMVVVSRNYGGILLGPDRFKHINNCARN ILVEKNYTNSPEBSKALGKNKKVRKDKKRNEH PRIVMATTMAMSFEWEWQYKFDPFTTLQPWUTTRQKQLAAWGSL LRKKGRLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYBLINGEDTEDEEFHGLDEATTLIRALQALQQBHABEIITUS DGPRRQVLLAGTCLPLLLTSHLSALQALQQBHABEIITUS DGPRRQVLLAGTCLPLLTSHLSALQALQQBHABEIITUS DGPRRQVLLAGTCLPLLTSHLSALQALQQBHABEIITUS DGPRRQVLLAGTCLPLLTSHLSALQALQQBHABEITLGGGST DPCKKTVCIYGKLDVQPAALAEDGWGSRPFTLVERDGKLHGRGST DDKGPVAGMINALEAYQKTGQBIPUNVRFCLEGMEESGSEGLDE LIFFARKUTFFROUDTVCLSDNYMLGKKKPCITYGLRGICTFFTR VBCSNKDLHSGVYGGSVHEAMTOLLLLMGSLVUKRGRILIFGIN VBCSNKDLHSGVYGGSVHEAMTOLLLLMGSLVUKRGRILIFGIN VBCSNKDLHSGVYGGSVHEAMTOLLLLMGSLVUKRGRILIFGIN VBCSNKDLHSGVYGGSVHEAMTOLLLLMGSLVUKRGRILLFGINFFILLGRILG	0333			
GSPTGGLFNTPPPTPPQDKRDFSSFQLLVEVALQRAAEMELQK QQDPSLPLLHTFIFLVSENPQ PREPURRYHGRRIT.GGRSGERGHMAEGDAGSDQRQNEETRAMAATY GBEWCVLDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKGQRRADLSNSLEETYIQNIGGSILVIMVEKIRD VLIQKSQMTEPGPDVKKKTBEEDVBCCDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATRINIVAKITYCEDKOTFIQDCBDDGSTA AGGRILHIMBILNVKNVWVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTINSFEBSSKALGKNKKVRRDKRRIBEN PIYQLNAPWLKGQRRADLSNSLEBIYIQNIGBSILVIMVEKIRD VLIQKSQMTEPGPDVKKKTBEBDVBCGDGDGTAAGGREUHMERGRRADLSNSLEBIYIQNIGBSILVIMVEKIRD VLIQKSQMTEPGPDVKKKTBEBDVBCCDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATRINIVAYRIYCEDKOTFILQDCBDGSTA AGGRILHIMBILNVKNWAVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTINSPESSKALGKNKKVRRDKKRNEH FDISETRTBVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATRINIVAYRIYCEDKOTFILQDCBDGSTA AGGRILHIMBILNVKNWAVVVSRWXGGILLGPDRFKHINNCARN ILVEKNYTINSPESSKALGKNKKVKRDKKRNEH FDISETRTBVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATRINIVAYRIYCEDKOTFILQDCBDGSTA AGGRILHIMBILNVKNWAVVVSRWXGGILLGPDRFKHINNCARN ILVEKNYTINSPESSKALGKNKKVKRDKKRNEH FFILYBLINGENTEDBEFBGFDRTILRALQALQGERABGILTUS ULSFCRLHKQSSMTVMBAQBSFLFNNVKLQRKLPVSSIQIVLBE LRKKGNLBWLDKSKSSFLIMWRPEBWGLIYQWVSRSGONNSV FTILYBLINGEDTEDBEFHGLDBATLIRALQALQGERKABILTUS DGRRRQVLLAGTCLPLLLTSHLSRAFKRRQTOCPPKTGSVTPPD SKGLQS KMAALTTLFKKYIDENQDRYIKKLAKWVALQSUSAWPEKRGFIRR MMEVAAADVKQLGGSVELVUIGKQKLPDGSFIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSBFFTLVERDCKLHGRGST DDKGPVAGWINALBAYQKTGQBIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFRDUDTVCLSDNYWLGKKKPCITYGLKGICYFFIR VBCSNKOLHSCVYGGSVHEAMTDLILLMGSLUDKRGNILLTPGIN EAVAAVYKESHKLYDDIDDFDIREFAKDVGAQILLHSHKKDILME			Ì	1
QQDPSLPLLHTPIPLVSENPQ  6596 2 1026 PRIPVRRYHGRRRIQGRSEGHMAEGDAGSDQRQBEEIRAMAATY GREWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNBYPGTAP PIYQLMAPWLKQQBRADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEEDVBCEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKOTPIQDCEDDGSTA AGGRLLHIMEILNVKNUMVVVSRWYGGILLGPDRPKHINNCARN ILVEKNYTINSPEBSSKALGKNKKVRKDKKRREH  6597 2 1026 PRLPVRRYHGRRRLQGRSGHMAEGDAGSDQRQNEKIRAMAAIY GEBRCVIDDCARIPCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLMAPWLKQQBRADLSNSLEBIYIQNIGBSILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEBVVCEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGSTA AGGRLLHHMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEBSSKALGKNKKVRKDKKRNEH  6598 1099 419 PRVRHATTMAMSFEWWQVKFPDPFFTLQPNUTTRQKQLAAWCSL LRKKSNLEWLDKSKSSFLIMWRRPEBWGKLIYQWVSRSGGNNSV VLSPCRLHKQSSMTVMEAQBSPLFNNVKLQRKLPVESIQIVLBE LRKKSNLEWLDKSKSSFLIMWRRPEBWGKLIYQWVSRSGGNNSV PTLYBLTNGEDTEDEEFHGLDBATLLRALQALQQBKRABIITVS DGPRRQVULIAGTCLPLLLTSHLSRAPKRRQTQCPPKTGSVTPPD SKGLQS  6599 164 1593 KMAALTTLFKYIDBNQDRYIKKLAKWVAIQSVSAMPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSBIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSRPFTLVERDGKLHGRGST DDKGPVAGWINALRAYQKTGQBIPVNVRFCLEGMEESGSGGLDB LIFARKDTFFRUDDYVCLSBNYMLGKKKPCLTYGGLGTFFIK VBCSNKOLHSGGYGGSVHRAMTDLILLLMGSLDVRRSGNILTPGIN VBCSNKOLHSGGYGGSVHRAMTDLILLMGSLDVRRSGNILTPGIN EAVAAVTKEEHKLYDDIDPDIBEFAKNOGQILLESHKKDILMH	-	ł	·	VCSMPLHSGQGEKPAAPFPRGELESPKPLVTPGSTLTLLTRAEA
1026   PRLPVRRYHGRRIQGRSRGHMAEGDAGSDQRQNEEIRAMAATY   GREWCVIDDCAKIFCIRISDIDDFKWTLCLQVMLPNEYBCTAP   PIYQLMAPWLKGQRADLSNSLBEITYQNIGESILYLWVEKIRD   VLIQKSQMTEPGPDVKKKTEEEDVBCBDLILACQPESSVKALD   FDISETRTEVEVERELPPIDHGIPITTORSTFQAHLAPVVCPKQV   KMVLSKLYENKKLASATHNIYAYRIYCEDKQTFLQDCBDDGSTA   AGGRILHIMEILNVKNVMVVVSRNYGGILLGPDRFKHINNCARN   ILVEKNYTNSPEBSSKALGKNKKVRKKKRRHEH   PRIPVRRYHGRRILQCRSRGHMAEGDAGSDQROBEIRAMAATY   GERWCVIDDCARIFCIRISDIDDPKWTLCLQVMLPNEYPGTAP   PIYQLMAPWLKGQERADLSNSLERIYIQNIGESILYLWVEKIRD   VLIQKSQMTEPGPDVKKKTEBEDVBCEDDLILACQPESSVKALD   FDISETRTEVEVERLPPIDHGIPITDRRSTFQAHLAPVVCPKQV   KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA   AGGRLHHMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN   ILVEKNYTNSPEBSSKALGKNKKVRKDKKRNEH   PRVENATMAMSFENFWQYRFDPPFTLQDNUTTRQKQLAAWCSL   VLSPCRLHKQSSMTVMEAQBSPLFNNVKLQRKLPVESIQIVLKE   LRKKSNLBWLDKSKSSFLIMWRRPEBWGKLYQWVSRSGGNNSV   FTLYELINGEDTEDEEFHGLDBATLLRALQALQQBKRABIITVS   DGPRRQVLLAGGCLPLLITSHLSRAPKRRQTQCPPKTGSVTPPD   SKGLQS   KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR   MMEVAAADVKQLGGSVELVDIGKQKLPDGSBIPLPPILLGRLGS   DPQKKTVCIYGHLDVQPAALEDGWDSRPFTLVERDGKLHGRGST   DDKGPVAGWINALRAYQKTGQBIPVNVRFCLEGMEESGSEGLDE   LIFARKDTFFRUDDVVCLSGDVRHGMKKPCILTYGRGCTYFFIK   VBCSNKOLHSGVYGGSVHRAMTDLILLMGSLVDKRSTNILTPGIK   EAVAAVTREBIKLVDDIDPDIBEFAKDVGQTLLHSHKKDILMH				GSPTGGLFNTPPPTPPEQDKEDFSSFQLLVEVALQRAAEMELQK
GBEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWILKGGERADLSINSLEEITIQNIGESILYIWVEKIRD VILQKSQMTEPGPDVKKKTBEEDVECEDDLILACQPESSVKALD FDISETRITEVEYEELPPIDHGIPITDRRSTPQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTPLQDCBDDGETA AGGRILHHMEILINVKNUWVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKRXREH  6597 2 1026 PRIPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIRAMAAIY GEBWCVIDDCAKIPCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWILKGQBRADLSNSLEBIYIQNIGBSILYHWVEKIRD VLIQKSQMTEPGGPVKKKTBEBDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIVAYRIYCEDKQTFLQDCEDDGETA AGGRILHHMEILNVKNVMVVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPRESSKALGKNKKVRKDKRNRH  6598 1099 419 PRVRWATTMAMSFEWFWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSPCRLHKQSSMTVMEAQBSPLPNNVKLQRKLEVESIQIVLKE LRKKGNLBWLDKSKSSFLIGNBKKVRKDKRNSH  6598 6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAQQSUSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPFILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSRPFTLVERDGKLHGRGST DDKGPVAGWINALKAYQKTGQBIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFFIL VBCSNKDLHSGYGGSVHEAMTDLIILMGSLVDKRGNILIPGIN VBCSNKDLHSGYGGSVHEAMTDLIILMGSLVDKRGNILIPGIN VBCSNKDLHSGYGGSVHEAMTDLIILMGSLVDKRGNILIPGIN EAVAAVFREEHKLYDDIDFDIREFAKDVGAQILLHSHKKDILMH				QQDPSLPLLHTPIPLVSENPQ
PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGGPUKKKTEEEDVEGEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKLASATENIYAYRIYCEDKQTFLQDCBDGGTA AGGRILHIMBILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYINSPESSKALGKNKKVRRDKKRNEH  6597 2 1026 PRLPVRRYHGRRRLQGRSGCHMAEGDAGSDQRQWEEIEAMAAIY GEBRCVIDDCAIIPCIRISDDIDDFKWTLCLQVMLPNEYBGTAP PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGGPDVKKKTEBEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRILHHMEILNVKNVMVVVSRWYGGILLGPDBFKHINNCARN ILVEKNYTNSPRESSKALGKNKKVRKDKRNEH  6598 1099 419 PRVENATTMAMSFENDWQYRPPFFTLQDKUDTRQKQLAAWCSL LRKKGNLEWLDRSKSSSLIMMRRPEEWGKLIYQWVSRSGONNSV VLSFCRLHKQSSMTVMEAQBSPLFNNVKLQRKLPVESIQIVLBE LRKKGNLEWLDRSKSSSLIMMRRPEEWGKLIYQWVSRSGONNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQALQGEHKABIITVS DGPRRQVILLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGGEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDDDYVCIGKYKKPCITYGLRGICYFFFIE VBCSNKDLHSGVYGGSVHEANTDLILLMGSLVDKRGNTLIPGIN VBCSNKDLHSGVYGGSVHEANTDLILLMGSLVDKRGNTLIPGIN VBCSNKDLHSGVYGGSVHEANTDLILLMGSLVDKRGNTLIPGIN	6596	2	1026	PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIRAMAAIY
VLIQKSQMTEPGPDVKKKTBEEDVBCBDDLILACQPESSVKALD FDISBTRTBVEVERLPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKLASATHNIYAYRIYCEDKQTPLQDCBDGETA AGGRLIHLMEILNVKNVMVVVSRNYGGILLGPDRFKHINNCARN ILVEKNYTNSPEBSSKALGKNKKVRKDKKRNEH  6597 2 1026 PRIPVRYHERRELQGRSRGHMAEGDAGSDQROMEBIEAMAATY GEBWCVIDDCAKIPCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPMLKGGRADLSNSLEBIYIQNIGESILYLWVBKIRD VLIQKSQMTEPGPDVKKKTEBEDVBCEDDLILACQPESSVKALD FDISBTRTBVBVEBLPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKLASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLHLMBILNVKNVMVVVSRNYGGILLGPDBFKHINNCARN ILVEKNYTNSPBESSKALGKNKKVRKDKKNRH  6598 1099 419 PRVRNATTMAMSFEWPWQYRFPPFTLQPNVDTRQKQLAAWCSL LRKKGNLBWLDKSKSSFLIMMRPPEEWGKLIYQWVSRSGQNNSV VLSFCRLHKQSSMTVMEAGBSPLFNNVKLQRKLYEVBSIQIVLKE LRKKGLBWLDKSKSSFLIMMRPPEEWGKLIYQWVSRSGONNSV FTLYBLTNGEDTEDEEFHGLDEATLLRALQALQAGBKRBIITVS DGPRRQVLLAGTCLPLLITSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPKKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIFLPPILLGRIGS DPQKKTVCIYGHLDVQPAALEDGWDBFFTLVERDGKLHGRGST DDKGPVAGMINALRAYQKTGQBIPVNVWFCLEGMESGSSEGLBB LIFARKDTFFKDVDYVCISDYWLGKKKPCITYGLRGICYFFIE VBCSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNTLIPGIN VBCSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNTLIPGIN EAVAAVTKEEHKLYDDIDFDIBEFAKDVGAQILLHSHKKDILMH				GREWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP
FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTPLQDCKDDGETA AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPESSKALGKNKKVRRDKKRNEH  6597 2 1026 PRIDVRRYHGRRIQGRSRGHMAEGDAGSDQRQNEBIRAMAIY GEBWCVIDDCAKIPCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLMAPMLKGQBRADLENSLBIYIQNIGBSILVLMVBKIRD VLIQKSQMTEPGPDVKKKTEBEDVBCCEDDLILACQPESSVKALD VLIQKSQMTEPGPDVKKKTEBEDVBCCEDDLILACQPESSVKALD KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHLMBILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPRESSKALGKNKKVRKDKKRNEH  6598 1099 419 PRVRWATTMAMSFEWPWQYRFPPFFIQPNVDTRQKQLAAWCGL VLSPCRLHKQSSMTVMEAQBSPLFNNVKLQRKLPVBSIQIVLBE LRKKGNLBWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV PTLYBLTNGEDTEDEFFHGLDEATLLRALQALQQBHRABIITVS DGPRRQVLLAGTCLPLLLTSHLSRAPKRRQTQCPPKTGSVTPPD SKGLQS  KMARLTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGETRR MBEVAAADVKQLGGSVELVDIGKQKLPDGSBIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSPFTLVERDGKLHGRGST DDKGPVAGMINALBAYQKTGQBIPVNVRFCLEEMBESSGSEGLDB LIFARKDTFFREDVDYVCISDNYMLGKKKPCITYGLRGICYFFFIR VBCSNKDLHSGVYGGSVHRAMTDLIILMGSLVDKRGNTLIPPGIN EAVAAVTREEHKLYDDIDFDIBEFAKDVGAQILLHSHKKDILMH			}	PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD
KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRILHIMBILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYITNSPERSSKALGKNKKVRKDKKRNEH  6597 2 1026 PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEBIRAMAAIY GEBMCVIDDCAKIFCIRISDDIDDRKWTLCLQVML?MEYPGTAP PIYQLNAPMLKGQERADLSNSLEBIYIQNIGESILYLWVBKIRD VLIQKSQMTEPGPDVKKKTEBBDVBCEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDGETA AGGRILHIMBILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYITNSPRESSKALGKNKKVRKDKKRNEH  6598 1099 419 PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQBSPLFNNVKLQRKLPVEBIQIVLEE LRKKGNLBWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEKKABIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRQTQCPPKTGSVTPPD SKGLQS  6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSBIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSPFFTLVERDGKLHGRGST DDKGPVAGWINALBAYQKTGQBIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFRDVDTVCLSDNYWLGKKKPCITYGLRGICYFFIE VECNNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTREEHKLYDDIDFDIREFAKDVGAQILLHSHKKDILMH				VI.IQKSQMTBPGPDVKKKTBEEDVBCBDDLILACQPESSVKALD
AGGRLIHIMBILINVKNVMVVVSRWYGGILIGPDRFKHINNCARN ILVEKNYTNSPEBSSKAIGKNKKURKDKKRNEH 6597 2 1026 PRIDVRRYHGRRRLQGRSGGHMAEGDAGSDORQNEBIBAMAAIY GEBWCVIDCAKIPCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPMLKGQBRADLSNSLEBIYIQNIGBSILVILWVBKIKD VLIQKSQMTEPGPDVKKKTEBDVBCEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKIYRNKKIASATHNIYAYRIYCEDKQTFLQDCEDDGBTA AGGRLIHIMBILINVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVERNYTNSPBESSKALGKNKKVRKDKKRNEH 6598 1099 419 PRVRMATTMAMSFENEWQYRFPPFFTLQENVDTRQKQLAAWCGL LRKKGNLBWILDKSKSSFLIMMRRPEEWGKLIYQWVGRSGQNNSV FTLYBLTNGEDTEDEEPHGLDBATLLRALQALQQBHKABIITVS DGPRRQVLLAGTCLPILLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS 6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSBIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSBFFTLVERRGKHGRGST DDKGPVAGWINALRAYQKTGQBIPVNVRFCLEGMEESGSBELDB LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIR VBCSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTKEBHKLYDDIDFDIBEFAKDVGAQTILHSHKKDILMH		<b>!</b> '		FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV
ILVEKNYTNSPESSKALGKNKKVRKDKKRNEH  6597 2 1026 PRLPVRYHGRRRLQGRSRGHMAEGDAGSDQRQNEBIRAMAAIY GERMCVIDDCAKIFCIRISDIDDFKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKGQGRADLSNSLEBIYIQNIGBSILYNEYPGTAP VLIQKSQMTEPGPDVKKKTEERDVRCEDDLILACQPESSVKALD VLIQKSQMTEPGPDVKKKTEERDVRCEDDLILACQPESSVKALD FDISETRTBVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYRNKKIASATHNIYAYRIYCEDKQTFLQDCGDDGBTA AGGRILHMBILNVKNWVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPESSKALGKNKKVRKDKKRNEH  6598 1099 419 PRVENHATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCGL LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYBLTNGEDTEDEFHGLDEATILRALQALQQEHKABIITVS DGPRRQVLLAGTCLPLLLTSHLSRAPKRRQTQCPPKTGSVTPPD SKGLQS  6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSBIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSBFFTLVERDGKLHGRGST DDKGPVAGWINALRAYQKTGGBIPVNVRFCLEGMEESGSEGLBG LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIR VBCSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEBKKLYDDIDFDIREFAKDVGAQILLESHKKDILMH		·	1	KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCBDDGBTA
6597 2 1026 PRLPVRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY GERWCVIDDCAKIPCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLMAPMLKGQBRADLSNSLEBIYIQNIGBSILYLWVBKIRD VLIQKSQMTEPGPDVKKKTEBEDVBCEDDLILACQPESSVKALD VLIQKSQMTEPGPDVKKKTEBEDVBCEDDLILACQPESSVKALD FDISETRTEVEVEBLPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHIMBILNVKNVMVVVSBWYGGILLGPDRFKHINNCARN ILVEKNYTNSPRESSKALGKNKKVRKDKKRNEH  6598 1099 419 PRVWATTMAMSFEWPWQYRFPDPFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQBSPLFNNVKLQRKLPVESIQIVLKE LRKKGNLBWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATILARALQALQQBHKABIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEFTLVERDGKLHGRGST DDKGPVAGWINALRAYQKTGGBIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKVDTYVCISDNYWLGKKKPCITYGLRGICYFFIR VBCSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEBHKLYDDIDFDIREFAKDVGAQILLHSHKKDILMH				
GEBWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKGQERADLSNSLEBIYIQNIGBSILYLWVBKIRD VLIQKSQMTEPGPDVKKKTEBBUVECEDDLILACQPESSVKALD FDISETTEVEVEBLPPIDHGIPITDRRSTFQAHLAFVVCPKQD KMVLSKLYRNKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHIMBILNVKNWWVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPBESSKALGKNKKVRKDKKRNEH  6598 1099 419 PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVWEAQBSPLFNNVKLQRKLPVESIQIVLKE LRKKGNLBWLDKSKSSFLIMWRRPEBWGLIYQWVSRSGQNNSV FTLYBLTNGEDTEDEEFHGLDEATLLRALQALQQBHKABIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  6599 164 1593 KWAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGBIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGS DDKGPVAGWINALEAYQKTGQBIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIR VECSNKDLHSGVYGGSVHFAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEBHKLYDDIDFDIBEFAKDVGAQILLHSHKKDILMH				
PIYQLNAPWLKGQERADLSNSLEBIYIQNIGBSILYLWVBKIRD VLIQKSQMTEPGPDVKKKTEBEDVBCEDDLILACQPESSVKALD FDISETRTBVEVEBLEP IDHGIP ITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKLASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHIMBILNVKNWWVVSBWYGGILLGPDRFKHINNCARN ILVEKNYTNSPRESSKALGKNKKVRKDKKRNEH  6598 1099 419 PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQBSPLFNNVKLQRKLPVBSIQIVLBE LRKKGNLBWLDKSKSSFLIMMRPEBWGKLIYQWVSRSGQNNSV FTLYBLTNGEDTEDEFFHGLDEATLLRALQALQQBHKABIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPALEDGWDSBFFTLVERRGKHGRGST DDKGPVAGWINALEAYQKTGQBIPVNVRFCLEGMEESGSEGLBG LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIR VBCCNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTKEBHKLYDDIDFDIBEFAKDVGAQTLLHSHKKDILMH	6597	2	1026	1 " " " " " " " " " " " " " " " " " " "
VLIQKSQMTEPGPDVKKKTEBEDVECEDDLILACQPESSVKALD FDISETRTEVAVEELPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYRKKLASATHNIYAYRIYCEKKQTFLQDCEDDGETA AGGRLLHIMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVBKNYTNSPBESSKALGKNKKVRKDKKRNEH  6598 1099 419 PRVRMATTMAMSFEWFWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLKE LRKKGNLBWLDKSKSSFLIMWRRPEBWGKLIYQWVSRSGQNNSV FTLYBLTNGEDTEDEEFHGLDEATLLRALQALQQEHKABIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSRFFTLVERRGCKLHGRGST DDKGPVAGWINALKAYQKTGQBIPVNVRFCLEGMEESGSEGLBG LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIK VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTKEEHKLYDDIDFDIREFAKDVGAQILLHSHKKDILMH		l		
FDISETRTBVBVEELPPIDHGIPITDRRSTFQAHLAFVVCPKQV KMVLSKLYBNKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRILHMBILINVKRWYVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPBESSKALGKNKKVRKDKKRNEH  6598 1099 419 PRVBMATTMANSFEWBWQYRFPPFFTLQPNVDTRQKQLAAWCGL VLSPCRLHKQSSMTVMEAQBSPLFNNVKLQRKLFVBSIQIVLKE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYBLTNGEDTEDEEFHGLDEATILRALQALQQEHKABIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSBIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSBFFTLVERDGKLHGRGST DDKGFVAGWINALRAYQKTGGBIPVNVRFCLEGMEESGSEGLBG LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIR VBCSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTREEHKLYDDIDFDIREFAKDVGAQILLHSHKKDILMH			l	· ·
KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLIHIMEILINVKNYMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPRESSKALGKNKKVRKKKRNEH  6598 1099 419 PRVRMATTMAMSFENFWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSPCRLHKQSSMTVMEAQBSPLFNNVKLQRKLFVESIQIVLKE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKABIITVS DGPRRQVLLAGTCLPLLITSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGETRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLFPILLGRIGS DPQKKTVCIYGHLDVQPAALEGMGDSPFTLVERDGKLHGRGST DDKGPVAGWINALRAYQKTGQBIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFRDVDYVCISDNYWLGKKKPCITYGLRGICYFFIR VECSNKDLHSGVYGGSVHFAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTKEEHKLYDDIDFDIERFAKDVGAQILLHSHKKDILMH			ł	
AGGRLLHLMEILINVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPRESSKALGKNKKVRKDKKRNEH  6598 1099 419 PRVEMATTMAMSFERDWQYRFPDFFTLQENVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQBSPLFNNVKLQRKLFVBSIQIVLKE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV PTLYELTNGEDTEDEEFHGLDEATLLRALQALQQBHRABIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGBIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPFILLGRIGS DPQKKTVCIYGHLDVQPAALEGMGDSPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQBIPVNVRFCLEGMEESGSEGLDB LIFARKDTFFRDVDYVCISDNYWLGKKKPCITYGLRGICYFFIR VECSNKDLHSGVYGGSVHRAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEBHKLYDDIDFDIREFAKDVGAQILLHSHKKDILMH		1		The state of the s
ILVEKNYTNSPRESSKALGKNKKVRKDKKRNEH  6598 1099 419 PRVRMATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQBSPLFNNVKLQRKLPVESIQIVLKE LRKKGNLBWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV PTLYBLTNGEDTEDEEFHGLDEATLLRALQALQQBHKABIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQBIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIR VECSNKDLHSGVYGGSVHFAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEBHKLYDDIDFDIREFAKDVGAQILLHSHKKDILMH				
6598 1099 419 PRVRMATTMAMSFEWEWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLFVESIQIVLKE LRKKGNLEWILDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYBLTNGEDTEDEEFHGLDEATLLRALQALQQEHKABIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSRFFTLVERDGKLHGRGST DDKGPVAGWINALRAYQKTGQBIPVNVRFCLEGMEESGSEGLBGL LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIR VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTREEHKLYDDIDFDIREFAKDVGAQILLHSHKKDILMH		]		I TO THE PROPERTY OF THE PROPE
VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLFVESIQIVLKE LRKKGNLBWLDKSKSSFLIMWRRPEBWGKLIYQWVSRSGONNSV FTLYBLTNGEDTEDEEFHGLDEATLLRALQALQQBHKABIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSRFFTLVERDGKLHGRGST DDKGPVAGWINALRAYQKTGQBIPVNVRFCLEGMEESGSEGLBGL LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIR VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEHKLYDDIDFDIREFAKDVGAQILLHSHKKDILMH				
LRKKGNLEWIDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS 6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPFILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSRPFTLVERDGKLHGRGST DDKGPVAGWINALRAYQKTGQBIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIR VECSNKDLHSGVYGGSVHRAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTKEEHKLYDDIDFDIERFAKDVGAQILLHSHKKDILMH	6598	1099	419	
FTLYBLTNGEDTEDEEFHGLDBATLLRALQALQQBHKABIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS 6599 164 1593 KMAALTTLFKYIDBNQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVBLVDIGKQKLPDGSRIPLPFILGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSBFFTLVERDGKLHGRGST DDKGPVAGWINALRAYQKTQQBIPVNVRFCLEGMEESGSEGLDB LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIR VBCSNKDLHSGVYGGSVHRAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTKEBHKLYDDIDFDIBEFAKDVGAQILLHSHKKDILMH		·		,
DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS 6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSRIPLPFILLGRLGS DPQKKTVCIYGHLDVQPAALEDGMDSRPFILVERDGKLHGRGST DDKGPVAGWINALRAYQKTGQBIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIR VECSNKDLHSGVYGGSVHRAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTKEEHKLYDDIDFDIREFAKDVGAQILLHSHKKDILMH				
SKGLQS  6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRIGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQBIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCLSDNYWLGKKKPCITYGLRGICYFFIR VECSNKDLHSGVYGGSVHFAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEHKLYDDIDFDIREFAKDVGAQILLHSHKKDILMH				
6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILIGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQBIPVNVRFCLEGMEESGSEGLBGL LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIR VECSNKDLHGGVYGGSVHFAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEHKLYDDIDFDIREFAKDVGAQILLHSHKKDILMH				,
MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQBIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VBCSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEHKLYDDIDFDIERFAKDVGAQILLHSHKKDILMH				
DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQBIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VBCSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEHKLYDDIDFDIERFAKDVGAQILLHSHKKDILMH	6599	164	1593	1
DDKGPVAGWINALKAYQKTGQBIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIK VBCSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTKEBHKLYDDIDFDIRRFAKDVGAQILLHSHKKDILMH		]	ļ	**
LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIR VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTREEHKLYDDIDFDIREFAKDVGAQILLHSHKKDILMH				· ·
VECSNKDLHSGVYGGSVHRAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTREBHKLYDDIDFDIBEFAKDVGAQILLHSHKKDILMH				
EAVAAVTKEBHKLYDDIDFDIRRFAKDVGAQILLHSHKKDILMH		}		
RWRYPSLSLHGIRGAFSGSGAKTVIPRKVVGKFSIRLVPNMTPE				
				RWRYPSLSLHGIRGAFSGSGAKTVIPRKVVGKFSIRLVPNMTPE

SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
no.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			VVGEQVTSYLTKKFARLRSPNEFKVYMGHGGKPWVSDFSHPHYL
			AGRRAMKTVFGVEPDLTREGGSIPVTLTFQEATGKNVMLLPVGS
			ADDGAHSQNEKLNRYNYIEGTKMLAAYLYBVSQLKD
6600	2	934	PGRLFRVAAMESAGLEQLLRBLLLPDTERIRRATBQLQIVLRAP
	ŀ		AALSALCDLIASAADPQIRQFAAVLTRRRLNTRWRRLAAEQRES
-	1	į	LKSLILTALQRETEHCVSLSLAQLSATIFRKEGLEAWPQLLQLL
			QHSTHSPHSPEREMGLLLLSVVVTSRPEAFQPHHRELLRLLNET
	}	}	LGRVGSPGLLFYSLRTLTTMAPYLSTKDVPLARMLVPKLIMAMO
			TLIPIDEAKACRALRALDELLESEVPVITPYLSEVLTFCLEVAR
			NVALGNAIRIRILCCLTFLVKVKSKALLKNRLLATLAAHPFPHC
	<u> </u>		GC .
6601	529	1420	PRAAARAPPPAVLRRDRRAATAPGAGEMTLHGPLAQRYFLNHIE
			KITTWQDPRKAMNQPLNHMNLHPAVSSTPVPQRSMAVSQPNLVM
			NHQHQQCMAPSTLSQQNHPTQNPPAGLMSMPNALTTQQQQQQKL
			RLQRIQMBRERIRMRQEBLMRQEAALCRQLPMEAETLAPVQAAV
			NPPTMTPDMRSITNNSSDPPLNGGPYHSREQSTDSGLGLGCYSV
			PTTPEDFLSNVDEMDTGENAGQTPMNINPQQTRFPDFLDCLPGT
5500			NVDLGTLESEDLIPLFNDVESALNKSEPFLTWL
6602	127	617	LLDFPALPKFVLAQSPKAGKPSTMTSMTQSLREVIKAMTKARNP
			BRVLGKITLVSAAPGKVICEMKVBEBHTNAIGTLHGGLTATLVD
			NISTMALLCTERGAPGVSVDMNITYMSPAKLGEDIVITAHVLKQ
6603	79	660	GKTLAFTSVDLTNKATGKLIAQGRHTKHLGN PVGPSSLAARTGLGHLPFLHRLASSRGLDMDLLQFLAFLFVLLL
0003	73	000	SGMGATGTLRTSLDPSLEIYKKMFRVKRREQLLALKNLAQLNDI
			HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGPFPQDEKLKD
			AFSHVVENTAFPGDVVLRFPRIVHYYFDHNSNWNLLIRWGISFC
			NCTCVFNQCPHSPILSIM
6604	3	688	TSTAOROGGERMSFRCCGRGGFNRGGGGGFNRGGSSNHFRGGG
0054	_	500	GGGGGGNFRGGGRGGFGRGGRGGFNKGODQGPPERVVLLGEFL
			HPCEDDIVCKCTTDENKVPYFNAPVYLKNKEQIGKVDE1FGQLR
	4		DFYFSVKLSENMKASSFKKLQKFYIDPYKLLPLQRFLPRPPGEK
			GPPRGGRGGRGGCRGGGRGGGRGGGGGGGGGGGGGGGGG
	•		GGFRGRGH
6605	7	B48	SGSRRGAMRAAGVGLVDCHCHLSAPDFDRDLDDVLEKAKKANVV
3000	•	5-10	ALVAVABHSGBPEKIMOLSERYNGFVLPCLGVHPVOGLPPEDOR
			SVTLKDLDVALPIIENYKDRLLAIGEVGLDFSPRFAGTGBOKEE
			QRQVLIRQIQLAKRLNLPVNVHSRSAGRPTINLLQEQGABKVLL
			HAFDGRPSVAMEGVRAGYFFSIPPSIIRSGQQKLVKQLPLTSIC
		•	LETDSPALGPEKOVRNEPWNISISABYIAOVKGISVEEVIEVTT
			QNALKLFPKLRHLLQK
6606	2	1682	FVRIRPRAEVANLSAHSASPIODAVLKRLSLLEDIVYROLNGLS
	_		KSLGLIEGYGGROKGGLPATLSPAEREKAKGPHEKYGYNSYLSE
			KISLDRSIPDYRPTKCKELKYSKOLPOISIIFIFVNRALSVILR
			SVHSAVNHTPTHLLKEIILVDDNSDEBELKVPLEEYVHKRYPGL
		1	VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP
į			VLSR1QENRKRV1LPSIDNIKODNFEVORYENSAHGYSWELWCM
			YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGRIGLLDPG
ļ			MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI
			GPYTKRNALRVABYWMDDYKSHVYIAWNLPLENPGIDIGDVSER
j			RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC
			LDQGPLENHTAILYPCHGWGPQLARYTKEGPLHLGALGTTTLLP
			DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG
	137	00.4	RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK
	1.57 1	986	VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT
6607			GTGTGGTGGT Charry and a second compact compact compact
6607			GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD KIEDELEMTMVCHRPEGLEOLEAQTNFTKRELQVLYRGFKNECP

	T 5 - 37	1 - 37 - 2	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
l	amino acid	amino acid residue of	P=Proline, Q=Glutamine, R=Arginine,
i	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
I	sequence	sequence	\=possible nucleotide insertion)
<u></u>	sequence	l —————	SGVVNEDTFKQIYAQFFPHGDASTYAHYLFNAFDTTQTGSVKFR
j .			DFVTALSILLRGTVHEKLRWTFNLYDINKDGYINOEEMMDIVKA
1	1	i .	IYDMMGKYTYPVLKEDTPROHVDVFFOKMDKNKDGIVTLDBFLE
1		ľ	SCQEDDNIMRSLOLFONVM
6608	224	1140	RPCFSSPTGLCPRLSYPMILLQHAVLPPPKQPSPSPPMSVATRS
1 3000	1	1	TGTLQLPPQKPFGQRASLPLAGEBELSKGGEQDCALBELCKPLY
i		1	CKLCNVTLNSAQQAQAHYQGKNHGKKLRNYYAANSCPPPARMSN
			VVBPAATPVVPVPPQMGSFKPGGRVILATENDYCKLCDASFSSP
1			AVAQAHYQGKNHAKRLRLAEAQSNSFSESSELGQRRARKEGNEF
ł			KMMPNRRNMYTVONNSGPYFNPRSRORIPRDLAMCVTPSGQFYC
ł	İ		SMCNVGAGREMEFRQHLESKOHKSKVSEQRYRNEMENLGYV
6609	1	443	FRLRCRRFRVAGGRLAGAGLRESRVPAPBORLSALTLLSWSAVT
İ			PAAEPGNFQLSPAEPRGPLASPVRAAPRAPCPAAKMSELNTKTS
j		ļ	PATNQAAGQEEKGKAGNVKKAKEBBEIDIDLTAPETEKAALAIQ
1			GKFRFQKRKKDPSS
6610	319	881	GRKSLCNLHIPIRPPLTYPDMYMGMMCTAKKCGIRFQPPAIILI
l .		1	YESKIKGKIRQRIMPVRNFSKFSDCTRAAEQLKNNPRHKSYLEQ
			VSLRQLEKLFSFLRGYLSGQSLAETMEQIQRETTIDPERDLNKL
İ			DDKBLAKRKSIMDBLFEKNQKKKDDPNFVYDIEVEFPQDDQLQS
			CGWDTESADEF
6611	978	212	PGCSGAGSRVWWLPALRHLAMGSTESSEGRRVSFGVDEBERVRV
	i	ļ	LOGVRISENVVNRMKBPSSPPPAPTSSTFGLQDGNLRAPHKEST
ł ·	1		LPRSGSSGGQQPSGMKEGVKRYBQKHAAIQDKLFQVAKREREAA
1			TKHSKASLPTGEGSISHBEQKSVRLARELESRBARLRRRDTFYK
l .	1		EQLERIERKNAEMYKLSSEQFHEAASKMESTIKPRRVERVCSGL
6612	1724	992	QAQILHCYRDRPHEVILCSDLVKAYQRCVSAAHKG VSTHASALSRTQGQPQRQPRAAASGAGAGTAGGGGSGGAEGSKM
6612	1/24	774	STRAQRVDDSPSTSGGSSDGDQRESVQQEPEREQVQPKKKEGKI
l	i		SSKTAAKLSTSAKRIQKELAEITLDPPPNCSAGPKGDNIYEWRS
	İ		TILGPPGSVYBGGVFFLDITFSPDYPFKPPKVTFRTRIYHCNIN
Į.	1		SQGVICLDILKDNWSPALTISKVLLSICSLLTDCNPADPLVGSI
l			ATQYMTNRAEHDRMARQWTKRYAT
6613	130	748	ELBLSSNMPEQSNDYRVAVFGAGGVGKSSLVLRFVKGTFRBSYI
1			PTVBDTYRQVISCDKSICTLQITDTTGSHQFPAMQRLSISKGHA
	1		FILVYSITSRQSLKELKPIYEQICBIKGDV3SIPIMLVGNKCDB
	1		SPSRBVQSSKARALARTWKCAFMETSAKLNHNVKBLFQELLNLB
1	ĺ		KRRTVSLQIDGKKSKQQKRKEKLKGKCVIM
6614	3	1191	SSAARAMRVLVRRCWGPPLAHGARRGRPSPQWRALARLGWEDCR
			DSRVREKPPWRVLFFGTDQFAREALRALHAARENKREELIDKLE
1			VVTMPSP8PKGLPVKQYAVQSQLPVYEWPDVGSGEYDVGVVASF
1			GRLINEALILKFPYGILNVHPSCLPRWRGPAPVIHTVLHGDTVT
			GVTIMQIRPKRFDVGPILKQETVPVPPKSTAKELEAVLSRLGAN
			MLISVLKNLPESLSNGRQQPMEGATYAPKISAGTSCIKWEEQTS
1			EQIFRLYRAIGNIIPLQTLWMANTIKLLDLVEVNSSVLADPKLT
	1	1	GQALIPGSVIYHKQSQILLVYCKDGWIGVRSVMLKKSLTATDFY
			NGYLHPWYQKNSQAQPSQCRFQTLRLPTKKKQKKTVAMQQCIB
6615	832	35	GRVGAGASAMSELPGDVRAFLREHPSLRLQTDARKVRCILTGHE
		•	LPCRLPBLQVYTRGKKYQRLVRASPAFDYAEFBPHIVPSTKNPH
	1		QLFCKLTLRHINKCPEHVLRHTQGRRYQRALCKYBECQKQGVEY
}			VPACLVHRRRREDOMDGDGPRPREAFWEPTSSDEGGAASDDSM
	i		TDLYPPRLFTRKDLGSTEDGDGTDDFLTDKEDEKAKPPREKATD
1			EGRRETTVYRGLVQKRGKKQLGSLKKKPKSHHRKPKSFSSCKQS
1			G
6616	347	1886	LLPPCQGARPLSSPPHASEDNLFLFWNCILCAFPHPSPQPLQYP
L	L		VWPLLLVITQIPAPRHLRNRPFSFSRGGLDSFSGSLSTPSICRS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
***	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<b>.</b>	sequence	bequence	\=possible nucleotide insertion)
	sequence		PAWVKMAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSP
<u> </u>	<b>,</b>		PPOPHPCHTCRGLVDSFNKGLERTIRDNPGGGNTAWEEENLSKY
ŀ	i	l	KDSETRLVEVLEGVCSKSDFECHRLLELSERLVESWWFHKQQEA
	1	j	PDLFOWLCSDSLKLCCPACTFGPSCLPCPGGTRRPCGGYGOCEG
	Ì		EGTRGGSGHCDCOAGYGGEACGOCGLGYPEAERNASHLVCSACF
		{	
	1		GPCARCSGPEESNCLQCKKGWALHHLKCVDIDECGTEGANCGAD
Į	Į	Į.	QFCVNTRGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKC
İ	1		LDVDECETEVCPGENKQCENTEGGYRCICAEGYRCMEGICVKEQ
i			IPESAGFFSEMTRDELVVLQQMFFGIIICALATLAAKGDLVFTA
		\	IFIGAVAAMTGYWLSERSDRVLEGFIKGR
6617	118	673	VWMAWQVSLLELEDRLQCPICLEVFKESLMLQCGHSYCKGCLVS
•	1	1	LSYHLDTKVRCPMCWQAVDGSSSLPNVSLAWVIEALRLPGDPEP
1			KVCVHHRNPLSLFCEKDQELICGLCGLLGSHQHHPVTPISTVCS
l	1	l	RMKEELAALFSELKQEQKKVDELIAKLVKNRTRIDGSAPSLCPC
	l		LGPATFTFL
6618	548	136	DGKVARRAPNSPAFQNDIYPLVSAPRATTAESPWSKVLQNTQCR
1			NVPKMTSERSRIPCLSAAAAEGTGKKQQEGRAMATLDRKVPSPE
İ			AFLGKPWSSWIDAAKLHCSDNVDLREAGKBGGKSREVMRLNKEA
			WKYGT
6619	246	842	PASSEVLTAAVMFLLLNCIVAVSQNMGIGKNGDLPRPPLRNEFR
f	ł		YFQRMTTTSSVEGKQNLVIMGRKTWFSIPEKNRPLKDRINLVLS
1			RELKEPPQGAHFLARSI.DDALKLTERPELANKVDMIWIVGGSSV
ł			YKRAMNHLGHLKLFVTRIMODFESDTFFSEIDLBKYKLLPEYPG
<u> </u>	<u> </u>		ILSDVQEGKHIKYKPEVCBKDD
6620	3	1879	NSRVDDFVARARMAARNEASQESALGAYSPVDYMSITSFPRLPE
ţ	į.		DEPAPAAPLRGRKDEDAFLGDPDTDPDSFLKSARLQRLPSSSSE
,			MGSQDGSPLRETRKDPFSAAAAECSCRQDGLTVIVTACLTFATG
			VTVALVMQIYFGDFQIFQQGAVVTDAARCTSLGIEVLSKQGSSV
			DAAVAAALCIGIVAPHSSGIGGGGVMLVHDIRRNESHLIDFRES
i .	1		APGALREETLQRSWETKPGLLVGVPGMVKGLHRAHQLYGRLPWS
ł			QVLAFAAAVAQDGFNVTHDLARALAEQLPPNMSERFRETFLPSG
	1	Į.	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ
l	1		HAGGVITERDFSNYSALVEKPVCGVYRGHLVLSPPPPPHTGPALI
İ	1	]	SALNILEGFNLTSLVSREQALHWVAETLRIALALASRLGDPVYD
ł	1.		STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYKLDGAPT
ì		]	AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS
l	Į.	}	WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA
1			LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV
			SIPHAANMG
6621	1	662	VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP
l	ł	t	AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT
l .		(	SVKV1GAQRRRSPSALATEVFEAHLGSHILQSLDGYVFALNQEG
]		1	KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK
			LPPGRGLLSQGTAKDGASSASSSSQSETPRPVVCFPPASDQFLL
6622	2	319	GRASGAQEETEAGGPERARAMBANMPKRKEPGRSLRIKVISMGN
1	1	1	AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN
L	<u> </u>		IFDMAGHPFFYEVRKPF
6623	1886	189	KALFEKVKKFRLHVBEGDILYAMYVRQTVLKVIKFLIIIAYNSA
l	1	1	LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF
}	1	1	VSIYGLTCLYTLYWLFYRSLREYSFEYVRQETGFDDIPDVKNDF
j	1	1	AFMLHMIDQYDPLYSKRFAVFLSKVSKNKLKQLNLNNEWTPDKL
<b>!</b>	<b>!</b>	<b>\</b>	ROKLOTNAHNRLELPLIMLSGLPDTVFEITELOSLKLEIIKNVM
·	!	!	IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD
l	1	[	MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI
l			LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMIN
1			LTELELVHCDLERIPHAVFSLLSLQELDLKENNLKSIEEIVSFQ
	•	1 .	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ľ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
1	sequence	Bequence	\=possible nucleotide insertion)
ļ	Bequence	ļ	HLRKLTVLKLWHNSITYIPEHIKKLTSLERLSFSHNKIEVLPSH
1		İ	LFLCNKIRYLDLSYNDIRFIPPKIGVLQSLQYFSITCNKVESLP
1			
i			DELYFCKKLKTLKIGKNSLSVLSPKIGNLLFLSYLDGKGNHFEI
6624	218	1786	LPPELGDCRALKRAGLVVEDALFETLPSDVREQMKTE
0024	210	1/86	GSRRGGGSRIPAVSTHVAPGRSVLRPFASGALRLRSLVKALGGC
1		1	RGRPSGLAHLSQETSHWRAKRSGRACLGDPPGBILRSFIMKCTA
Į.	1	}	REWLRVTTVLFMARAI PAMVVPNATLLEKLLEKYMDEDGEWWIA
j			KORGKRAITDNDMOSILDLHNKLRSQVYPTASNMEYMTWDVELE
1			RSAESWAESCLWEHGPASILLPSIGQNLGAHWGRYRPPTFHVQSW
1			YDEVKDPSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGC
ł		i	AINLCHNMNIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCS
1	1		ACPPSFGGGCRENLCYKEGSDRYYPPRREETNBIERQQSQVHDT
			HVRTRSDDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTCNRYEC
Į			PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITR
į.			QGRKHYFIKSNRNGIQTIGKYQSANSFTVSKVTVQAVTCETTVE
6625			QLCPFHKPASHCPRVYCPRKLYASKSTLCSCNWNSSLP
6625	1124	543	PGPRGGGGLLSTKALGRSRGLGMHPGPSSGGTEGGVPTALRPP
1	:		GPLVPSTSDDNLLKNIELFDKLALRFHGRLLFLKDVLGDBICCW
1			SFYGQGRKINEVCCTSIVYNTEKKQTKVEFPEARIFEETLNILI
	1		YETPRGPDPALLEATGGAAGAGGGAGRGEDEENREHRVRRIHVRR
6626			HITHDERPHGQQIVFKD
6626	3	1498	SAVEFVYTDRFHLIGISVEFLCSLRSDATMESITACLHALQAL
1			LDVPWPRSKIGSDQDSGIBLLNVLHRVILTRESPSIQLASLEVV
1	]		RQIICAAQEHVKEKRRSAEVDDGAAEKETLPEFGEGKDTGGLVP
i .			GKSLVFATLELCVCILVRQLPELNPKLTGSPGVKATKPQILLED
I			GSRLVSAALVILSELPAVCSPEGSISILPTILYLTIGVLRETAV KLPGGQLSSTVAASLQALKGILSSPMARABKSRTAWTDLLRSAL
ľ			TTILDCWDPVDETHQBLDEVSLLTAITVFILSTSPEVTTIPCLQ
	1		KRCIDKFKATLEIKDPVVQIKTYQLLHSIPQYPNPAVSYPYIYS
			LASCIMEKLQEIDKRKPENTAELEIFQEGIKVLETLVTVAREHH
	·		RAQLVACLLPILISFLLDENSIGSATSIMENDHDFALQNLMQIG
ł			PQYSSVFKSLVASSPALKARLEAAIKGNQRSVKVKIPTSKYTKS
l .	l i		PGKNSSIQLKTSFL
6627	1	697	GIPHLSSRDMTGTPGAVATRDGEAPERSPPCSPSYDLTGKVMLL
	<u> </u>	<b>5</b> ,	GDTGVGKTCFLIQFKDGAFLSGTFIATVGIDFRNKVVTVDGVRV
Ì	]		KLQIWDTAGQERFRSVTHAYYRDAQALLLLYDITNKSSFDNIRA
1			WLTEIHEYAQRDVVIMLLGNKADMSSERVIRSEDGETLAREYGV
j			PFLETSAKTGMNVELAFLAIAKELKYRAGHQADEPSFQIRDYVE
	[		SOKKRSSCCSFM
6628	1	1861	QCAEFGGGGGGGGGGGGGGGGGGGGERNKENERPSAGSKAN
[	-	1002	KEFGDSLSLBILQIIKESQQQHGLRHGDFQRYRGYCSRRORRLR
!	]		KTINFKMGNRHKFTGKKVTEBILITDNRYLLLVIMDAERAWSYAM
1			QLKQKANTEPRKRFHLLSRLRKAVKHAEELERLCESNRVDAKTK
l			LEAQAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIYEKLASAFTE
[			EQAVLYNORVEEISPNIRYCAYNIGDOSAINELMOMRLRSGGTR
			GLLAEKLEALITOTRAKQAATMSEVEWRGRTVPVKIDKVRIPLL
(			GLADNEAAIVQAESEETKERLFESMLSECRDAIQVVREELKPDQ
1			
			KQRDYILEGEPGKVSNLQYLHSYLTYIKLSTAIKRNENMAKGLQ RALLQQQPEUDSKRSPRPODLIRLYDIILONLVELLOLPGLEED
[	]		KAFQKEIGLKTLVFKAYRCFFIAQSYVLVKKWSEALVLYDRVLK
	[		YANEVNSDAGAPKNSLKDLPDVQELITQVRSEKCSLQAAAILDA
1			NDAHQTETSSSQVKDNKPLVERFETFCLDPSLVTKQANLVHPPP
	ľ		GFQPIPCKPLFFDLALNHVAFPPLEDKLEQKTKSGLTGYIKGIF
6620-			GFRS
6629	5653	4549	GATPLGSVGGRTGKMDAATLTYDTLRFAEFEDYPETSEPVWILG
L]	L l		RKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGC

			· · · · · · · · · · · · · · · · · · ·
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ľ	amino acid residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	sequence	\=possible nucleotide insertion)
<b> </b>	Bequence	<del> </del>	MLRCGQMIFAQALVCRHLGRDWRWTQRKRQPDSYFSVLWAFIDR
1	1		KDSYYSIHQIAQMGVGEGKSIGQWYGPNTVAQVLKKLAVFDTWS
1			SLAVHIAMDNTVVMEBIRRLCRTSV2CAGATAFPADSDRHCNGF
ŀ	1		PAGAKVTNRPSPWRPLVLLIPLRLGLTDINKAYVETLKHCFMMP
ļ			QSLGVIGGKPNSAHYPIGYVGERLIYLDPHTTQPAVEPTDGCFI
	i		PDESFHCQHPPCRMSIAELDPSIAVVRGGHLSTQAFGAECCLGM
1	ļ		TRKTFGPLRFFFSMLG
6630	2	423	LVQCGGTRRRSANGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS
Į.	ł		LGDQYVKDEFRRHKTVGSDEAQRFLQEWKVYATALLQQANENRQ
			NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI
1	İ		SBSMKPKF
6631	2	423	LVQCGGIRRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS
ı	1		LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANENRQ
1			NSTGKACFGTFL?EEKLNDFRDEQIGQLQELMQEATKPNRQFSI
L			SESMKPKF
6632	1273	588	WNSRGRTQRGAA2LAPAAAMKAVVQRVTRASVTVGGEQISAIGR
1			GICVLLGISLEDTQKRLEHMVRKILNLRVFKDESGKHWSKSVMD
	l		KQYEILCVSQFTLQCVLKGNKPDFHLAMPTBQABGFYNSFLEQL
1	l '		RKTYRPELIKDGKFGAYMQVHIQNDGPVTIELESPAPGTATSDP
			KQLSKLEKQQQRKEKTRAKGPSESSKERNTPRKEDRSASSGAEG DVSSEREP
6633	1145	617	ATGRHEGVPTLEGIIOOLVNGIITPATIPSLGPWGVLHSNPMDY
0033	1113	) ""	ANGANGLDAIITOLLNOFENTGPPPADKEKIQALPTVPVTEEHV
		`	GSGLECPVCKDDYALGERVROLPCNHLFHDGCIVPWLEOHDSCP
1			VCRKSLTGONTATNPPGLTGVSFSSSSSSSSSSSSSSNKNATSNS
6634	1	1134	CGGTPRKGSGPRRRLPMARLRDCLPRLMLTLRSLLFWSLVYCYC
1			GLCASIHLLKLLWSLGKGPAQTFRRPAREHPPACLSDPSLGTHC
j		1	YVRIKDSGLRPHYVAAGERGKPLMLLLHGFPEFWYSWRYQLREF
			KSBYRVVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLGY
ł		i	SKCVLIGHDNGGMIAWLIAICYPEMVMKLIVINFPHPNVFTEYI
1	ĺ		LRHPAQLLKSSYYYPFQIPWFPEFMFSINDFKVLKHLFTSHSTG
			IGRKGCQLTTKDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH
Į.	ł		HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTTLSEASH
(625	1420	470	WLQQDQPDIVNKLIWTFLKBETRKKD
6635 ·	1420	4/0.	EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGGAEPRPLPLSYRLIDGEAALPAVVFLHGLFGSKTNFNSIAK
		1	ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG
			LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS
}		1	HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHI.
		ĺ	LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL
			LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI
		1	AAIRGPLV
6636	1514	1801	SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAB
[		ĺ	QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD
			DEGDGVF
6637	2	1501	CSSSPCPHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI
			Kasedslsvlberncsdpggpvngyqkitggpglingrhakigt
		{	VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD
			LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG
			DLPMGYOHLHTOLOYECISPFYRRIGSSRRTCLRTGKWSGRAPS
1			CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW
1			FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR
			DDDRDEKTIQSLQISAITLHPNYDPILLDADIAILKLLDKARIS
[			TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL
			RSGVVSVVDSLLCBBQHEDHGIPVSVTDNMFCASWEPTAPSDIC
			TARTGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	1	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /*possible nucleotide deletion,
	amino acid	sequence	
	sequence		\=possible nucleotide insertion)
			TKVLPFKDWIERNMK
6638	1391	224	GGIPQAGGKMAAPWWRAALCECRRWRGFSTSAVLGRRTPPLGPM
		į	PNSDIDLSNLERLEKYRSFDRYRRRAEQEAQAPHWWRTYREYFG
	}		BKTDPKEKIDIGLPPPKVSRTQQLLERKQAIQELRANVEEERAA
	1		RLRTASVPLDAVRAEWERTCGPYHKQRLAEYYGLYRDLFHGATF
	<b>!</b>	J	VPRVPLHVAYAYGEDDLMPVYCGNEVTPTEAAQAPEVTYEAEEG
	Į.		SLWTLLLTSLDGHLLRPDAEYLHWLLTNIPGNRVAEGQVTCPYL
	]	ļ	PPFPARGSGIHRLAFLLFKQDQPIDFSEDARPSPCYQLAQRTFR
	ĺ		TFDFYKKHQRTMTPAGLSFFQCRWDDSVTYIFHQLLDMREPVFE
			FVRPPPYHPKQKRFPHRQPLRYLDRYRDSHKPTYGIY
6639	2046	1268	IGCFIMDGGDDGNLIIKKRFVSEAELDERRKRRQEEWEKVRKPB
	1	]	DPBECPBEVYDPRSLYERLQEQKDRKQQEYBEQFKFKNMVRGLD
	1	i	BDBTNFLDBVSRQQELIEKQRREKELKELKBYRNNLKKVGISQB
	Į.		NKKEVEKKLTVKPIETKNKPSQAKLLAGAVKHKSSESGNSVKRL
	I		KPDPEPDDKNQEPSSCKSLGNTSLSGPSIHCPSAAVCIGILPGL
		ł	GAYSGSSDSESSSDSEGTINATGKIVSSIFRTNTFLEAP
6640	117	1043	VLEPPDVSMAESEDRSLRIVLVGKTGSGKSATANTILGEEIFDS
0040	]/	1043	RIAAQAVTKNCQKASREWQGRDLLVVDTPGLFDTKESLDTTCKE
	}	ļ	ISRCIISSCPGPHAIVLVLLLGRYTBEBQKTVALIKAVPGKSAM
	1	i	KHMVILFTRKEBLEGQSFHDFIADADVGLKSIVKECGNRCCAFS
	1	ì	NSKKTSKAEKESQVQBLVBLIEKMVQCNEGAYPSDDIYKDTEBR
		1	LKOREEVLRKIYTDQIMEEIKLVEEDKHKSEEKKEKEIKLLKLK
		<u> </u>	YDEKIKNIREEARRNIFKDVFNRIWKMLSEIWHRFLSKCKFYSS
			SAAVGRRSEVRGCAPRPRILRSARRMDPVPGTDSAPLAGLAWSS
6641	1.	894	ASAPPRGFSAISCTVRGAPASFGKSFAQKSGYFLCLSSLGSLR
		1	NPQENVVADIQIVVDKSPLPLGFSPVCDPMDSKASVSKKKRMCV KLLPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK
		[	
		ľ	APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS
	İ	i	TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF
			GDLTIKSLADIBREYNYGYVVEKTAAARLPPSVS
6642	22	1296	PLEERMMTKMDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTE
	L		
i		1	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV
			HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCBILQVGELP
			HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCBILQVGBLP NBGRNDYHPMFFTHDRAPRBLFGICIQLLNKTWKEMRATAEDFN
			HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAFEBLFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSBILRLRQSER
			HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAFEBLFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSBILRLRQSER MSQDDFQSPPIVBLREKIQPBILBLIKQQRLNRLCEGSSFRKIG
			HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NEGRNDYHPMFFTHDRAFEELFGICIQLINKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQPKSKLRSLSYSBILRLRQSER MSQDDFQSPPIVBLREKIQPBILBLIKQQRIMRLCEGSSFRKIG NRRRQERFWYCRLAINHKVLHYGDLDDNPQGBVTFESLQEKIPV
			HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAFBELFGICIQLLNKTWKEMRATABDFN KVMQVVRBQITRALPSKPNSLDQFKSKLRSLSYSBILBLRQSER MSQDDFQSPPIVELREKIQPBILBLIKQQRLNRLCEGSSFRKIG NRRRQERFWYCRLALNHKVLHYGDLDDNPQGBVTFRSLQBKIFV ADIKATVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDETLNF
			HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NEGRNDYHPMFFTHDRAFBELFGICIQLLNKTWKEMRATARDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSBILBLRQSER MSQDDFQSPIVBLREKIQPBILBLIKQQRLNRLCEGSSFRKIG NERRQERFWYCRLALNHKVLHYGDLDDNPQGBVTFRSLQBKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLBLAFSILYDPDETINF IAPNKYEYCIWIDGLSALLGKDMSSBLTKSDLDTILSMEMKLRL
			HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAFEBLFGICIQLLNKTWKEMRATARDFN KVMQVVRBQITRALPSKPMSLDQFKSKLRSLSYSBILRLRQSER MSQDDFQSPPIVKLREKIQPBILBLIKQQKLNRLCEGSSPRKIG NRRRQERFWYCRLALNHKVLHYGDLDDNPQGBVTFRSLQBKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDSTINF IAPNKYEYCIWIDGLSALIGKDMSSBLTKSDLDTLLSMEMKLRL LDLENIQIPBAPPPIPKBPSSYDFVYHYG
6643	3049	2265	HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAFEBLFGICIQLLNKTKKEMRATAEDFN KVMQVVRBQITRALPSKPMSLDQFKSKIRSLSYSBILRLRQSER MSQDDFQSPPIVKLREKIQPEILBLIKQQKLNRLCEGSSFRKIG NRRQERFWYCRLALNHKVLHYGDLDDNPQGBVTFBSLQBKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLBNIQIPBAPPPIPKEPSSYDFVYHYG SIHAPAEGRTRGRLAEKPKMLTRKTKLWDINAHITCRLCSGYLI
6643	3049	2265	HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAFEBLFGICIQLINKTWKEMRATABDFN KVMQVVRBQITRALPSKPNSLDQYKSKLRSLSYSBILRLRQSER MSQDDFQSPPIVBLRBKIQPBILBLIKQQKLMRLCEGSSFRKIG NRRQRRFWYCRLALNHKVHYGDLDDNPQGBVTFBSLQBKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDETLNF IAPNKYEYCIWIDGLSALIGKDMSSELTKSDLDTLLSMBMKLRL LDLBNIQIPBAPPPIPKBSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTYTEGLHTFCRSCLVKYLBENNTCPTCRIVIHQSHPLQYIG
6643	3049	2265	HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAFEBLFGICIQLINKTWKEMRATABDFN KVMQVVRBQITRALPSKPNSLDQYKSKLRSLSYSBILRLRQSER MSQDDFQSPPIVBLRBKIQPBILBLIKQQKLMRLCEGSSFRKIG NRRQRRFWYCRLALNHKVHYGDLDDNPQGBVTFBSLQBKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDETLNF IAPNKYEYCIWIDGLSALIGKDMSSELTKSDLDTLLSMBMKLRL LDLBNIQIPBAPPPIPKBSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLBENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLYPGLQBABMRKQRBFYHKLGMBVPGDIKGETC
6643	3049	2265	HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHEMFFTHDRAFBELFGICIQLINKTWKEMRATABDFN KVMQVVRBQITRALPSKPNSLDQFKSKLRSLSYSBILRLRQSER MSQDDFQSPPIVBLREKIQPBILBLIKQQRLNRLCEGSSFRKIG NRRGQRFFWYCRLAINHKVHYGDLDDNPQGBVTFRSLQBKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDETINF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTILSMBMKLRL LDLBNIQIPBAPPPIPKBPSSYDFVYHYG SIHAPAEGRTRGRLAEKPKMLTRKIKLMDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLBENNTCPTCRIVTHQSHPLQYIG HDRTMQDIVYKLVFGLQBABMRKQREFYHKLGMBVPFGDIKGETC SAKQHLDSHRNGETKADDSSNKEAABEKPBEDNDYHRSDEQVSI
6643	3049	2265	HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAFEBLFGICIQLINKTWKEMRATABDFN KVMQVVRBQITRALPSKPNSLDQYKSKLRSLSYSBILRLRQSER MSQDDFQSPPIVBLRBKIQPBILBLIKQQKLMRLCEGSSFRKIG NRRQRRFWYCRLALNHKVHYGDLDDNPQGBVTFBSLQBKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDETLNF IAPNKYEYCIWIDGLSALIGKDMSSELTKSDLDTLLSMBMKLRL LDLBNIQIPBAPPPIPKBSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLBENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLYPGLQBABMRKQRBFYHKLGMBVPGDIKGETC
6643	3049	2265	HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAPBELFGICIQLLNKTWKEMRATARDFN KVMQVVRBQITRALPSKPNSLDQFKSKLRSLSYSBILBLRQSER MSQDDFQSPIVBLREKIQPBILBLIKQQRLNRLCEGSSFRKIG NRRRQBRFWYCRLALNHKVLHYGDLDDNPQGBVTFRSLQBKIPV ADIKATVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDETLNP IAPNKYBYCIWIDGLSALLGKDMSSBLTKSDLDTLLSMBMKLRL LDLBNIQIPBAPPPIPKBPSSYDFVYHYG SLHAPAEGRTRGRLABKPKMLTRKTKLWDINAHLTCRLCSGYLI DATTVTECLHTFCRSCLVKYLBENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBABMRKQREFYHKLGMBVPGDIKGSTC SAKQHLDSHRNGBTKADDSSNKBAABBKPBEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFLAKKLNLSSFNBL DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL
		2265	HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAPBELFGICIQLLNKTWKEMRATARDFN KVMQVVRBQITRALPSKPNSLDQFKSKLRSLSYSBILBLRQSER MSQDDFQSPIVBLREKIQPBILBLIKQQRLNRLCEGSSFRKIG NRRRQBRFWYCRLALNHKVLHYGDLDDNPQGBVTFRSLQBKIPV ADIKATVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDETLNP IAPNKYBYCIWIDGLSALLGKDMSSBLTKSDLDTLLSMBMKLRL LDLBNIQIPBAPPPIPKBPSSYDFVYHYG SLHAPAEGRTRGRLABKPKMLTRKTKLWDINAHLTCRLCSGYLI DATTVTECLHTFCRSCLVKYLBENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBABMRKQREFYHKLGMBVPGDIKGSTC SAKQHLDSHRNGBTKADDSSNKBAABBKPBEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFLAKKLNLSSFNBL DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL
6644	3049		HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAFEBLFGICIQLINKTWKEMRATABDFN KVMQVVRBQITRALPSKPNSLDQPKSKLRSLSYSBILRLRQSER MSQDDFQSPPIVBLREKIQPBILBLIKQURINBLCEGSSFRKIG NRRQERFWYCRLALNHKVLHYGDLDDNPQBBVTFBSLQBKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLBLAFSILYDPDBTINF IAPNKYEYCIWIGGLSALLGKDMSSBLTKSDLDTILSMEMKLRL LDLBNIQIPBAPPPIPKEPSSYDFVYHYG SLHAPABEGRTRGRLABKPRMIJTRKTKLWDINAHITCRLCSGYLI DATTYTECLHTFCRSCLVKYLBENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVXLVPGLQBABMRKQREFYHKLGMBVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAABEKPBEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNBL DILCNEBILGKDBTLKFVVVTRWFRKAPLLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFINLGGEMLYILDQR
			HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAFEBLFGICIQLINKTWKEMRATABDFN KVMQVVRBQITRALPSKPNSLDQYKSKLRSLSYSBILRLRQSER MSQDDFQSPPIVBLRBKIQPBILBLIKQQKLMRLCEGSSFRKIG NRRQRRFWYCRLALNHKVLHYGDLDDNPQGBVTFBSLQBKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDETINF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTTLSMBMKLRL LDLBNIQIPBAPPPIPKBSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTYTECLHTFCRSCLVKYLBENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLYPGLQBAEMRKQRKFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAABEKPERDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSPNEL DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL FRPLATEPRGSSPVOLVSSTWSVRTLPILLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMBELFKPQELYSKKALR
			HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAPEBLFGICIQLINKTWKEMRATABDFN KVMQVVRBQITRALPSKPNSLDQVKSKLRSLSYSBILRLRQSER MSQDDFQSPPIVBLRBKIQPBILBLIKQQRLMRLCEGSSFRKIG NRRQGRFPWYCRLAINHKVHYGDLDDNPQGBVTFBSLQBKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDETINF IAPNKYEYCIWIDGLSALLGKDMSSBIJTKSDLDTILSMBMKLRL LDLBNIQIPBAPPPIPKBPSSYDFVYHYG SLHAPAEGRTTRGRLAEKPKMLTRKIKLMDINAHITCRLCSGYLI DATTVTECLHTFCRSCIVKYLBENNTCPTCRIVHQSHPLQYIG HDRTMQDIVYKLYPGLQBABMRKQRBFYHKLGMBVPGDIKGETC SAKQHLDSHRNGBTKADDSSNKBAABBKPBEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKINLSSFNBL DILCNBEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPILFINLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMBBLFKPQELYSKKALR TYYERLAHASIMKLNQASNDKLYDLMTMAFKYQVLLCPRPKDVL
			HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAPEBLFGICIQLINKTWKEMRATABDFN KVMQVVRBQITRALPSKPNSLDQPKSKLRSLSYSBILRLRQSER MSQDDFQSPPIVBLREKIQPBILBLIKQQRLNRLCEGSSFRKIG NRRRQRRFWYCRLAINHKVLHYGDLDDNPQGBVTFRSLQRKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDETINF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTILSMBMKLRI. LDLBNIQIPBAPPPIPKBPSSYDFVYHYG SIHAPABGRTRGRLAEKPKMLTRKIKLMDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLBENNTCPTCRIVHQSHPLQYIG HDRTMQDIVYKLYPGLQRAEMRKQREPYHKLGMBVPGDIKGGTC SAKQHLDSHRNGBTKADDSSNKBAABBKPBEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKINLSSFNBL DILCNBEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVTIPLLFINLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNKFMBELFKPQELYSKKALR TYYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPROVIL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ
			HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAPBELFGICIQLINKTWKEMRATABDFN KVMQVVRBQITRALPSKPNSLDQPKSKURSLSYSBILBLRQSER MSQDDFQSPPIVBLREKIQPBILBLIKQQRLNRLCEGSSFRKIG NRRQGRFPWYCRLALNHKVUHYGDLDDNPQGBVTFRSLQBKIFV ADIKAIVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDETLNP IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMBMKLRL LDLBNIQIPBAPPPIPKBPSSYDFVYHYG SIHAPAEGRTRGRLAEKPKMLTRKIKLMDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLBENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBABMRKQRBPYHKLGMBVPGDIKGGTC SAKQHLDSHRNGSTKADDSSNKBABEBKPBEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFLAKKLNLSSFNBL DILCNEEILGKDHTLKFVVVTRWFFKKAPLLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFINLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNKFMBELFKPQELYSKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LUTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMPLKDKVQNNNGRFVLPVSGPVPWGT
			HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAPERLFGICIQLINKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQPKSKLRSLSYSBILRLRQSER MSQDDFGSPPIVBLREKIQPBILBLIKQURLNRLCEGSSFRKIG NRRQERFWYCRLALMHKVLHYGDLDDNPQGBVTFBSLQBKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDBTIMP IAPNKYEYCIWIGCLSALLGKDMSSBLTKSDLDTILSMEMKLRL LDLENIQIPBAPPPIPKEPSSYDFVYHYG SIHAPABGRTRGRLABKPRMITRKTKLMDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLBENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBABMRKQRBFYHKLGMBVPGDIKGSTC SAKQHLDSHRNGSTKADDSSNKEABEBKPBEDDDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKJNLSSFNBL DILCNEBILGKDBTILKFVVVTRWFKKAPLLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFINLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMBBLFKPQELYSKKALR TYYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLTFFQDLHIRVSMFLKDKYQNNNGRFVIPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL
			HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAPEBLFGICIQLINKTWKEMRATABDFN KVMQVVRBQITRALPSKPNSLDQYKSKLRSLSYSBILRLRQSER MSQDDFQSPPIVBLRBKIQPBILBLIKQUKINBLCEGSSFRKIG NRRQRRFWYCRLALNHKVLHYGDLDDNPQGBVTFBSLQBKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDBTINP IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTILSMEMKLRL LDLBNIQIPBAPPPIPKBPSSYDFVYHYG SLHAPAEGRTRGRLABKPMITRKTKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLBENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREPYHKLGMBVPGDIKGETC SAKQHLDSHRNGETKADDSSNKBAABEKPBEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNBL DILCNBEILGKDHTLKFVVVTRWFBKRAPLLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFINLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMBBLFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSFTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMPLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEBVKR IFFKHGGRYVPAPKEGSFEFYGDRVL KLGTIMYSVNQPVRTHVSGSSKNLASWTQESIAPNPLAKEBLNF
			HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAPEBLFGICIQLINKTWKEMRATABDFN KVMQVVRBQITRALPSKPNSLDQYKSKLRSLSYSBILRLRQSER MSQDDFQSPPIVBLRBKIQPBILBLIKQQKIMBLCEGSSFRKIG NRRQRRFWYCRIAINHKVHYGDLDDNPQGBVTFBSLQBKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDETINF IAPNKYBYCIWIDGLSALLGKDMSSEITKSDLDTILSMBMKLRL LDLBNIQIPBAPPPIPKBSSYDFVYHYG SIHAPAEGRTRGRLABKPKMITRKIKLWDINAHITCRLCSGYLI DATTVTECHTFCRSCLVKYLBENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBABMKKQRBFYHKLGMBVPGDIKGETC SAKQHLDSHRNGBTKADDSSNKBABEBKPBENDMYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNBL DILCNBEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDILL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFINLGGEMLYILDQR LRAQNIPGDKARKVINDIISTMFNKFMBBLFKPQELYSKKALR TVYBRLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMPLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGBEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVBTHVSGSSKNLASWTQBSIAPNPLAKEBLNF LARLMGMBIKKPSGPBPGPRLNLPTTDEEBEQAALTRPEBLSY
			HQDTYIRIVLENSSREDKHECPFGRSAIBLTKMLCEILQVGBLP NBGRNDYHPMFFTHDRAPEBLFGICIQLINKTWKEMRATABDFN KVMQVVRBQITRALPSKPNSLDQYKSKLRSLSYSBILRLRQSER MSQDDFQSPPIVBLRBKIQPBILBLIKQUKINBLCEGSSFRKIG NRRQRRFWYCRLALNHKVLHYGDLDDNPQGBVTFBSLQBKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLBLAPSILYDPDBTINP IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTILSMEMKLRL LDLBNIQIPBAPPPIPKBPSSYDFVYHYG SLHAPAEGRTRGRLABKPMITRKTKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLBENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREPYHKLGMBVPGDIKGETC SAKQHLDSHRNGETKADDSSNKBAABEKPBEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNBL DILCNBEILGKDHTLKFVVVTRWFBKRAPLLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFINLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMBBLFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSFTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMPLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEBVKR IFFKHGGRYVPAPKEGSFEFYGDRVL KLGTIMYSVNQPVRTHVSGSSKNLASWTQESIAPNPLAKEBLNF

SEQ	Predicted	Predicted end	Dmino and an analysis and an a
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	ĺ.	\=possible nucleotide insertion)
6645	6530	4646	FVEGLAGYVYKAASEGKVLTLAALLLNRSESDIRYLLGYVSQQG
i	j		GQRSTPLIIAARNGHAKVVRLLLEHYRVQTQQTGTVRFDGYVID
1	1		GATALWCAAGAGHFEVVKLLVSHGANVNHTTVTNSTPLRAACFD
1		<b>[</b>	GRLDIVKYLVENNANISIANKYDNTCLMIAAYKGHTDVVRYLLE
1	1		QRADPNAKAHCGATALHFAAEAGHIDIVKELIKWRAAIVVNGHG
			MTPLKVAAESCKADVVELLLSHADCDRESRIEALELLGASFAND
	ļ		RENYDIIKTYHYLYLAMLERFQDGDNILBKEVLPPIHAYGNRTE
	·		CRNPQELESIRQDRDALHMEGLIVRERILGADNIDVSHPIIYRG
1			AVYADNMBFEQCIKLWLHALHLRQKGNRNTHKDLLRFAQVFSQM
ì	ł		IHLNETVKAPDIECVLRCSVLEIBQSMNRVKNISDADVHNAMDN
ŀ			YECNLYTFLYLVCISTKTQCSBEDQCKINKQIYNLIHLDPRTRE
	i i		GPTLLHLAVNSNTPVDDPHTNDVCSFPNALVTKLLLDCGARVNA VDNEGNSALHIIVQYNRPISDPLTLHSIIISLVRAGAHTDMTNK
1			QNKTPLDKSTTGVSEILLKTQMKMSLKCLAARAVRANDINYODO
1			IPRTLEEFUGPH
6646	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY
1			EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTI.
1			KKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWATAL
			TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWPLD
i			FKVLPQRAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA
			GSERAEEKQDSRKPLLEL
6647	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY
1 .			EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTL
			EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL
			TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLD
1			FKVLPQEABEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA
6648	413	897	GSERAERKQDSEKPILIRL
. 0040	472	037	RNCWNCFTKYPNSPPEDIDHKDSYLITRSIMAEPDYIEDDNPEL IRPQKLINPVKTSRNHQDLHRELLMNQKRGLAPQNKPELQKVME
			KRKRDQVIKQKBEEAQKKKSDLBIELLKRQQKLBQLELBKQKLQ
			BEQENAPEFVKVKGNLRRTGOBVAQAQES
6649	1357	832	WIPRAAGIRHEVKWDVKEIMSOHNIYVDALLKEFEOFNRRLNEV
			SKRVRIPLPVSNILWEHCIRLANRTIVEGYANVKKCSNEGRALM
1 !			QLDPQQFLMKLEKLTDIRPIPDKEFVETYIKAYYLTENDMERWI
			KEHREYSTKQLTNLVNVCLGSHINKKARQKLLAAIDDIDRPKR
6650	32	765	LVPLVFSLLVQSCKQVYRSIAMKFVPCLLLVTLSCLGTLGQAPR
			QKQGSTGEEFHFQTGGRDSCTMRPSSLGQGAGEVWLRVDCRNTD
			QTYWCEYRGQPSMCQAFAADPKSYWNQALQELRRLHHACQGAPV
			LRPSVCREAGPQAHMQQVTSSLKGSPEPNQQPEAGTPSLRPKAT
1 1			VKLTEATQLGKDSMEELGKAKPTTRPTAKPTQPGPRPGGNEEAK
			KRAWEHCNKPFQALCAFLISFFRG
6651	3425	1353	AKELLKVGDFSLCAGPYONTADIMENLSKEPLASFVSESFDISA
	1	*	CGIATEHVKIDNSGEGLTARAGSETLSRDGEVGVNSDMHYELSG
	ļ		DSDLDLLGDCRNPRLDLEDSYTLRGSYTRKKDVPTDGYESSLNF
	l		HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCVPPYVQIR
] ]			DLHGILRTYANFSITKBLKDTMRTSHGLRRHPSFSANCGLPSSW
ļ Ì	. }		TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGDSQHSASSANV
1	1		FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP RPQGQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL
1 1	ŀ	i	NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN
	]		DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKRA
[ ]	į		CKSTFLFYLVETEDKSFFVRTKNLLRKGGHTEIRPOHFCOAFHR
	1		ENDTLIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV
1 1	İ		LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLINGNG
] [	ļ		RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELLH
j	•		YHQCDSRSSTKAEILKCLLNLQIQHIDARFAVLLTDKPTIPREV

SEQ	Predicted	Predicted end	Daving hold assessed assessed as a second
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
""	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	1 1		PKNNGILVTDVNNFIENIEKIAAPFRSSYW
6652	2	1343	IPGSTISCSCHSRRLRGGSPAPRISLGAASPRPRPPSLPLPLPL
5022	ļ <del>-</del>		PFPLFLPTRPARRAWIRSRRASEWVGKMEVPRLDHALNSPTSPC
1			EEVIKNLSLEAIQLCDRDGNKSQDSGIAEMEELPVPHNIKISNI
i	ļ		TCDSFKISWEMDSKSKDRITHYFIDLNKKENKNSNKFKHKDVPT
1			KLVAKAVPLPMTVRGHWFLSPRTEYTVAVQTASKQVDGDYVVSE
1			WSEIIEFCTADYSKVHLTQLLEKAEVIAGRMLKFSVFYRNQHKE
1			YFDYVREHHGNAMOPSVKDNSGSHGSPISGKLEGIPFSCSTEFN
1			TGKPPQDSPYGRYRFEIAAEKLFNPNTNLYFGDFYCMYTAYHYV
ł			ILVIAPVGSPGDEFCKQRLPQLNSKDNKPLTCTEEDGVLVYHHA
1			QDVILEVIYTDPVDLSLGTVAEITGHQLMSLSTANAKKDPSCKT
1			CNISVGR
6653	170	1910	FFLEPRLRPFPASRARPVPARTRPSPLHPCCFCFEGGGSMLSPQ
ŀ			RVAAAASRGADDAMESSKPGPVQVVLVQKDQHSFELDEKALASI
		*	LLQDHIRDLDVVVVSVAGAFRKGKSFILDFMLRYLYSQKESGHS
l			NWLGDPERPLTGFSWRGGSDPETTGIQIWSEVFTVEKPGGKKVA
Į.			VVLMDTQGAFDSQSTVKDCATIFALSTMTSSVQIYNLSQNIQED
1			DLQQLQLFTEYGRLAMDEIFQKPFQTLMFLVRDWSFPYBYSYGL
			QGGMAPLDKRLQVKEHQHEBIQNVRNHIHSCPSDVTCFLLPHPG
Į į			LQVATSPDFDGKLKDIAGEFKEQLQALIPYVLNPSKLMEKEING
1			\$KVTCRGLLBYFKAYIKIYQGEDLPHPKSMLQATARAYNLAAAA
			SAKDIYYNNMEBVCGGEKPYLSPDILEBKHCBFKQLALDHFKKT
1			KKMGGKDFSFRYQQELEBEIKELYENFCKHNGSKNVFSTFRTPA
1 .			VLFTGIVALYIASGLTGFIGLEVVAQLFNCMVGLLLIALLTWGY
	·		IRYSGQYRELGGAIDFGAAYVLEQASSHIGNSTQATVRDAVVGR
			PSMDKKAQ
6654	1	705	RTSLSPSQCSSFNLAMASAGMQILGVVLTLLGWVNGLVSCALPM
i			WKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQMQCKVYDSLLAL
1			PODLOAARALCVIALLVALFGLLVYLAGAKCTTCVKEKDSKARL
			VLTSGIVFVISGVLTLIPVCWTAHAVIRDFYNPLVARAQKRELG
			ASLYLGWAASGLLLLGGGLLCCTCPSGGSQGPSHYMARYSTSAP
			AISRGPSRYPTKNYV
6655	341	16	KDAYMPKKGLLALALVFSLPVPAABHWIDVRVPEQYQQBHVQGA
1			INIPLKEVKERIATAVPDKNDTVKVYCNAGRQSGQAKEILSEMG
6656			YTHVENAGGLKDIAMPKVKG
0000	2	1212	TELPPRPANLATOPPLSPLRALAPLPEKPGAVPPPOKRMAKVAK
			DINPGVKKMSLGQLQSARGVACLGCKGTCSGFEPHSWRKICKSC
			KCSQEDHCLTSDLEDDRKIGRILMDSKYSTLTARVKGGDGIRIY
			KRNRMIMTNPIATGKDPTFDTITYEWAPPGVTQKLGLQYMELIP KBKQPVTGTEGAFYRRRQLMHQLPIYDQDPSRCRGLLKNELKLM
	,		EEFVKQYKSEALGVGKVALPGQGGLPKEEGKQQKKPEGARTTAA
1 1	•		TINGSLSDPSKEVEYVCBLCKGAAPPDSPVVYSDRAGYNKOWHP
			TCFVCAKCSEPLVDLIYFWKDGAPWCGRHYCESLRPRCSGCDEI
1 1			IPAEDYORVEDLAWHRKHFVCEGCEOLLSGRAYIVTKGOLLCPT
1	İ		CSKSKRS
6657	830	2120	LLTCQERAGDCLLSASTMKEVVYWSPKKVADWLLENAMPEYCEP
			LEHFTGQDLINLTQEDFKKPPLCRVSSDNGORLLDMIETLKMEH
			HLBAHKNGHANGHLNIGVDIPTPDGSPSIKIKPNGMPNGYRKEM
			IKIPMPBLERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER
			VPPKEVQPPLPDTFFDHFNRVOWAFSICEINGMILVGLWLIOWL
1 1			LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK
			LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL
ļ	ļ		TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV
			AYYITTRLFWWYHTMANQOVLKBASQMNLLARVWWYRPFQYPEK
	ſ		NVQGIVPRSYHWPPPWPVVHLSRQVKYSRLVNDT
6658	35	855	HCCALGAPGSPYRGLYFSSAAPCTAPRKAKHOSTLEGLTKRMLM

WO 01/53312

		· · · · · · · · · · · · · · · · · · ·	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\-possible nucleotide insertion)
_	_		FDPVPVKQEAMDPVSVSYPSNYMESMKPNKYGVIYSTPLPEKFF
1			QTPEGLSHGIQMEPVDLTVNKRSSPPSAGNSPSSLKFPSSHRRA
	1		SPGLSMPSSSPPIKKYSPPSPGVQPFGVPLSMPPVMAAALSRHG
			IRSPGILPVIQPVVVQPVPFMYTSHLQQPLMVSLSERMENSSSS
			MQVPVIBSYEKPISQKKIKIEPGIBPQRTDYYPEEMSPPLMNSV
}	<b>!</b>		SPPOALLOR
6659	18	523	BPQRGDCBTWFQNCSLPKFVCFFCWGFWLWRAHSMSNLHSLPGL
l	1		RGLTSISRNQLQCTNAMRVINNYQRRWKNQNTFLLATFANVVNV
i			CGNPTITCPHNRTLNNCHHSGVQVPLMYCNLTTPSPQNISNCRY
ł			AQTPANMFYIVACDNRDQRRDPPQYPVVPVHLHTII
6660	514	1707	CAASLDCRHHLCEPDMKLVWPSAKLLQAAAGASARACDSVTSNV
[			LPLLLEQFHKHSQSSQRRTILEMLLGFLKLQQKWSYEDKDQRPL
í	[		NGPKDQLCSLVFMALTDPSTQLQLVGIRTLTVLGAQPDLLSYED
1			LELAVGHLYRLSFLKEDSQSCRVAALEASGTLAALYPVAFSSHL
1			VPKLABBLRVGBSNLTNGDEPTQCSRHLCCLQALSAVSTHPSIV
Ī	İ		KETLPLILQHLWQVNRGNMVAQSSDVIAVCQSLRQMARKCQQDP
	Į		RSCWYFHQTAIPCLLALAVQASMPEKEPSVLRKVLLEDEVLAAM
1			VSVIGTATTHLSPBLAAQSVTHIVPLFLDGNVSFLPENSFPSRF
j			QPFQDGSSGQRRLIALLMAFVCSLPRNVSKHIWEVLLFNLDKVT
j			PG .
6661	179	430	GVHAASGTLSATWLARAKMFDSLAKAGKYLGQAAKLMIGMPDYD
I	• 		NYVEHMRVNHPDQTPMTYEEFFRERQDARYGGKGGARCC
6662	185	423	RELPKPAPAQPAS IHCARFSGVTPPTAKTAMSDGNTAFNALMYC
i .	1		GPKADDGNIFSACAPASSAVKASVSVAQPGQAVIP
6663	3	1005	RPVLSSRVDDFVPPLPETSGRRKKLERMYSVDRVSDDIPIRTWF
1			PKENLFSFQTASTTMQAISNFRKHLRMVGSRRVKAQTFAERRER
1			SFSRSWSDPTPMKADTSHDSRDSSDLQSSHCTLDEAFEDLDWDT
	ŀ		EKGLEAVACDTEGFVPPKVMLISSKVPKAEYIPTIIRRDDPSII
ł			PILYDHEHATFEDILBBIERKLNVYHKGAKIWKMLIFCQGGPGH
ŀ			LYLLKNKVATFAKVEKBEDMIHFWKRLSRLMSKVNPEPNVIHIM
1			GCYILGNPNGEKLFQNLRTLMTPYRVTFBSPLELSAQGKQMIET
L	L		YFDFRLYRLWKSRQHSKLLDFDDVL
6664	58	968	PRLLRLPRSVVVMDSPWDELALAFSRTSMFPFFDIAHYLVSVMA
<b>!</b>			VKRQPGAAALAWKNPISSWFTAMLHCFGGGILSCLLLAEPPLKF
			LANHTNILLASSIWYITFFCPHDLVSQGYSYLPVQLLASGMKEV
			TRTWKIVGGVTHANSYYKWGWIVMIAIGWARGAGGTIITNFERL
1			VKGDWKPEGDEWLKMSYPAKVTLLGSVIPTFQHTQHLAISKHNL
			MFLYTIFIVATKITMMTTQTSTMTFAPFEDTLSWMLFGWQQPFS
			SCEKKSEAKSPSNGVGSLASKPVDVASDNVKKKHTKKNE
6665	171	1278	DERRLACROVVTQQRSELYPGFQKRQRFLPKAGEEAAAQGGRHL
			PGRWLGPGCTQNPCSVHTATGPEPRKLPLLPPDSPNSGYPKEPA
l			ALCPGIPSPCRMTHQDLSITAKLINGGVAGLVGVTCVFPIDLAK
1			TRLQNQHGKAMYKGMIDCLMKTARAEGFFGMYRGAAVNLTLVTP
1			BKAIKLAANDFFRRLLMEDGMQRNLKMEMLAGCGAGMCQVVVTC
1	i .		PMKMLKIQLQDAGRLAVHHQGSASAPSTSRSYTTGSASTHRRPS
]			ATLIAWELLRTQGLAGLYRGLGATLLRDIPFSIIYFPLPANLNN
			LGFNELAGKASFAHSFVSGCVAGSIAAVAVTPLDVLKTRIQTLK
	J i		KGLGEDMYSGITDCAR
6666	498	2868	MTTFLPVPQMMAGFSFGTFGNPPMESPSAWQTIHQPFIVSCLTL
			WSPGCWPQPIQKEGVGLWDIRKPQSSLLRYGGNLSLQSAMSVRF
			NSNGTQLLALRRRLPPVLYDIHSRLPVFQFDNQVYFNSCTMKSC
1			CFAGDRDQYILSGSDDFNLYMWRIPADPEAGGIGRVVNGAFMVL
			KGHRSIVNQVRFNPHTYMICSSGVKKIIKIWSPYKQPGCTGDLD
(			GRIEDDSRCLYTHEEYISLVLNSGSGLSHDYANQSVQEDPRMMA
	Ì		FFDSLVRREIBGWSSDSDSDLSESTILQLHAGVSERSGYTDSES
			SASLPRSPPPTVDESADNAFHLGPLRVTTTNTVASTPPTPTCED
L			The state of the s

			the second of th
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			AASRQQRL9ALRRYQDKRLLALSNESDSEENVCEVELDTDLFPR
		Í	PRSPSPEDESSSSSSSSSSEDEEELNERRASTWORNAMRRKQKT
	1		TREDKPSAPIKPTNTYIGEDNYDYPQIKVDDLSSSPTSSPERST
	1		STLEIQPSRASPTSDIESVERKIYKAYKWLRYSYISYSNNKDGE
			TSLVTGEADEGRAGTSHKDNPAPSSSKEACLNIAMAQRNQDLPP
	1	1	BGCSKDTFKEETPRTPSNGPGHEHSSHAWAEVPRGTSQDTGNSG
	ł		SVEHPFETKKLINGKALSSRABEPPSPPVPKASGSTLINSGSGNCP
	•	1	RTQSDDSEBRSLETTCANHNNGRLHPRPPHPHNNGQNLGELEVV
			AYSSPGHSDTDRDNSSLTGTLLHKDCCGSRMACETPNAGTRKDP
		L	TDTPATDSSRAVHGHSGLKRQRIBLEDTDSENSSSKKKLKT
6667	171	1310	ABEVERLAAMRSDSLVPGTHTPPIRRRSKFANLGRIPKPWKWRK
	1	•	KKSEKFKHTSAALERKISMRQSREELIKRGVLKEIYDKDGELSI
			SNEEDSLENGQSLSSSQLSLPALSEMBPVPMPRDPCSYEVLQPS
		1	DIMDGPDPGAPVKLPCLPVKLSPPLPPKKVMICMPVGGPDLSLV
			SYTAQKEGQQGVAQHHHTVLPSQIQHQLQYGSHGQHLPSTTGSL
	ļ		PMHPSGCRMIDELNKTLAMTMQRLESSBQRVPCSTSYHSSGLHS
	Ì		GDGVTKAGPMGLPEIRQVPTVVIBCDDNKENVPHESDYEDSSCL
	l	·	YTREEEEEBDEDDDSSLYTSSLAMKVCRKDSLAIKPSNRPSKR
			ELBEKNILPROTDEERLELROQIGTKL
6668	714	358	TLAVATGPALTLRCHVCTSSSNCKHSVVCPASSRFCKTTNTVEP
	1		LRGNLVKKDCAESCTPSYTLQGQVSSGTSSTQCCQEDLCNEKLH
			NAAPTRTALAHSALSIGLALSILAVILAPSI
6669	459	1207	KDBETRKDYDYMLDHPEBYYSHYYHYYSRRLAPKVDVRVVILVS
			VCAISVPQFFSWWNSYNKAISYLATVPKYRIQATEIAKQQGLLK
	ì		KAKEKGKNKKSKEEIRDBEENIIKNIIKSKIDIKGGYQKPQICD
	į		LLLFQIILAPFHLCSYIVWYCRWIYNFNIKGKRYGERERLYIIR
	}		KSMKMSKSQFDSLEDHQKETFLKRELWIKENYEVYKQEQEEELK
			KKLANDPRWKRYRRWMKNEGPGRLTFVDD
6670	184	594	VARI*GEAAKMSSEPPPPYPGGPTAPLLEEKSGAPPTPGRSSPA
	ł	1	VMQPPPGMPLPPADIGPPPYEPPGHPMPQPGFIPPHMSADGTYM
	<b>!</b>		PPGFYPPPGPHPPMGYYPPGPYTPGPYPGPGGHTATVLVPSGAA
	<u> </u>		TIVIV
6671	1	763	LPAEKPRSAPNMAGGROGPQLTALLAAWIAAVAATAGPEBAALP
	1	ſ	PEQSRVQPMTASNWTLVMEGEWMLKFYAPWCPSCQQTDSEWEAF
	1	1	AKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIPRR
			YRGPGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFS
	l l	}	ISGKIWHLHNYFTVTLGIPAWCSYVFFVIATLVFGLSMDLVL*V
	L	<b> </b>	ISQCNWDPPYRHVS*/RPSTNLGVHTAHTSKHLRL
6672	304	1089	APGSKPVQFMDFEGKTSFCMSVFNLSNAIMGSGILGLAYAMAHT
		1	GVIFFLALLCIALLSSYSTHLLLTCAGIAGIRAYEQLGQRAFG
	{	Į.	PAGKVVVATVICLHNVGAMSSYLFIIKSELPLVIGTFLYMDPEG
	[	1	DWFLKGNLLIIIVSVLIILPLALMKHLGYLGYTSGLSLTCMLFF
	1	1	LVSVIYKKFQLGLCYRATMKQQWESEALVGTPQPRDSTAAVKAQ
	l	L	MFHS+LTGVLTQWPIMAPAFVCHPGGAGPSITELCRAFQAQD
6673	1116	1963	LQIQTHHTHHGARVTHLGSHQLLANAGTMLCRQQSSSMAPAFSQ
	l .	1	SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEQG*G*GLNV
	l	[	WLCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPNP*HSSIGAE
			NAVPRP+QG+KVNPSGQERQS\WVLPLPVPGEPLKLPGLPG+NK
			SFSRV/SGSKGKWILPRQLM+AS+R\TPRPVPGTQWVPITW/PL
	]	1	ITWH*SAPTPPLKACPAPRPSDPCSSCLSCPCVTQHPRFSDTGW
	ĺ	1	FGAGHCHSSCDFTRKGAAGGPG
6674	ī	440	LEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL
	-		HVLFHSDGSKNFDGFHAIYREITACSSSPCFHDGTCVLDKAGSY
		1	KCACLAGYTGORCENLLEERNCSDPG/WPSQWVPBNNRGPWAYQ

SEQ Predicted beginning nucleotide location nucleotide location corresponding to first amino acid sequence location sequence Sequ	partic Acid, E= ne, G=Glycine, =Lysine, sparagine, ginine, ine, Unknown, *=Stop deletion, ion)
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence sequence 277 1678 GNWPTERMAFLONPTITIAHLRQSHVTS LOCATION (CORN - PSC) SUBJECT (CORN - PSC	ne, G=Glycine, =Lysine, sparagine, ginine, ine, Onknown, *=Stop deletion, ion)
location corresponding to first amino acid residue of amino acid sequence  277  location corresponding to first amino acid residue of amino acid sequence  16675  corresponding to first amino acid residue of amino acid sequence codon, /=possible nucleotide	=Lysine, sparagine, ginine, ine, ine, onknown, *=Stop deletion, ion)
corresponding to first amino acid residue of sequence sequence corresponding to first amino acid residue of amino acid sequence sequence sequence corresponding to first amino acid residue of sequence sequence sequence corresponding to first amino acid sequence sequence sequence corresponding to first amino acid sequence sequence sequence corresponding to first amino acid sequence sequence sequence corresponding to first amino acid sequence sequence sequence sequence corresponding to first amino acid sequence, sequence sequence sequence corresponding to first amino acid sequence sequence sequence sequence corresponding to first amino acid sequence sequence sequence sequence corresponding to first amino acid sequence sequence sequence corresponding to first amino acid sequence sequence sequence corresponding to first amino acid sequence sequence corresponding to first amino acid sequence sequence corresponding to first amino acid sequence corresponding to fir	sparagine, ginine, ginine, ine, ine, a=Stop deletion, ion) DOTGMCEMVLIDHDVD
to first amino acid residue of S=Serine, T=Threonine, V=Val. residue of amino acid sequence sequence sequence S=Serine, T=Threonine, V=Val. (Codon, /=possible nucleotide insert: 6675 277 1678 GNWPTERMAFLDNPTILAHIRQSHVTSI LEKIHPPSMPGDSGSKIQGSNGETQGYV	ginine, ine, ine, Unknown, *=Stop deletion, ion) DDIGMCEMVLIDHDVD
amino acid residue of sesidue of amino acid sequence sequence sequence 277 1678 GNWPTERMAPLONPTILAHIRQSHVTSI LEKIHPPSMPGDSGSKIQGSNGETQGYV	ine, Onknown, *=Stop deletion, ion) DDTGMCEMVLIDHDVD
amino acid residue of sesidue of amino acid sequence sequence sequence 277 1678 GNWPTERMAPLONPTILAHIRQSHVTSI LEKIHPPSMPGDSGSKIQGSNGETQGYV	ine, Onknown, *=Stop deletion, ion) DDTGMCEMVLIDHDVD
residue of amino acid w=Tryptophan, Y=Tyrosine, X=1 amino acid sequence Codon, /=possible nucleotide insert.  6675 277 1678 GNWPTERMAFLDNPTITLAHIRQSHVTSI LEKIHPPSMPGDSGSKIQGSNGETQGYV	Onknown, *=Stop deletion, ion) DOTGMCEMVLIDHDVD
amino acid sequence Codon, /=possible nucleotide   sequence   =possible nucleotide insert.   6675   277   1678   GNWPTERMAFLDNPTITLAHIRQSHVTS  LEKIHPPSMPGDSGSKIQGSNGETQGYV	deletion, ion) DOTGMCEMVLIDHDVD
sequence \=possible nucleotide insert.  6675 277 1678 GNWPTERMAFLDNPTIILAHIRQSHVTSI LEKIHPPSMPGDSGSKIQGSNGETQGYV	ion) DDTGMCEMVLIDHDVD
6675 277 1678 GNWPTERMAFLDNPTITLAHLRQSHVTSI LBKIHPPSMPGDSGSKIQGSNGETQGYV	DDTGMCEMVLIDHDVD
LBKIHPPSMPGDSGSKIQGSNGETQGYV	
	INGSADII22MDLGIK
KKSLKEKPPISGKQSILSVRLEQCPEQL	
GTTATKKIDVYLPLHSSQDRLLPMTVVT	Masarvodliglicwo
YTSEGREPKLNDNVSAYCLHIABDDGEV	d <b>tdfppldsn</b> epihkf
GFSTLALVEKYSSPGLTSKESLFVRINA	ahgpsbiqvdntkvtm
KEILLKAVKRRKG9QKVSGSRADGVFEE	HEZIMOQVTAIOIQEO
HYKSFKVSMIHKLRFTTDVQL/GCALFF	GVLRKRAAPVDCLRPS
ADTWROEQIGCCGAACAALRS+DSHKC+	EGISGDKVRIDPVTNQ
KASTKFWIKOKPISIDSDLLCAC\DLAE	
6676 277 1678 GAWPTERMAPLDNPTILLAHIRQSHVTS	
LEKIHPPSMPGDSGSRIQGSNGRTQGYV	
RRSHTAQRIBRIRKERQNQIKCKNIQWK	
KKSTKEKBBISGKÖSITZAKITÄNY	
GTTATKKIDVYLPLHSSQDRLLPMTVVT	
YTSEGREPKLNDNVSAYCLHIABDDGEV	
GFSTLALVEKYSSPGLTSKESLFVRINA	
KEILLKAVKRRKGSQKVSGSRADGVFEE	
HYKSFKVSMIHRLRFTTDVQL/GCALFP	
ADTWRQEQIGCCGAACAALRS+DSHKC+	
Kastkfwikqkpisidsdllcac\dlag	B
6677 277 1678 GNWPTERMAFLDNPTIILAHIRQSHVTS	DDTGMCEMVLIDHDVD
LEKIHPPSMPGDSGSBIQGSNGBTQGYV	YAQSVDITSSWDFGIR
RRSNTAORLERLRKERONQIKCKNIQWK	ernskosaqelkslfe
KKSLKEKPPISGKQSILSVRLEQCPLQL	NNPFNEYSKPDGKCHV
GTTATKKIDVYLPLHSSQDRLLPMTVVT	
YTSEGREPKLNDNVSAYCLHTAEDDGEV	
GFSTLALVEKYSSPGLTSKESLFVRINA	
KRILLKAVKRRKGSOKVSOSRADOVPEE	
HYKSFKVSMIHRLRFTTDVQL/GCALFP	
ADTWROEQIGCCGAACAALRS*DSHKC*	
KASTKFWIKQKPISIDSDLLCAC\DLAE	
6678 221 865 GPSNQSSGSLSLIVTGCSSYWS*INDTC	
PRPCSQLPMSQGCLWHLDCCCPWVPYIP	
LLGSDQBSVGLRDLCVFVNFLLHVLLGL	
FLFFLLLQGGCHCLVLFANLVSQAPQIG	
HHPLPLVVGRWDAVKHLETVQSGLASLG	
6679 2 786 LEFARGAMPFLGODWRSPGONWVKTVDG	
SSYCNKEVYNKENLFNSLNYD/SCSQEE	
QRKWIYVHKGSTKBRHGYCTLGBAPNRL	
RLLBLIAKSQLTSLSGIAQKNFMNILEK	
KLLQTLYTSLCTLVKRVGKSVLVGNINM	
NIQITRVSGQAQPPPGSGSLHRDTGQTR	
6680 1498 2951 PLCTLPLMPSALPGWAGERWEKQWPLA/ P\RKNEPDTHCPRGEARPEV*HLPKPHS	
/NQVSPPQPM*GAEENGDQRGGKERAGE	ELINASSELTAAPUP?
EVHRNLQTFPGLPSRGGGP/GGAGTQGS	WARGEQUY/SPLLPAS
MQRSQAGLPGWEAGLVESPTHHIPALRP	eginatgbafpsttcs
SGP\PAPPGPTGLRPGGGSSSGGHG**P	glpvgkv/galgaaqd
PQSQGRGPTQGTVGTEMLLSGLGSAKAC	PAARPAVP*LPSDPAS
TIPKKGTRGFGEGPGVLQERNRWVVGRA	QGFTSADAAGTAPPGV
*LPAPLSQPPGATEPQVRACGMAPPSPG	TSGRLVANGRHPGPOV
AGGCPPGAGCWGSQPRGSQRCPRTYTHS	DIGHGRAPCDDRCWH*
WODPPSSPRTGCLPGIPARQAYSAPRTR	CONCIDENTANCELD
	ONT ATMICANTAL TH
FQGGGGG	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
No.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
)	amino acid	residue of	S=Serine, T=Threonine, V=Valine, .
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i i	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	)	\=possible nucleotide insertion)
6681	1169	511	INYIYYNQQQRAFHELK\EKLMSAPALGLPDLTKLFTLHVSERE
0001	2205	]	KMTVGVLTQTVGPWSRPGAYLSKQLDGVSKGWPPCPRALAATAL
			LAQEADELTLRONLNRKSPHA\VVTLINTEGHH*LINARLTRYQ
		}	TLLCENPHKTIEVSNT/LNPATLLLVTRSPVKHNCLEVLDSVYS
j .		ļ	SRPNLRDHP*TSVDWKLYVDGSGFANPCKVTLKKETSPAPVTPR
1		ł ·	s
6682	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
0002	100	1	VRRRIBLIQDFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
		ł	YOLSLKPERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG
ļ '		<b>\$</b>	FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN
			PLOTDAABNNVCDINSVHGLFATGTIEGRVECWDPRTRNRVGLL
		l	D\AP+TVSQQIQR+TSLPTISALKFN\GALTMAVGTTTGQVLLY
1		<b>\</b>	DLRSDKPLLVKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK
		l	NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL
i	ſ	í	GPAPRWCSFLDNLTBELEENPESNE
6683	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
		ł	VRRRIBLIQDFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
l .	İ		YQLSLKFERCLDSEVVTFEILSDDYSKTVFLHNDRYIBPHSQSG
}	1	<b>)</b>	FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN
!			PLQTDAAENNVCDINSVHGLFATGTIEGRVECWDPRTRNRVGLL
			D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTITGQVLLY
ł	1	Ì	DIRSDKPLLVKDHQYGLPIKSVHPQDSLDLILSADSRIVKMWNK
l	Į.	(	NSGKIFTSLBPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL
ĺ		[	GPAPRWCSFLDNLTERLERNPESNE
6684	111	527	GLRGGTSRGRAGREPRYAAGVLCVVAGYCQSPCPPGGRGREAPA
		Į.	PD\SGRRHA*RPA*WLGGPGGDSGGREEGGS/GELQRAMESKMG
	l		ELPLDINIQEPRWDQSTFLGRARHFFTVTDPRNLLLSGAQLEAS
]			RNIVQNYR
6685	258	1473	KLLGDNFEGFCNKFELSDSENGSNS*QSPL\FDRLFDPDPQKVL
			QGVIDMKNAVIGNNKQKANLIVLGAVPRLLYLLQQETSSTELKT
}	,		BCAVVLGSLAMGTENNVKSLLDCHIIPALLQGLLSPDLKFIRAC
	<b>,</b>	ţ	LRCLRTIFTSPVTPERLLYTDATVIPHLMALLSRSRYTQEYICQ
l			IFSHCCKGPDHQTILFNHGAVQNIAHLLTSLSYKVRMQALKCFS
Ì	}	1	VLAFENPQVSMTLVNVLVDGELLPQIFVKMLQRDKPIKMQLTSA
1	<b>!</b>	<b>!</b>	KCLTYMCRAGAIRTDDNCIVLKTLPCLVRMCSKBRLLEBRVEGA
1	ĺ	1	BTLAYLIEPDVBLQRIASITDHLIAMLADYFKYPSSVSAITDIK
1		1	RLDHDLKHAHELRQAAFKLYASLGANDEDIRKKVSLGEGRPPVL
-		000	TASRQGVTST DSVTFDDLAVDFTPKEWTLLDPTQRNLYROVMLENYKNLATVGY
6686	310	927	
	i	1	QLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV
	1	1	LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN
Į		1	SENTFECYLYGVDFLITLHKKTSTGEQRSVFSHVWKKPSSLNPDV
			VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT
6687	181	915	EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST
l	l	ĺ	IGETSNRSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRRHGSESR
i	ł	i	SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR
1	}	1	IRPROLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV
	l	ĺ	PLATGLTGORLLGVPIIVQASQABKNRLAAMANNLQKGNGGPMR
-	1855	<u> </u>	LYVGSLHFNTTEDMLRGIFEPFGKV
6688	1025	1	ABVPNYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF
i	[ ·	1	SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD
	1	1	LPSDGGTGFFSLAGDSSTRLSSLAFISFSLSSVSVGSSAGTTS
1		1	STSVGSVVAAPTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE
l .	l	[	VAVICGSKGAGASGSASCSSRAGKTTRATAASSMPSGTSSFSTC
i	Ĩ	I	TMSELEELFSLPSPAPLLSKLFTSSGSIAICCQDSGPSDTGRLS
]		E .	VCQLWLADSDTGKLSDCQEVVTVGDSGGLTCPELSLGRM*MSLL

Desinning   coation   corresponding   coation   corresponding   cofficient   coation   corresponding   cofficient   coation   corresponding   cofficient   coation   corresponding   cofficient   coation	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Solitation   Coxtesponding	ID	1	P	(A=Alanine, C=Cvateine D=Acnartic Acid R=
Cocation   Corresponding   Co first   Contresponding   Co	NO:		ſ	Glutamic Acid. F=Phenylalanine G-Glucine
L=Leucine, M=Methionine, N=Apgaingine, perfoline, Q=Glutamine, R=Arginine, amino acid residue of amino acid sequence   S=Serine, T=Threonine, V=Valine, N=Gerine, T=Threonine, V=Valine, N=Gerine, T=Threonine, V=Valine, N=Gerine, T=Threonine, V=Valine, N=Gerine, T=Threonine, V=Valine, N=Gerine, T=Threonine, V=Valine, N=Gerine, T=Threonine, V=Valine, N=Gerine, T=Threonine, V=Valine, N=Gerine, T=Threonine, V=Valine, N=Gerine, T=Threonine, V=Valine, N=Gerine, T=Threonine, V=Valine, N=Gerine, N=Gerine, V=Valine, N=Gerine, N=Gerine, V=Valine, N=Gerine, N=Gerine, V=Valine, N=Gerine, N=Gerine, N=Gerine, V=Valine, N=Gerine, N=	1			HaHistidine IaIsoleucine Kalveine
to first amino acid residue of amino acid residue of amino acid amino acid asequence of servine, Threnomine, V-Valine, amino acid asequence sequence of codon, /-possible nucleotide deletion)  6689 640 1299 SSNAYMFORSSNERSPERNYFYTHLECPTMISST  SSNAYMFORSSNERSPERNYFYTHLECPTMISST  SSNAYMFORSSNERSPERNYFYTHLECPTMISST  SSNAYMFORSSNERSPERNYFYTHLECPTMISST  SSNAYMFORSSNERSPERNYFYTHLECPTMISST  SSNAYMFORSSNERSPERNYFYTHLECPTMISST  SSNAYMFORSSNERSPERNYFYTHLECPTMISST  SSNAYMFORSSNERSPERNYFYTHLECPTMISST  SSNAYMFORSSNERSPERNYFYTHLECPTMISST  AMDSTRAICAGANAMFORSSNERSPERNYFYTHLECPTMISST  FFSDSISFCESSSPCKW*FYSSKYGONALLSSNLSNGPGGSSS  ORNSLITHDIOMSCALLSTCONFYLRERVSYSSENTHLELDIAGSSCONFYLRERVSYSSENTHLECPTMISST  GGSARREPGNISPHSQKCSALLSTCONFYLRERVSYSSENTHLECPTMISST  GGSARREPGNISPHSQKCSALLSTCONFYLRERVSYSSENTHLEDVAN  FFSDSISFCENTSPHSQKCSALLSTCONFYLRERVSYSSENTHLEDVAN  GGSARREPGNISPHSQKCSALLSTCONFYLRERVSYSSENTHLEDVAN  GGSARREPGNISPHSQKCSALLSTCONFYLRERVSYSSENTHLEDVAN  GGSARREPGNISPHSQKCSALLSTCONFYLRERVSYSSENTHLEDVAN  GEKLNNYFTHENDSFTSGNINAVGCGGAKRHIONGESTITLEDVAN  GEKLNNYFTHENDSFTSGNINAVGCGGAKRHIONGESTITLEDVAN  GEKLNNYFTHENDSFTSGNINAVGCGGAKRHIONGESTITLEDVAN  GEKLNNYFTHENDSFTSGNINAVGCGGAKRHIONGESTITLEDVAN  GEKLNNYFTHENDSFTSGNINAVGCGAKRHIONGESTITLEDVAN  GEKLNNYFTHENDSFTSGNINAVGCGAKRHIONGESTITLEDVAN  GEKLNNYFTHENDSFTSGNINAVGCGAKRHIONGESTITLEDVAN  GERLNNYFTHENDSFTSGNINAVGCGAKRHIONGESTITLEDVAN  GERLNNYFTHENDSFTSGNINAVGCGAKRHIONGESTITLENGEN  GERLNNYFTHENDSFTSGNINAVGCGAKRHIONGESTITLENGEN  GERLNNYFTHENDSFTSGNINAVGCGAKRHIONGESTITLENGEN  GERLNNYFTHENDSFTSGNINAVGCGAKRHIONGESTITLENGEN  GERLNNYFTHENDSFTSGNINAVGCGAKRHIONGESTITLENGEN  GERLNNYFTHENDSFTSGNINAVGCGAKRHIONGESTITLENGEN  GERLNNYFTHENDSFTSGNINAVGCGAKRHIONGESTITLENGEN  GERLNNYFTHENDSFTSGNINAVGCGAKRHIONGESTITLENGEN  GERLNNYFTHENDSFTSGNINAVGCGAKRHIONGESTITLENGEN  GERLNNYFTHENDSFTSGNINAVGCGAKRHIONGESTITLENGEN  GEGEBOGGRNILAGETINGCHANGENGENGENGENGEN  GEGEBOGGRNILAGETINGCHANGENGENGENGENGENGENGENGENGENGENGENGENGEN	1	corresponding		L≈Leucine M=Methionine N-Acnaragine
amino acid residue of amino acid sequence  6689  640  1299  SSASYIROYSSSSDBEINTVITVOLICEPTYTSST SSASYATARTSTEDTYARSICAL SERVELLES ABBORDAN ABBORDANIC SASYATARTSTEDTYARSICAL SERVELLES ABBORDANICAL SERVELLES				P=Proline. O=Glutamine P-Arrinine
Residue of amino acid sequence   Refuence			1	S=Serine, T=Threonine V=Valine
sequence seq	1	1		W=Tryptophan V=Turosine V=Unknown +-Chan
Sequence   \_\epossible muclectide insertion	1	amino acid		Codon. /=nossible nucleotide deletion
SSAVIPOYSSSDSRIMTYPTVILLCEPOTTSST	1		1 - 1	\mpossible nucleotide incertion)
SSABYATSATSISTIAPSGSLKKRIGHLGALDSSSTFICTS		<b>-</b>		SSAVI PGYSSSSDSPLATUDITYDI I COPOTECCT
ABBSTFRICSPBVSDTSSDSSGKUNVLILIPSKUSI 1-SCPGGSSS FPSDSISPCRP-SUSVOSABLISBUSDGFGGSSS FPSDSISPCRP-SUSVOSABLISBUSDGFGGSS ORNSLTARQLAWSI-*ATRX*-KUNACHPICLSSKKSAL-1-SLANGRI GGSARRQCHISPSWGCCASTCCOPPUT.REVESVSSENTH-IS- GGS90 1 442 GTRGKMATLGPLGSWQCWRRCLSARDGSRHLLILLLIGSGGG QOVENQTYETH.REBISLS.RYGGVSTCSSSLMMIMGNAMVY YURLTPIMOSKGGLALMRIVPCPLROWELQUER-HIGGGKKUL\ GGGLAINTYKDRMOP  1 287 1401 LETTESBEKARRYKDBPSQLANVYGGSKENLIGGKKUL\ GGGLAINTYKDRMOP  LEGGGLATINTYKDRMOP  DTWEENQLIGAAGKULVRDWHLENYSHLAVGYGASKEDALITUNGSS GYEIKNSVEPTORUGSFHAMRHINTAIRFPAGSSSLVWRRKP HENDAFSNLVHCSKGGFLIGONIDIFDLRGKSLKSNITTUNGSS GYEIKNSVEPTORUGSFHAMRHINTAIRFPAGSSSLVWRRKP HENDAFSNLVHCSKGGFLIGONIDIFDLRGKSLKSNITTUNGSS GYEIKNSVEPTORUGSFHAMRHINTAIRFPAGSSSLVWRRKP HENDAFSNLVHCSKGGFLIGONIDIFDLRGKSLKSNITTUNGSS GYEIKNSVEPTORUGSFHAMRHINTAIRFPAGSSLVWRRKP CSLCKARSPRKMUTTERQCHTSTGKYPECHECKAPLKSKRINT HOWTHTICKKYVICSECGKGFIOKOMLIVERGINTIKKREVILTSKGD LEPKIQUTRIKLIKHVUCSECGKGFIOKOMLIVERGINTIKKREVILTSKGD LEPKIQUTRIKLIKHVUCSECGKGFIOKOMLIVERGKRIKTUNG GKEHSGGFINKLARTLRGCHICHGEVYLAVSSLEWFRENSKSEW CSLEKAPGRKRAMT.TERGCHTSTGKYPECHECKAPLKKRINT HOWTHTICKKYVILTSCHAMPTORUTYARSIENFRENSKSEW CSLEKAPGRKRAKERKENLOHILLIGEVYLVARSIENFRENSKSEW DGLAMDARGKRINTALBETTERGKYVECKLYTISKERIPHLIDDLGGEL LAQAVOATRINTIKCFILNVCPAYTSHRI ISRAVERMAMGVEQOLL DESSISLIKUCKYYNINSPHDILIETTSGEVELSDFDLLWGTSH SCLUVFQPVLWPEYTFMILFFBAILQPOMNISVLQK ROBGHSGGFINKLARTLRGCLANGVECHTULDHILDDLGGEL LAQAVOATRINTIKCFILNVCPAYTSHRI ISRAVERMAMGVEQOLL DESSISLIKUCKYYNINSPHDILIETTSGEVELSDFDLLWGTSH SCLUVFQPVLWPEYTFMILFFBAILQPOMNISVLGK ROBGHSGGFINKLARTLRGCHAMPTORUTYARSIENFRENSKER CHELGGILDQDGITARRAGPFERGOPHILSPTLLWGTSH SCLUVFQPVLWPEYTFMILFFBAILQPOMNISVLGK RUHGLAGHTSPATART STANDARTHANGVERQUELCH LAQAVOATRINTIKCFILNVCPAYTSHRI ISRAVERMAMGVEQOLL DESSISLIKUCKYYNINSPHDILIPTIGGFPAAHHIGFAAA LAVOPSGCHTEP, POEVWPSLIFIGDAYARROKSLLQUIGTHIPV NAAAGKPQUTTGGGFTAABGPFRAGDFTGSFPAAHHIGFAAA LAVOPSGCHTEP, POEVWPSLIFIGDAYARROKSLLQUIGTHIPV NAAAGKPQUTTGGGTTAABGPFRAGDFTGGFTAAHTGFAAA LAVOPSGCHTEP, POEVWPSLIFIGDAYARROKSLLQUIGTHIPV NAAAGKPQUTTGGGTTAABGPFRAGATY ISR	6689	640	1299	SSASVATCATCICDTARCCCI VI VIICI I CAI DOCCOTTO COMO
PFEDS 19FCPSSSSFCRN* FVSSKVSGNALLSERIGEGGSSS GRRSLTARGLASSLASSLASTAL 1-SLANGE GGSASRREGRISPHSGNCSALSTACTNVI KPREVSVSSKNYPAL GGSASRREGRISPHSGNCSALSTACTNVI KPREVSVSSKNYPAL GGSASRREGRISPHSGNCSALSTACTNVI KPREVSVSSKNYPAL GGSASRREGRISPHSGNCSALSTACTNVI KPREVSVSSKNYPAL GGSASRREGRISPHSGNCSALSTACTNVI KPREVSVSSKNYPAL GGSASRREGRISPHSGNCSALSTACTNVI KPREVSVSSKNYPAL GGSASRREGRISPHSGNCSALSTACTNVI KPREVSVSSKNYPAL GOVGAGTYPSTILKREHSLSK PYGGVSTGSSSLIMLINGNAMMYNY YTRLTPDMGSRGGALMRRVPCPLROMBELQVHFKTHGGRKRILL GOVGAGTYPSTILKREHSK PYGGVSTGSSSLIMLINGNAMMYNY YTRLTPDMGSRGGALMRRVPCPLROMBELQVHFKTHGGRKRILL LEVETSSEKARRYKORDSGNAVFORGKKINLAGAGSSTLAVBRREGR LEVETSSEKARRYKORDSGNAVFORGKKINLAGAGSSTLAVBRREGR LEGGGLATTTEOGHSGACGDTWKVDHVLERIGGSESLAVBRREG HERDAFRINTVHCSKOPILLGOMPHI PELIGRSKSHLTILVNQS GFETKINSVEYTONGUS FVIANHURLHTATKFPASQKLISTKSQR GFETKINSVEYTONGUS FVIANHURLHTATKFPATATARFITARCLANGUS FVIANHURLHTATKFPATATARFITARCLANGUS FVIANHURLHTATKFPATATARFITARGHTATARFITARGHTATARFITARGHTATARFITARGHTATARFITARGHTATARFITARGHTATARHITARGHTATARGHTATARGHTATARHITARACLANGUS FVIANHURLHTATKFPATATARFITARGHTATARGHTATARGHTATARGHTATARGHTATARGHTA		""		
GRISTITARQIANSI-ATKIF HRACHRICLISEKESAI-ISLAIQRI GGSASRIKURI SPINSOKCSAI SYCKOPUL YERVISUSSEKINIGA GGSASRIKURI SPINSOKCSAI SYCKOPUL YERVISUSSEKINIGANIMMYK YIRLITPIMIGEKGALMIKUPCI ELRIMIKLUPUL KILLIGEGGGI OQVQAGQTYEYIKKEERISKEY YQGVUTGSSSIMAIMAMYK YIRLITPIMIGEKGALMIKUPCI ELRIMIKLUPUK KIHCHGGKKILI-I GGGLAI WYTKDIMOD  ELRITORISE OLA WYTKURI SAINAY YOR GKKIN QAQES ITLEDVAN DETWEBENQLIGAAQKOLYRUWULKINISAI QAGSAI SITLEDVAN DETWEBENQLIGAAQKOLYRUWULKINISAI QAGSAI SITLEDVAN DETWEBENQLIGAAQKOLYRUWULKINISAI QAGSAI SITLEDVAN LEGGGUMT TIEDGIH SACACDI WYDWULKINISAI GSESLAVRIKKIN LEGGGUMT TIEDGIH SACACDI WYDWULKINISAI GSESLAVRIKKINI LEGGGUMT TIEDGIH SACACDI WYDWULKINISAI GSESLAVRIKKINI LEGGGUMT TIEDGIH SACACDI WYDWULKINISAI GSESLAVRIKKINI LEGGGUMT TIEDGIH SACACDI WYDWULKINISAI GSESLAVRIKKINI LEGGGUMT TIEDGIH SACACDI WYDWULKINISAI GSESLAVRIKKINI LEGGGUMT TIEDGIH SACACDI WYDWULKINISAI GSESLAVRIKKINI LEGGGUMT TIEDGIH SACACDI WYDWULKINISAI GSESLAVRIKKINI LEGGGUMT TIEDGIH SACACDI WYDWULKINISAI GSESLAVRIKKINI LEGGGUMT TIEDGIH SACACDI WYDWULKINISAI CHARLITAI KURGHEKHI AN TIEDGIH TIED	ļ			PPSDSTSPCPCCCCPCVD+FUCCVUICONETICODICONADAGGG
GGSASRRÇANISPISQUESALSYCONFULREREUSUSSINYPAL  6690 1 442 GTGGMMATISPIGSGWORREGLSARICSKILLLILLILLISGUESGUE  OOVGASOTPSYLKRERSLERPYGGWOTGSSSLMAIMONAMWAYT YTRLTPPMORSKGALMREVELRIDWILLDILLISGUESGUE  GDGLAIWYTKDRNOP  18THESSEKARRYKORPSQLNAVFQGKRINJOAQBSSITLEDVAN DETWESBULLGAARGDLYRDWILERYSNIVAVGYQASKEPDALFY LEQGRQLMTIEDGHISGACGDJWKVDWLERISSNIVAVGYGASKEPDALFY LEQGRQLMTIEDGHISGACGDJWKVDWLERIGGSSLWARKRE HERDAFRIN LYNGKSKGFILLGOCHDIFTDIGKSHINITAVAGYGASKEPDALFY LEQGRQLMTIEDGHISGACGDJWKVDWLERIGGSSLVARRKER HERDAFRIN LYNGKSKGFILLGOCHDIFTDIGKSHINITAVAGYGASKEPDALFY LEQGRQLMTIEDGHISGACGDJWKVDWLERIGGSSLVARRKER HERDAFRIN LYNGKSKGFILLGOCHDIFTDIGKSHINITAVAGYGASKEPDALFY LEQGRQLMTIEDGHISGACGDJWKVDWLERIGGSSLVARRKER HERDAFRIN LYNGKSKGFILLGOCHDIFTOKKSHINITAVAGYGAKEPALFY GGERIAGRAFTH COSKORPH GOKAPHT COSKORPH	i	1		OPNSI TAPOLAMSI + ATTECHNA CHONGI COMBOAL AND CHORN
COUCHAGOT PETILIBRIES SERVICIONES SENDIFICATION	1		ļ	CCCVCDACALOPROUNCOVI ON CONTRACTABLISMOS PROUNCES
GOVGAGOTPSYLKRERSISSKY YGGVOTSSSISHIMIGNAMWMY YTRLTPDMQSKQGALWNRVPCPLRDWRLQVBFXTHOGGKRIL\ GOGLALWYTKDRWQP DFTWERQLGAAQKOLKPOMAPOSOKKMIQAQBSTTLEDVAL DETWERQLGAAQKOLKPOMAPOSOKKMIQAQBSTTLEDVAL DETWERQLGAAQKOLKPOMAPOSOKKMIQAQBSTTLEDVAL LBQGQLWTTEDGIHSGACSDIWKVDHVLBRIQAGBSTTLEDVAL LBQGQLWTTEDGIHSGACSDIWKVDHVLBRIQAGBSTLTEDVAL LBQGQLWTTEDGIHSGACSDIWKVDHVLBRIQAGSSILTLEVAG GTEIRNSVERTINGRESPHANNERLHATIKPPASQKLISTTSQD LSPRUQKTRILBKHRUCSGCKAFIKKSKLIDRUQWHTGEKPH CSLCEKAPSKKFWLTERGHERTTGEKEFY RECPECKAFIKKSEKIN HQKTHTGEKPYICSBCGRGFIQUGNLIVHQRIHTGEKPH CSLCEKAPSKKFWLTERGHERTTGEKEFY RECPECKAFIKKSEKIN HQKTHTGEKPYICSBCGRGFIQUGNLIVHQRIHTGEKPH CSCLGERGPSKFWLTERGHTTGEKEFY RECPECKAFIKKSEKIN HQKTHTGEKPYICSBCGRGFIQUGNLIVHQRIHTGEKPH CSCLGERGPSKFWLTERGHTTGEKEFY RECPECKAFIKKSEKIN HQKTHTGEKPH CSBCGRGFIQUGNLIVHQRIHTGEKPH CSCLGERGPSKFWLTERGHTTGEKFY RECPECKAFIKKSEKIN HQKTHTGEKPH CSBCGRGFIQUGNLIVHQRIHTGEKPH CSCLGERGPSKFWLTERGHTTGEKFY RECPECKAFIKKSEKIN HQKTHTGEKPH CSBCGRGFIQUENTITGE CSCLGERGPSKFWLTERGHTTGEKFY RECPECKAFIKKSEKIN HQKTHTGEKPH CSBCGRGFIQUENTITGE CSCLGERGPSKFWLTERGHTTGEKTY CSCLGERGPTTGEN FROM THE CSBCGLESHIJDLIQGT LAQAVQATKAYNKCILAVCPATTSRHEISNAVERHAGVEGGLL DPSDISSSLLDKCLTTRSPHPDILIFTSGEVELDFLIMGTSH SCLLWFQFVLMPEYTFWILIFRAILQFQMHSVLQK  GOGLAGAGKFRYNKTCHAVCPATTSRHEISNAVERMAMVEGGLL DPSDISSSLLDKCLTTRSPHPDILIFTSGEVELDFLIMGTSH SCLLWFQFVLMPEYTFWILIFRAILQFQMHSVLQK  GOGLAGAGKFRYNKTCHAVCPATTSRHEISNAVERMAMVEGGLL DPSDISSSLLDKCTTRSPHPDILIFTSGEVELDFLIMGTSH LAQAVQATKHNKCCHAVCPATTSRHEISNAVERMAMVEGGLI DPSDISSSLLDKCLTTRSPHPDILIFTSGRVELDFLIMGTSKX SCLLWFQFVLMPEYTFWILIFRAILQFQMHSVLQK  GOGLAGAGKFRYNKTHAVCPATTSRHEISNAVERMAMVEGGLI DPSDISSSLLDKCLTTRSPHPDILIFTSGRVELDFLIMGTSNA LAQAVGATKHTRKSCHFYGAGFPERQDPWGSPGISLPAHIGFAAA LAVGPSGCHTEP\PPDEWPSLFLIGGAYAARDKSKLIQGTTHV NAAGKRQUTCAKFYRGABFPERQDPWGSPGISLPAHIGFAAA LAVGPSGCHTEP\PPDEWPSLFLIGGAYAARDKSKLIQGTTHV NAAGKRQUTCAKFYRGATTSAUGTPTTGFTATATAFTTTSSGRVELGTASMI LAVGPSGCHTEP\PPDEWPSLFLIGGAYAARDKSKLIQGTTHV NAAGKRQUTCAKFYRGATTSAUGTPTTGFTATATAFTTSSGRVELGTASMI LAVGPSGCHTEP\PPDEWPSLFLIGGAYARRKALIKFTFHERDVTTALD LATATSTAGYATA	6690	1	442	CADCAMP ALI COL COMOCADO CADO CODA A LA CADA CADA CADA CADA CADA CADA CA
TIRLIPDMQSKQGALMNRVPCFILRDMKLQVHPKIHGQGKKNL\s    GGGLAIN WYKDRMQD    LKTETSEEKARRYKDRPSQLNAVFQEQKRMIQAQESITLEDVAN     DETWIEWGLLIGAAQKOLKTROMMENYSMLVAVGYQASKPDALFY     LEGGGLAIN WYTEOGHISGACSDI WKVPUKEJGSELVANRKRVC     HERDAFENI VHCSKSCFILLGONIDI FDLRGKSLKSSILTLIVAQSS     GYEIKNSVERTINGUSS PILANHRIKELHIN PRAPAQKLISTKOQE     GYEIKNSVERTINGUSS PILANHRIKELHIN URGRIHTGEKPH     CSLCEKAPSRKYMLTEHQRIHTGEKPY KECPECKARALKKSRILAN     KORTHICKEKRY ICSSCGREFIOKGMLIVAGRIHTGEKPH     CSLCEKAPSRKYMLTEHQRIHTGEKPY KECPECKARLKKSRILAN     KORTHICKEKRY ICSSCGREFIOKGMLIVAGRIHTGEKPH     CSLCEKAPSRKYMLTEHQRIHTGEKPY KECPECKARLKKSRILAN     KORTHICKEKRY ICSSCGREFIOKGMLIVAGRIHTGEKPH     CSLCEKAPSRKYMLTEHQRIHTGEKPY KECPECKARLKKSRILAN     KORTHICKEKRY ICSSCGREFIOKGMLIVAGRIHTGEKPH     CSLCEKAPSRKYMLTHANGRIHTGEKPY KECPECKARLKKSRILAN     KORTHICKEKRY ICSSCGREFIOKGMLIVAGRIHTGEKPH     CSLCEKAPSRKYMERKEKRICKHGVCITRVLGDIHLIPLIQUE     TAQAVQATKRYNKCILANVCRAYTSRHEI SHAVERMAMOVEGGLI     DESDISSSLILDKCLTYRIFIARILIZAGVAKAKCOVE     RQBGHSQGPHKLAETLRWCLILLEUTVYAFSIENFRKSKSK     COLMDLARQKFSRIMBEKKEKICKHGVCITRVLGDIHLIPLIQUE     DESDISSSLIDKCLTYRIFIARILIZAGVAHASVAKCOVE     RQBGHSQGPKKLAETLRWCLILLEUTVYAFSIENFRKSKSK     COLMDLARQKFSRIMBEKKEKICKHGVCITRVLGDIHLIPLIQUE     TAQAVQATKRYNKKELAVVCRAYTSRHEISNAVERMAWCXGGLI     DESDISSSLIDKCLTYRISPHPDILITRTSGEVYLGDIHLIPLIQUE     TAQAVQATKRYNKRELAVCRAYTSRHEISNAVERMAWCXGGLI     DESDISSSLIDKCLTYRISPHPDILITRTSGEVYLGDIHLIPLIQUE     TAQAVQATKRYNKMKLELAVCRAYTSRHEISNAVERMAWCXGGLI     DESDISSSLIDKCLTYRISPHPPILITRTSGEVYLGDIHLIPLIQUE     TAQAVQATKRYNKMKLELAVCRAYTSRHEISNAVERMAWCXGGLI     DESDISSSLIDKCLTYRISPHPPILITRTSGEVYLGTA     SCLLIHLAPPGATTPSQFLSSVSTETASSVRQAAESRQBELFVR     EVHSLGQILPQDGITARARMILEYVI GRADAFSKLIQGATHAV     RAAGKRQUVTGAKFYRAMSLEYVI GRADAFSKLIGGATHAV     RAAGKRQUVTGAKFYRAMSLEYVI GRADAFSKLIGGATHAV     RAAGKRQUVTGAKFYRAMSLEYVI GRADAFSKLIGGATHAV     RAAGKRQUVTGAKFYRAMSLEYVI GRADAFSKLIGGATHAV     RAAGKRQUVTGAKFYRAMSLEYVI GRADAFSTAYTI KIR     RPSTQSGRPGTMEQAITTPTTAYTARI TISSSGRVURGATSAN     TSPDGSPILAGALAILTRAGATHAV	5555		772	OOMCACOTERVI EDRUCI CERROCUCTUSCO EDI MONTE DE LA CONTRACTOR DE LA CONTRAC
GOGLAIWYTKORMOP	. 1			WILL TRUMCKOCK DEPOTE OF THE CONTROL OF THE CONTROL OF THE CONTROL OF T
A				
DPTWEEWQLLQAAQKDLYRDWOLKNYSNLVAVQYQASKPDALFY LEQGEQUMTIEDGHEGACSDUWKVDHVLERLQSESLVWRRKEY HERDAFERI VUCCKSCOFLLGOMDITICKSGLKSNLTLVWQSK GYEI KNSVEPTGNIOS FILIANNIERLHTA I KPPASQKLISTKSQS 1 SPKINGKTRKLEKHVCSECGKAP I KKSRLTDHQVMHTIGEKDF CSLCEKAPSRKFMLTERGRTHTGEKPYECPECGKAPLKKSRLANI HOKTHTIGEKPYI CSECGKAP I KKSRLTDHQVMHTIGEKDF CSLCEKAPSRKFMLTERGRTHTGEKPYECPECGKAPLKKSRLANI HOKTHTIGEKPYI CSECGKAP I KKSRLTDHQVMHTIGEKDF CSLCEKAPSRKFMLTHEGRTHTGEKPYECPECGKAPLKKSRLANI HOKTHTIGEKPYI CSECGKAP I KKSRLTDHQVMHTIGEKDF CSLCEKAPSRKFMLTHEGRTHTGEKPYECPECGKAPLKKSRLANI HOKTHTIGEKPYI CSECGKAP I KKSRLTDHQVMHTIGEKDFI CSEC CSCLCEKAPSRKFMITTEGKPYECPECGKAPLKKSRLANI HOKTHTIGEKPYI CSECGKAP I KKSRLTDHQVMHTIGEKPYI CNE CSCLCEKAPSRKFMITTEGKPYECPECKAPLKKSRLANI HOKTHTIGEKPYI CSECGKAP I KKSRLTDHGWHTHGEKPYI CNE CSCLGEKAPSRKFMATTIKAGPMPHTHA I MOORREYAAKCOVE ROGGHSQGFNKLABTILRWCINIG ILEUTYVAFSI ENNKERKSKLOVE LOLMDLARQKFSKIMBEKEKKLOKHGVCIRVILGDHLLDLOLOGEL LORDVAARNINKCFLINVCFAYTSRHISINGAVEKAMAVEKGGLL DPSDI SESLLDKCLYTNIS PHPDLIKTYVAFSI ENNFERSKSEV DGLMDLARQKFSKIMBEKEKLOKHGVCIRVILGDHLUPTORTSH SCLVFQPVLMPEYTFMITLFAGEVCIRVILGDHLUPTORTSH SCLVFQPVLMPEYTFMITLFAGEVCIRVILGDHLUPTORTSH SCLVFQPVLMPEYTFMITLFAGEVCIRVILGGTHAWAVEKGGLI DPSDI SESLLDKCLYTNIS PHPDLILI RTTSGEVRLSDFLLDVTSH SCLVFQPVLMPEYTFMITLFAGEVCIRVILGGTHAWAVEKGGLI DPSDI SESLLDKCLYTNIS PHPDLILI RTTSGEVRLSDFLLDVTSH EVHSLGGILLPQDGLTARAGPPEAQDPMGSPGISLPANHIGFANA LAVOPSCCHTEP AND THE STANKENDALSKOLLIGGTHAW NAAAGKPQVTTGAKFYRGMSLEYYG I EADDNPFPDLSVYFLP EVHSLGGILLPQCCLTARAGPPEAQDPMGSPGISLPANHIGFANA LAVOPSCCHTEP AFTENDARATASSVERQAAESRQHELIPVR EVHSLGGILLPQCCLTARAGPPEAQDPMGSPGISLPANHIGFANA LAVOPSCCHTEP AFTENDARATASSVERQAAESRQHELIPVR EVHSLGGILLPQCCCTARAGPPEAQDPMGSPGISLPANHIGFANA LAVOPSCCHTEP AFTENDARATASSVERQAAESRQHELIPVR EVHSLGGILLPQCCCTARAGPPEAQDPMGSPGISLPANHIGFANA LAVOPSCCHTEP AFTENDARATASSVERQAAESRQHELIPVR EVHSLGGILLPQCCCTARAGPPEAQDPMGSPGISLPANHIGFANA LAVOPSCCHTEP AFTENDARATASSVERQAAESRQHELIPVR EVHSLGGILLPQCCCTARAGPPEAQDPMGSPGISLPANHIGFANA LAVOPSCCHTEP AFTENDARATASSVERQAAESRQHELIPVR EVHSLGGILLPQCCCTARAGPPEAQDPMG	6601	202	7.407	
LENGERUMTIEUGHESGACSDUMKVDHVLERLOSSESLVINTERENG HERDAFERI VURCENSCPLLGOMBI FLORKSLKSHLYILIVANGES GYEI KNSVEPTONGDSPLLAGNHDI FLORKSLKSHLYILIVANGES GYEI KNSVEPTONGDSPLLAGNHDI FLORKSLKSHLYILIVANGES GYEI KNSVEPTONGDSPLLAGNHDI FLORKSLKSHLYILIVANGES GYEI KNSVEPTONGDSPLLAGNHDI FLORKSLKSHLYILIVANGE CSLCEKARPSKEPHLITERGETHTGEKPEGCEGKAFIKKSELNI ESPHQKTTELLARIGHUCSSCCKAFIKKSHLATIKOGNETHTGEKPYICNEG CSLCEKARPSKEPHLITERGETHTGEKPEGCEGKAFIKKSELNI HOKKTHTGEKPYICSECGKOFIQKOMLIVHORIHTGEKPYICNEG (*KGEJIGORTHLAGHAFIKOCHALIGILEVTVYARSI ENFKREKSKEK ROGEGISOGFNKLAETLERWCLAHIGILEVTVYARSI ENFKREKSKEK DOLMMLARQKYSEIMBEKEKLQHEVCLRVLODLHLLJDLOGEI IAQAVQATKNINKCFLINVCFAYTSRHEISSAVERMAWCVRGGLL DPSDISSELLDKCLTYNRSPHPDILETSGEVELSDFLLWGTSH SCLVFQPVUMPEYTFWNLFFEAILQFQMNHSVLQK ROGEGISOGFNKLAETLERWCLAHIGILEVTVYARSI ENFKREKSEV DGLMDLARQKYSEIMBEKEKLQKIGVCLRVLAGDHLLPUTGSEL LAQAVQATKNINKCFLINVCFAYTSRHSI SNAVREMAWSVRGGLL DPSDISSELLDKCLTYNRSPHPDILETTSGEVELSDFLLWGTSH SCLVFQPVUMPEYTFWNLFFEAILQFGOMNISVLQK ROGEGISOGFNKLAETLERWCLAHIGTUTGATSHEISNAVREMAWSVRGGLL DPSDISSELLDKCLTYNRSPHPDILITTSGEVELSDFLLWGTSH SCLVFQPVUMPEYTFWNLFFEAILQFGOMNISVLQK SCLVFQPVUMPEYTFWNLFFEAILQFGOMNISVLQK SCLVFQPVUMPEYTFWNLFFEAILQFGOMNISVLQK SCLVFQPVUMPEYTFWNLFFEAILQFGOMNISVLQK SCLVFQPVUMPEYTFWNLFFEAILQFGOMNISVLQK SCLVFQPVUMPEYTFWNLFFEAILQFGOMNISVLQK SCLUFGCFCHTEP, PDEVEPSLISVSTITTASSVERGABESRQHELIPVR RVHSLGGILPQDGLTARAGPPERAGDPSGFGISLPAAHIGFAAA LAVOPSCCHTEP VFDEVEPSLFLGDAYARARDKSKLLQLGTTHVV NAAGKPQVDTGAKFYRGMSLEYYGI RADDNFPFDLSVYFLP WHAAGKPQVDTGAKFYRGMSLEYYGI RADDNFPFDLSVYFLP CHAMBAGARPQVDTGAKFYRGMSLEYYGI RADDNFPFDLSVYFLP DENNIAGVQVPROTISLKLKGTNOTGGSGGISLPAAHIGFAAA LAVOPSCCHTEP VFDEVEPSLFLGDAYARARDKSKLLQLGTTHVV NAAGKRQVDTGAKFYRGMSLEYYGI RADDNFPFDLSVYFLP DENNIAGVQPROTISLKLKGTNOTGGSGGSGISLPAAHIGFAAA LAVOPSCCHTEP VFDEVEPSLFLGDAYARRDKSKLLQLGTTHV NAAGKPQVDTGAKFYRGMSLEYYGI RADDNFPFDLSVYFLP DENNIAGVQPROTISLKLKGTNOTGGSGGGISLPAAHIGFAAA LAVOPSCCHTEP VFDEVEPSLFQDAYARRUSKERICIGLGSGAFTATHAG DENNIAGVQPROTISLKLKGTNOTGGSGAVPYTGGNGESTAFMI TSPDGPFINLSRLINLTKYSQKPKLAKALLERI HHERDIVKTAL TSPDGPFINLSRLINLTKY	0091	201	1401	DETECTSES KARRYKDRPSQLNAV PQEQKKMIQAQBSITLEDVAV
HERDAFENI VICSKSOFILLGORIDI FDLEGKSLKSNITIVNOSS GYBI INSVEPTINGSS FLANHRICHTAI KFPASCKLISTKSOE IS PKIQKTRKLEKHEVCSECGKAFI KKSWLTDHQMAITGEKPHE CSLCEKAPSRKFMITERQRTHTGEKPY ECPGGKAPLKKSRIMI HOKTITIGEKPY IC GEGCKGFI (ORGINLI VRQRI HTGEKPY IC NE HOKTITIGEKPY IC GEGCKGFI (ORGINLI VRQRI HTGEKPY IC NE /GREFI (ORTCLI LANIQRIPHTER  178 939 WIKEGELSLWERFCANT I KRAGPMPKHIAFIMDENREYAKKOVE DOLMDLARQKPSRIMBEKERLQKHGVCI INVIGOLHILIP LOLQKII I TQAVQATKNINKCHLAVCHAVTSRIRI SINAVERMAWOVSOGILL DESDI SESLLI DKCLYTIRS PHIPDI LI LETSGEVRILS DEPLIMOTSH SCLVPQPVLWPEYTFWINLFEATLQPQMHISVLQK RQEGHSQGFINKLASTILRUCLINI.GI ILEVTVYAPS I ENPKRESKSEV OLIMDLARQKPSRIMBEKERLQKHGVCI TRVINGDIHLLIP LOLQKII DESDI SESLLIDKCLYTIRS PHIPDI LI LETSGEVRILS DEPLIMOTSH RQEGHSQGFINKLASTILRUCLINI.GI ILEVTVYAPS I ENPKRESKSEV OLIMDLARQKPSRIMBEKERLQKHQVCI TRVINGDIHLLIP LOLQKI RQEGHSQGFINKLASTILRUCLINI.GI ILEVTVYAPS I ENPKRESKSEV OLIMDLARQKPSRIMBEKERLQKHQVCI TRVINGDIHLLIP LOLQKI RQEGHSQGFINKLASTILRUCLINI.GI ILEVTVYAPS I ENPKRESKSEV OLIMDLARQKPSRIMBEKERLQKHQVCI TRVINGSHEN TRVINGSTERMAMOVEQGIL DESDI SESLLIDKCLYTINS PHIPDI LI LETSGEVELS DEPLILAQTSH SCLUWPQDVLWPEYTFWINLFEATLQKHINSVLQK BEVESLGQI LPQDGLTARAGPPBAQDPHGSPGISLPANHIGFAAA LAVGPSGCHTEP J PODEWPS LI LIGADAYARROKSILL [GLGTTHVV NAAAGKPQVUTGARFYRGMSLEYYGI RADDRIPPTDLSVYYLP EVHSLGQI LPQDGLTARAGPPBAQDPHGSPGISLPANHIGFAAA LAVGPSGCHTEP J PODEWPS LI LIGADAYARROKSILL [GLGTTHVV NAAAGKPQVUTGARFYRGMSLEYYGI RADDRIPPTDLSVYYLP SAAGKPQVERRAFISUPAAMASSEMEPLILLAMSYPRREKEFQLCAD LAVGPSGCHTEP J PODEWPS LI LIGADAYARROKSILL [GLGTTHVV NAAAGKPQVOTGARFYRGMSLEYYGI RADDRIPPTDLSVYYLP RADGRAFYRGMSLEYICHADDRIPPTDLSVYTLP REPSTQSGRPGTMRQAITTRTAYTARP I TESSGRFVULGTASMIL SPOCIES PROFINIS, TRVINKYSOK KALALIEVI PHIHERDVKTALD LAALSTEHSQYKOMWWK/DQ I EKCYYRVGMYRBAEKQI KISS PPLETIRRINSRALRGES FEKNERGBGVBAEKKI I SLLGKLRNIS LQTDKPPI PLURREVUTDUNQYLEYQOSILINESDGKSRMYSP WLLV LECYMYRRI HEAR I \ 1 LQSP PLUFYDFREKSKECONFYGSQES I LALCTHLQQL LRTITEDLD \ NRQLKDEFFKLLQLI SINGEI SVOL SLLGGESSSQNTNVINSLEDLKPPI LLINDMEILWSLLENCK 6699 325 492 EGELP PARRVLIPRAMTASAQPEGR	1	1		LEGGEOLEMATERICATION CONTINUES CONTI
GYBIRNSVEPTGNEDSKIHANHERLHTAIKPASCKILISTKSOM LSPKHOKTRKLEKHHVCSECCKAPIKKSWLITDEVMITGEKPHE CSLCERAPSRKPMLTEBORTHTTSEKPYECPECGKAPIKKSRILISH HOKTHTIGERPYICSECKOFIOKGNLIVHORIHTGEKPYECNE (/KGFIOKTCLIANIORPHTER ROEGHSOGFINLASTLEWCLINIGLIEVTVYAPSIENEKRSKSKW DGLØMIJAROKPSKIMBEKEKILOKHGILEVTVYAPSIENEKRSKSKW DGLØMIJAROKPSKIMBEKEKILOKHGILEVTVYAPSIENEKRSKSKW LAQAVQAYKNYNKCPLAWCPAYTSRHEISHAVREMAMGVEGGLI LAQAVQAYKNYNKCPLAWCPAYTSRHEISHAVREMAMGVEGGLI DPSDISESLLDKCI,YTNRSPHPDILLTSTGEVRISHDFLIMOTSH SCLUVEQVULWBEYTFWILFBAILQFOMNISVLQK ROEGHSOGFINLASTLEWCLINIGLIEVTVAPSIENFKRSKSKW ROEGHSOGFINLASTLEWCLINIGLIEVTVAPSIENFKRSKSKW ROEGHSOGFINLASTLEWCLINIGLIEVTVAPSIENFKRSKSKW ROEGHSOGFINLASTLEWCLINIGLIEVTVAPSIENFKRSKSKW ROEGHSOGFINLASTLEWCLINIGLIEVTVAPSIENFKRSKSKW ROEGHSOGFINLASTLEWCLINIGLIEVTVAPSIENFKRSKSKW ROEGHSOGFINLASTLEWCLINIGLIEVTVAPSIENFKRSKSKW ROEGHSOGFINLASTLEWCLINIGLIEVTVAPSIENFKRSKSKW ROEGHSOGFINLASTLEWCLINIGLIEVTVAPSIENFKRSKSKW ROEGHSOGFINTARGPERATIEWCLINIGLIEVTVAPSIENFKRSKSKW ROEGHSOGFINTARGPERATIEWCLINIGLIEVTVAPSIENFKRSKSKW ROEGHSOGFINTARGPERATIEWCLINIGLIEVTVAPSIENFKRSKSKW ROEGHSOGFINTARGPERATIEWCLINIGLIEVTVAPSIENFKRSKSCW ROEGHSOGFINTARGPERATIEWCLINIGLIEVTVAPSIENFKRSKSCW ROEGHSOGFINTARGPERATIEWCLINIGLIEVTVAPSIENFKRSKSCW ROEGHSOGFINTARGIEWERKERTURGLETVARGKERSKER ROEGHSOFFINISTARTERCINICALIELEPTORGKRRSKSKW ROEGHSOGFINTARGERIANIELEPTORGENSTARTIEKTSCOFFINISTORGKRS ROEGHSOGFINTARGERTURGLETVARGERSCHELDPTARKSCW ROEGHSOGFINISTORGHSTARKSCW ROEGHSOGFI	1 1			DEGE QUATTED GTHS GACSDIWK V DHV LERLQSESLVNRRKPC
ISPKHQKTRKLEKHENCESCCKAFIKKSRLITHGQWHTIGEKPHE   CSLCEAPSRYRMITEBIORTHTEKPYPICPECGRAPIKKSRLNI   HQKTHTGEKPYICSECGKGFIQKGNILIVEQRIHTGEKPYICNEC   // OKGFIQKTCLIANIQRPHTER   A	1			
CSLCRKAPSRKMLITHIGKTHIGKERYECGKAPILKKSRILAN	i l			GIBIANSVEFTGNGDSFEHANHKKEHTAIKFPASQKLISTKSQF
HORTHTGERPYICSEGGRSFIQKGMLIVHQRIHTGERPYICNEG //GRSPIQKTCLIAHQRPHTER  339 WILKEGELSLÜKERFCANIIKAGPMPKHTAFIMDGNRRYAKKCOVE ROEGISOGENKLAFTLRWCINIG LLEVTVYAFSLENKRRSKU DGLMDLARQKFSRLMEKKEKLQKHGVCIRVIGDLHLLPLDLQKI IAQAVQATKNYNKCFLNVCFAYTSRHEISBAVREMANGVSQGLL DPSDISESLLDKCLYTINSPHPDILIBTSGEVRISDPLWGTSH SCLVKPQFVLWBPSTPWINLFBAILQFQMMBSVLQK ROEGISQGPIKLAFTLRWCINIGILBTVTVAFSLENKRKSKU ROEGISQGPIKLAFTLRWCINIGILBTVTVAFSLENKRKSKSV DGLMDLARQKFSRIMBERKELGKHGVCIRVIGDLHLLPLDLQKL IAQAVQATRNYNKCFLNVCFAYTSRHEISBAVREMANGVSQGLL DPSDISESLLDKCLYTINSPHPDILIBTSGEVRISDPLWGTSH SCLVPQPVLWBPSTYBMLFBAILQFQMNHSVLQK BYHDIGGILPQDGITARAGPPBAILQFQMNHSVLQK EVHSIGGILPQDGITARAGPPBAILQFQMNHSVLQK BYHDIGGILPQDGITARAGPPBAQDPMGSPGISLPAHIGFAAA LAVGPSGCHTEP/PDEWBSLPLGDAYAARDKSKLLQLGITHVV NAAAGKPQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYYLP BYHDIGGILPQDGITARAGPPAQDPGSSGISLPAAHIGFAAA LAVGPSGCHTEP/PDEWBSLPLGDAYAARDKSKLLQLGITHVV NAAAGKPQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYYLP BYHSIGGILPQDGITARAGPADPMGSGGISLPAAHIGFAAA LAVGPSGCHTEP/PDEWBSLPLGDAYAARDKSKLLQLGITHVV NAAAGKPQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYYLP C6695 292 613 SILLMIAPPGAYTPSQDLSVSTSTASSVERQAAESRQHELPVR RYHSIGGILPQDGITARAGPADPMGSSGISLPAAHIGPAAA LAVGPSGCHTEP/PDEWBSLPLJLAMSYFRRKGPLCAD LAVGPSGCHTEP/PDEWBSLPLJLAMSYFRRKGPLCAD LAVGPSGCHTEP/PDEWBSLPLJLAMSYFRRKGPLCAD LAVGPSGCHTEP/SDEWBSLPLJLAMSYFRRKGPLCAD LAVGPSGCHTEP/SDEWBSLPLJLAMSYFRRKGPLCAD LAVGPSGCHTEP/SDEWBSLPLJLAMSYFRRKGPLCAD LAVGPSGCHTEP/SDEWBSLPLJLAMSYFRRKGPLCAD LAVGPSGCHTEP/SDEWBSLPLJLAMSYFRRKGPLCAD LAVGPSGCHTEP/SDEWBSLPLJLAMSYFRRKGPLCAD LAVGPSGCHTEP/SDEWBSLPLJLAMSYFRRKGPLCAD LAVGPSGCHTEP/SDEWBSLPSGVAPTROMGSBARGNERIFGTSML TSPDGPPINLSRLNLTKYSQKPKLAKALIKYIFHHENDVKTALD LAALSTEHSQKNWMMK/DQIEKCYYRVGMRBAKQIKSS TSPDGPPINLSRLNLTKYSQKPKLAKALIKYIFHHENDVKTALD LAALSTEHSQXKNWMMK/DQIEKCYYRVGMRBAKQIKSS LAALSTEHSQXKNWMMK/DQIEKCYSVARGMSRAKGRSKMYTSP LLVLCCHMRRTHEAT/1GDPADYAFASGQOSSAVTTIKDR LQTDKPFIPLVERKVDTUJMNQVLKYQQSGSAYTTIKDR LQTDKPFIPLVERKVDTUJMNQVLKYQGSGSANFTSGKSEGNFYGGSB ILALCTHLQQLIRTIEDLD\REFILLDLKPFILLINMEHMSLLSNCK SLAGGESSSQNTNVLNSLEDLKPFILLINMEHMSLLSNCK SLAGGSSSSQNTNVLNSLEDL				COLORA HORNING WINDS THE COLORA HORNING WAS A STREET OF THE COLORA HORNING WINDS THE COLORA HORNING WAS A STREET OF THE C
				CSLCERAFSREFILTRHORTHTGERPYECPECGRAFLKKSRLNI
178   939   WIKEGELSIMERFCANTIKAGPHEKHAFIMDGNRRYAKKQUE   RQEGHSQFNKLABTLWCLINLEVTYAFSIEMFKRSKSKE   DCIMDLARQKFSRLMEKEKIQKHGVCIRVICGIHLIPJIDJQKI   IAQAVQATKNYNKCFLNVCFAYTSRHEISRAVREMAWGVEQGIL   IAQAVQATKNYNKCFLNVCFAYTSRHEISRAVREMAWGVEQGIL   IAQAVQATKNYNKCFLNVCFAYTSRHEISRAVREMAWGVEQGIL   DPSDISESILDKCLYTNRSPHPDILIERTSGEVRLSDFILWQTISH   SCLUVRQPVUMPEYTFWALFEATLQFOMNISVLQK   RQEGHSQGPNKLAFTLWCLINLGILEVTYYAFSIEMFKRSKSEV   DCIMDLARQKFSRLMEEKEKLQKHGYCIRVIGDIHLIPJDLQKI   IAQAVQATKNYNKCFLNVCFAYTSRHEISRAVREMAMGVEQGIL   IAQAVQATKNYNKCFLNVCFAYTSRHEISRAVREMAMGVEQGIL   DPSDISESILDKCLYTNRSPHPDILIERTSGEVRLSDFILWQTSH   SCLUVRQPVUMPEYTFWALFAGSVERQAAESRQHELPVR   EVHSLQQILAPGGATFSQFLSSVSTETAASSVERQAAESRQHELPVR   EVHSLQQILAPGGATFSQFLSSVSTETAASSVERQAAESRQHELPVR   EVHSLQQILAPGGATFSQFLSSVSTETAASSVERQAAESRQHELPVR   REVHSLQQILAPQGCLTARAGPPEAQDPWSPGISLPAAHIGFAAA   LAVGPSGCHTEP \PDSVWPSLFIGDAYAARDKSKLIQLGITHVV   NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFPDLSVYFLP   EVHSLQQILAPQGCLTARAGPPEAQDPWSPGISLPAAHIGFAAA   LAVGPSGCHTEP \PDSVWPSLFIGDAYAARDKSKLIQLGITHVV   NAAAGKPQVDTGAKFYRGMSLEYYGIEADDNPFPDLSVYFLP   EVHSLGQILAPQGAAFARGKSERQHELPVR   EVHSLGQILAPQGAAFARGKSERQHELPVR   EVHSLGQILAPQGAAFARGKSERQHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGSERGHELPVR   EVHSLGQILAPQGAAFARGAAFARGSERGAAFARGA	1			VOICETORMOLITATION   VOICETO
RQEGISQGPNKLABTIRWCINI.GILEVITVYAFSIENFKRSKSKU DGIMDLARQKFSRLMBEKEKLQKHGVCIRVLGDLHLLPJDLQEL IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEGGLL DRSDISESLLDKCLYTINSPHPDILETSGEVRLSDFLLWGTSH SCLVFQPVLWPEYTFWILFATLQFQMNHSVLQK RQEGISQGPNKLABTLRWCINI.GILEVITVYAFSIENFKRSKSEV RQEGISQGPNKLABTLRWCINI.GILEVITVYAFSIENFKRSKSEV DGIMDLARQKFSRLMBEKEKLQKHGVCIRVLGDLHLLPJDLQEL LAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVVEGGL DPSDISESLLDKCLYTINSPHPDILITTSGEVRLSDFLLWGTSH SCLVFQPVLWPEYTFWNLFFATLQFQMNHSVLQK BUHSLAQLILPQDGLTARAGPPERADPWSSPGISLPAHTGFAAA LAVGPSGCHTEP\FDEVWPSLFIGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGARFYRGMSLEYYGIRADDNPFPDLSVYFLP EVHSLGQILPQDGLTARAGPPERADDAYBDRSKLIQLGITHVV NAAAGKFQVDTGARFYRGMSLEYYGIRADDNPFPDLSVYFLP EVHSLGQILPQDGLTARAGPPERADDAYBDRSKLIQLGITHVV NAAAGKFQVDTGARFYRGMSLEYYGIRADDNPFPDLSVYFLP EVHSLGQILPQDGLTARAGPPERADDAYBPERASKLIQLGITHVV NAAAGKFQVDTGARFYRGMSLEYYGIRADDNPFPDLSVYFLP EVHSLGQILPQDGLTARAGPPERADDNPFPDLSVYFLP EVHSLGQILPQDGLTARAGPPERADDNPFPDLSVYFLP BVSCGCHTEP\FDEVWPSLFLIGADAYARDKSKLIQLGITHVV NAAAGKFQVDTGARFYRGMSLEYYGIRADDNPFPDLSVYFLP AAAAGKFQVDTGARFYRGMSLEYYGIRADDNPFPDLSVYFLP FVRGRVGGRWAFLSVPAAMSSEMEPLLLAWSYFRRKFQLCAD LAGAGSGCHTEP\FDEVWPSLFLIGATYARRAFTTSSSGRFVRLGTASML DBNATAQVPRPGTSLKLPDTNOTGGPSQAVRPITQBGRPITGFL RPSTQSGRPGTMEQAIRTPRTTAYTARPITSSSGRFVRLGTASML TSPDGPPTINLSRALRFGSKRVMAVVPASISGQDVGSFAYITTIKDR TSPDGPPTINLSRALRFGSKRVMAVVPASISGQDVGSFAYITTIKDR TSPDGPPTINLSRALRFGSKRVMAVVPASISGQDVGSFAYITTIKDR LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRBAEKQIKSS LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRBAEKQIKSS LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRBAEKQIKSS LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRBAEKQIKSS LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRBAEKQIKSS LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRBAEKQIKSS LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRBAEKQIKSS LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRBAEKGIKSGCAFF ULLV\ECYMYRRIBEAT\LQSFPILLDDLFDUFKSKEQNFYGSQES IIALCTHLQQLIRTIEDLD\ENQLKDEPFKLLQISLWGEISVDL SL\SGGSSSGNTWVINSLEDLKPPILLINDMEHLWSLLSNCK 6698 6698 668 754 VGSCCAGASGSCKKEKCKCTSKERGECAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	6692	128	020	WINDOW OF MEDICANTINA COMPANY AND AND AND AND AND AND AND AND AND AND
DGIMDLARQKYSRIMBEREKIQKHGVCIRVLGDIHLLDIJQKI IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAGWGGLI DPSDISESLLDKCLYTTRSPHPDILLRTGGWRLSDFLLWGTSH SCLVFQPVLWPEYTFWNLFBAILQFQMNHSVLQK  8093 MIKEGELSLMERFCANTIKAGPMRKHAFIMGGNRRYAKKCQVE RQBGHSQGRMKLABTIKARCINLGILBVTVYAFSIENFKRSKSEV DGIMDLARQKYSRIMEBKEKLQKHGVCIRVLGDIHLLPJDLQGLI IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFILWGTSH SCLVFQPVLWPEYTFWNLFFRAILQFQMSHSVLQK SCLVFQPVLWPEYTFWNLFFRAILQFQMSHSVLQK SCLVFQPVLWPEYTFWNLFFRAILQFGMSHSVLQK EVHSLGQILPQDGLTARAGFPERAQDPMSGPGISLPAAHIGFAAA LAVGFSGCHTEP \PDEWBPSLFLGDAYAARDKSKLLQGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYFLP EVHSLGQILPQDGLTARAGPPEAQDPWSGPGISLPAAHIGFAAA LAVGFSGCHTEP \PDEWBPSLFLGDAYAARDKSKLLQGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYFLP EVHSLGQILPQDGLTARAGPPEAQDPWSGPGISLPAAHIGFAAA LAVGFSGCHTEP \PDEWBPSLFLGDAYAARDKSKLLQGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYFLP EVHSLGQILPQDGLTARAGPPEAQDPWSGPGISLPAAHIGFAAA LAVGFSGCHTEP \PDEWBPSLFLGDAYAARDKSKLLQGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYFLP EVHSLGQILPQDGLTARAGPPEAQDPWSGPGISLPAAHIGFAAA LAVGFSGCHTEP \PDEWBPSLFLGDAYAARDKSKLLQGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYFLP EVHSLGQILPQDGLTARAGPPEAQDPWSGFGISLPAAHIGFAAA LAVGFSGCHTEP \PDEWBPSLFTGDAYAARDKSKLLQGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYFLP BEVRGRVGERWAFFLSVPAAMSSEPEPLLLAMSYFRRRRGCOLGA LACTGMLESSPYDOAAMILARALIEMYJIDEDUDGGIAEMML DENNAIAQVPRPGTSLKLPGTNOTGGPSQAVRPITQAGRPITGFL RPSTQSGRRGTMRQAIRTPRTAYTARPITSSSGFVRLGTASML TSPDGPPINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD LAALSTEHSQYKDMWWK\QDIEKCYYNVGMYRBABKQIKSS LAALSTEHSQYKDMWWK\QDIEKCYYNVGMYRBABKQIKSS LAALSTEHSQYKDMWWK\QDIEKCYNVGSGESSGFVGUVTSCKKNBFCV ULV\BCYMYRRIBEAI\TQSPPLDYPUVKRESKEQNFYGSGES LAALSTEHSQYCDUVTDUNQULKYQQSLLNBSDGKSRWFYSP WLLV\BCYMYRRIBEAI\TQSPPLDYPUVKRESKEQNFYGSGES IIALCTHLQQLIRTITEDLD\ENQFYLQQSLLNBSDGKSRWFYSP ULLV\BCCMYRRIBEAI\TQSPPLDYPUVKRESKEQNFYGSGES IIALCTHLQQLIRTITEDLD\ENGFYLDLDNDHEHWSLLSNCK 6698 668 754 VGSCACASSCKCECKCTSCKKSGCRAFP	0052	170	233	MIABGELSLWERFCANTIKAGPMPKHIAFIMDGNRRYAKKCQVE
IAQAVQATKNYINKCFLAVCFAYTSHE ISNAVREMAMGURGGIL DPSDISESILDKCLYTNRS PHPDILIRTSGEVRLSDFILWQTSH SCLUFQPULWPETTFMANLFRATLQPQMNHSULQK RQEGHSQGPNKLASTILRWCLNIGILEVTVYAFSIENFRESKSEV RQEGHSQGPNKLASTILRWCLNIGILEVTVYAFSIENFRESKSEV DGIAMDLARQKFSRIMBEKLQKHGVCTRUIGDHILDHDLQGEL IAQAVQATKNYINKCFLNVCFAYTSRHEISNAVREMAMGURQGIL DPSDISESILDKCLYTNRSPHPDILIRTSGEVRLSDFILWQTSH SCLUFQPVLWMPETTFMALLGFQMNHSULQK G694 292 813 SLLLHLAPFGAYTFSQPLSSVSTETASSVRQAAESRQHELPVR EVHSLGQILPQDGITARAGPPEAQDPMGSPGISLPAAHIGFAAA LAVGPSGCTTEP\FDEWPBSLFILGDAYAARDKSKLIQUGITHVV NAAACKFQVDTGAKFYRGMSLEYYGIRADDMFFPDLSVYFLP EVHSLGQILPQDGITARAGPPEAQDPMGSPGISLPAAHIGFAAA LAVGPSGCTHTEP\FDEWPBSLFILGDAYAARDKSKLIQUGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDMFFPDLSVYFLP EVHSLGQILPQDGITARAGPPEAQDPMGSPGISLPAAHIGFAAA LAVGPSGCTHTEP\FDEWPSLFILGAVAARDKSKLIQUGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDMFFPDLSVYFLP EVHSLGQILPQDGITARAGPPEAQDPMGSPGISLPAAHIGFAAA LAVGPSGCTHTEP\FDEWPSLFILGAVAARDKSKLIQUGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDMFFPDLSVYFLP EVHSLGQILPQDGATARAGPPEAQDPMGSPGISLPAAHIGFAAA LAVGPSGCTHTEP\FDEWPSLFILGAVAARDKSKLIQUGITHVV NAAAGKPQVDTGAKFYRGMSLEYYGIRADDMFFFDLSVYFLP BFVRGRVGERWAFISVPAAMSSEMEPLILAMSFFRRKFGJCACD LCTQMLEKSPYDQAAMILKARALIFENYJTBIDVDQEGIAEMML DENNAIAQVERPGTSLKLPGTNOTGGSSQAVRPITQAGRPITGFL RPSTQSGRRGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML TSPDGPFINLSRLNLTKYSQKPKLAKALIEKYJPHHENDVKTALD LAALSTEHSQYKDWWMK/QDIEKCYYRVGMYRRABKQUKSS FYSTQSGRSGNYNDHTNSRLEDLRWFYRGMSGRSWFYSP ULLV\ECTMYRRIHEAI\QSPIDTPVFKESKEQNFYGSQES ILALCTHLQQLIRTIRDLD\ENQYLKYQQSILNESDGKSRWFYSP WLLV\ECTMYRRIHEAI\QSPIDTPVFKESKEQNFYGSGES ILALCTHLQQLIRTIRDLD\ENQYLKYQQSILNESDGKSRWFYSP BLLV\ECTMYRRIHEAI\QSPIDTPVFKESKEQNFYGSGES ILALCTHLQQLIRTIRDLD\ENQYLKYQGSFILGISLWGEISVDL SI\SGGSSSQNTNVINSLEDLKPFILLINDMEHWSLLSNCK 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	1 1			NOT AND ADOLESS PRESENT CONTRACTOR SELECTION OF THE PROPERTY O
DPSDISESLLDKCLYTNRSPHPDILIETSGEVRLSDFILMQTSH SCLVFQPVLWPEYTFWILFEATLQPQMNHSVLQK RCLFQPVLWPEYTFWILFEATLQPQMNHSVLQK RQEGHSQGFNKLAFTLRWCLNLGILEVTVYAFSIENFKRSKEVL DGLMDLARQKFSRIMEBKEKLQKHGVCIRVIGDLHILLPLDLQEL IAQAVQATRNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL IAQAVQATRNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL IAQAVQATRNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL DPSDISESLLDKCLYTNSPHPDILIETSGEVRLSDFILMQTSH SCLVFQPVLMPEYTFWNLFRATLQFQMNHSVLQK SCLVFQPVLMPEYTFWNLFRATLQFQMNHSVLQK SCLVFQPVLMPEYTFWNLFRATLQFQMNHSVLQK BYSILGILPQGGLTARAGPPERQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\PDEVWPSLFIGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDNPFPDLSVYFLP EVHSLGQILPQGGLTARAGPPERQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFIGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDNPFPDLSVFFLF EVHSLGQILPQGGLTARAGPPERQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFIGDAYAARDKSKLIQLGITHVV NAAAGKPQVDTGAKFYRGMSLEYYGIRADDNPFPDLSVFFLF EVHSLGQILPQGGLTARAGPPERQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFIGDAYAARDKSKLIQLGITHVV NAAAGKPQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVFFLF EVHSLGQILPQGGLTARAGPPERQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFYGIRADAYFRRKKFQLCAD BYRGRGVGERWAPLSVPAAMSSEMEPLILAWSYFRRKFQLCAD LCTQMLEKSPYDDAWAILKARALIERWYTDEIDVDQBGIARMML DENATAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL RPSTQSGRPGTMRQAIRTPETAYTARPITSSSGRFVRLIGTSSML TSPDGPFPINLSRINLITXYSQKPKLARALIERYIPHHENDVKTALD LAALSTEHSQYKDWWK/DQIEKCYYRVGMYRRABKQIKSS LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRRABKQIKSS LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRRABKQIKSS LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRRABKQIKSS LQTDKPFIPLVRKFVDTDIWNQYLAYQQSILNRSDGKSRWFYSP WLLV\ECYMYRRIHEAI\IQSPPIDYFVFKSKEQNFYSGQGS IIALCTHLQQLIRTIEDID\SNOLKDEFFKLLGISLKURNE ULV\ECYMYRRIHEAI\IQSPPIDYFVFKSKEQNFYSGQGS IIALCTHLQQLIRTIEDID\SNOLKDEFFKLLGISLKURNE SL\SGGESSQNTNVLNSLEDILKPFILLNDMEHLWSLLSNCK 6699 325 492 EGELP/PARRVLFRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	1 1			TAGAMOATIVAN WAREKERLIQKHGVCTRVLGDLHLLDLDLQKL
SCLUFGPULMPBYTEMNLFEATLQFQMNHSVLQK	1 1			DECREER I DECLARATE DIDENT THE COMMENT OF THE COMME
178   939   Wikegelswerfcaniikagpmpkhtafimdgnryakkcqve   RQBGHSQBPhstaetlrwclnigilbytvyafsienfrrsksev   DGIMDLARQKFSILMBEKEKIQKHGVCIRVLGDLHLLPLDLQEL   IAQAVQATKNYNKCFLNVCFAYTSRHEISMAVERMAMJVEQGLL   IAQAVQATKNYNKCFLNVCFAYTSRHEISMAVERMAMJVEQGLL   DPSDISESLLDKCLYTNRSPHPDILIRTSGEVELSDFLLWQTSH   SCLVFQPVLWPEYTFWNLFBAILQFQMNHSVLQK   SCLVFQPVLWPEYTFWNLFBAILQFQMNHSVLQK   EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA   LAVGPSGCHTEP\PDEVWPSLFICGDAYAARDKSKLIQLGITHVV   NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP   EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA   LAVGPSGCHTEP\PDEVWPSLFICGDAYAARDKSKLIQLGITHVV   NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP   EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA   LAVGPSGCHTEP\FDEVWPSLFICGDAYAARDKSKLIQLGITHVV   NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP   EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA   LAVGPSGCHTEP\FDEVWPSLFICDDAYAARDKSKLIQLGITHVV   NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP   RPSTQSGRPGTMEQAIFTPATAATTARPITSSSGFFVRLGTASMIL   LCTQMLEKSPYDQAAWILKARALIEMVYIDEIDVDQBGIAEMMIL   DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPTTGFL   RPSTQSGRPGTMEQAIFTPATTATTARPITSSSGFFVRLGTASMIL   LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYREABKQIKSS   PPLFILRIKMSRALRPGSRKVMAVVPASISGQDVGSFAYLTIKDR   LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYREABKQIKSS   LQTDKPFILJUTHRHKSFFFEKKERBGVEAEKKAISLLISKLKMS   LQTDKPFIPLJVBKFVDTDIMQVILBYQQSILMRSDGKSRWFYSP   WLLV\ECYMYRRIHEAI\QSPPIDYFDVFKESKEQNFYGSQES   IIALCTHLQQLIRTIEDJD RNQLKDBFFKLLQISJWGEISVDL   SL\SGGESSQNTNVLNSLEDLKPBFILLINDMEHLWSLLSNCK   SL\SGGESSQNTNVLNSLEDLKPBFILLINDMEHLWSLLSNCK   SCGESSQNTNVLNSLEDLKPBFILLINDMEHLWSLLSNCK   SCEELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV   GGGLP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV   GGGLP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV   LGGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV   LGGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV   LGGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV   LGGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV   LGGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV   LGGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV   LGGELP/PARRVLPRAMTASAQPRGRRPGVGVGVV	1		•	CONTROL INDEPENDED BEST OF CHARGES OF
RQBGHSQGPNKLAETLRWCLNLGILEVTYVAFS1ENFRRSKSEV DGLMDLARQKFSRLMEBKEKLQKHGVCIRVLGDLHLLPLDLQEL IAQAVQATRNINKCFLINVCFAYTSRHEISNAVREMAMGVEQGIL DFSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH SCLVFQPVLMPEYTFWNLFFAILQFQMNHSVLQK SCLVFQPVLMPEYTFWNLFFAILQFQMNHSVLQK EVHSLGQILPQGGLTARAGPFEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQIGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYFLP EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQIGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIBADDNPFFDLSVYFLP EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQIGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIBADDNPFFDLSVYFLP AAAAGKFQVDTGAKFYRGMSLEYYGIBADDNPFFDLSVYFLP FVRGRVGERWAPLSVPAAMSSEMEPLLLAWSYFRRKFQLCAD LCTQMLEKSPYDQAAWILKARALTEMVYIDBIDVDGBGIAEMML DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL RPSTQSGRFOTMEQAAIRTTRTAYTARPITSSSGRFVRLGTASML TSPDGPPINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD LAALSTEHSQYKDWWWK/DQIBKCYYRVGMYRRABKQIKSS TSPDGPPINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD LAALSTEHSQYKDWWWK/DQIBKCYYRVGMYRRABKQIKSS PPLFILRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR LQTDKPFIPLVBKRVDTDIWNQYLEYQQSLMSEGOKSRFYYSP WLLV\ECYMYRRIHEAI\QSPPIDYFDVFKESKEQNFYGSQES IIALCTHLQQLIRTIEDLD\RNQLKDEFFKLLQISJMGEISVDL SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSGCRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	6693	178	030	WINDCELCOMEDICANTIVACIONAMICA ENGLISHED
DGIMDLARQKFSRIMBEREKLQKHGVCIRVIGDLHILIPLDLQEIL IAQAVOARTKNYNKCFLNVCFAYTSRHEISNAVREMAMGVEQGIL DPSDISBSILDKCLYTHRSPHPDILIRTSGEVRLSDFILWQTSH SCLVFQPVLWPEYTFWNLFBAILQFQMNHSVLQK BCLVFQPVLWPEYTFWNLFBAILQFQMNHSVLQK EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFIGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNFFFDLSVYFLP EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFIGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNFFFDLSVYFLP EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFIGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNFFFDLSVYFLP EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFIGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNFFFDLSVYFLP EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFYGDAAFILAWSYFRRKFQLCAD DENAIAQVPRPGTSKLPGTNGTGGPSQAVRPITQAGRPITGFL RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML TSPDGPFINLSRLNILTKYSQKPKLAKALIEYIFHHENDVKTALD LAALSTEHSQYKDWWWK/DQIEKCYYRVGWYRBABKQIKSS TSPDGPFINLSRLNILTKYSQKPKLAKALIEYIFHHENDVKTALD LAALSTEHSQYKDWWWK/DQIEKCYYRVGWYRBABKQIKSS PPLFIRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR LAALSTEHSQYKDWWWK/DQIEKCYYRVGWYRBABKQIKSS IPPLITKVIDTAHRHKSEFFFKHGBEGVBAEKKAISLLSKLRNB LQTDKPFIPLVEKFVDTDIWNQYLBYQQSLLNESDGKSRWFYSP WLLV\CCYMYRRIHEBAI\IQSPPIDYFDVFKESKEQNFYGSQES IIALCTHLQQLIRTIEDLD\CNOFFFKLLQISLWGETSVDL SL\SGGSSSSQNTNVINSLEDLKPFILLINDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	1	270	, , , ,	POECHSOCHMEN APPLIANCE METAL THE THE CONTROL OF THE PROPERTY O
IAOAVOATKNYNKCFLNVCFAYTSRHEISNAVREMAMGVEQGLL DPSDISESLLDKCLYTNRSPHPDLILIRTSGEVRLSDFILWQTSH SCLVFQPVLWPEYTFWNLFKAILQFQMNHSVLQK SCLVFQPVLWPEYTFWNLFKAILQFQMNHSVLQK EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFILGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKKYRGMSLEYYGIRADDNPFFDLSVYFLP EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFILGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYFLP EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFILGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYFLP EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFILGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYFLP FRVRGGRFQTMFQAAWILKARALTEMVYIDBIDVDQBGIAEMML DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGFPTTGFL RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML TSPDGPPINLSRLNLTRYSQKPKLAKALIEYIPHHENDVKTALD LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRRABKQIKSS FPLFIRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR LQTDKPPIPLVEKFVDTDIWNQYLEYQQSILNESDGKSRWFYSP WLLV\SCYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQGS IIALCTHLQQLIRTIEDLD\ENQLKDEPFKLLQISLWGEISVDL SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	1 1			DCIMDIADOVPCDIMPPPPPT OVICTOR OD 17 1 DE DE
DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH SCLVFQVVLWPETTFWILFRAILDFQMINHSVLQK  SCLVFQVVLWPETTFWILFRAILDFQMINHSVLQK  SULSLEDGILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFYLGDAYAARDKSKLIQLGITHVV NAAAGKPQVDTGAKFYRGMSLEYYGIRADDNPFPDLSVYFLP  6695 292 813 SILLHLAPPGAYTPSQPLSSVSTETASSVRQAAESRQHELPVR EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFYLGDAYAARDKSKLIQLGITHVV NAAAGKPQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYFLP  6696 1 782 PRVRGRVGERWAPLSVPAAMSSEMEPLLLAWSYFRRKKFQLCAD LCTQMLEKSPYDQAAWILKARALTEMVYIDEIDVDQBGIAEMML DENAIAQVPRPGTSLKLPGTNOTGGPSQAVRPITQAGRPITGFL RPSTQSGRPGTMEQAILTARYTARPITSSGKPVRLGTASML LAALSTEHSQYKDWWWK/DQIEKCYYRVSMYRBABKQIKSS 6697 3 782 PPLFTLRENSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR LQTDKPFIPLVBKKFVDTDIWNQYLKYQQSILINBGDGKSRWFYSP WLLVLSCYMYRRIHEAI\QSPPILDYFDVFKESKEQNFYGSQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGBISVDL SL\SGGESSSQNTNVLNSLEDLKPFILLMDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	{			TACATION TO THE TACK TO THE TA
SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK  SILLHLAPPGAYTFSQPLSSVSTETASSVRQAAESRQHELFVR EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEWPSLFIGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYFLP  6695 292 613 SLLHLAPPGAYTPSQPLSSVSTETASSVRQAAESRQHELFVR EVHSLGQILPQDGLTARAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEWPSLFIGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYFLP  6696 1 782 PRVRGRVGERWAFISVPAAMSSEMEPLILAWSYFRRKFQLCAD LCTQMLEKSPYDQAAWILKARALTEMVYIDEIDVDQBGTARMML DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL RPSTQSGRPGTMEQAIRTPETAYTARPITSSSGRFVRLGTASML TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHEDVKTALD LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRBABKQIKSS 6697 3 782 PPLFIRRLNSRALRPGSRRVMAVVPASLSGQDVGSFAYLTIKDR IPQILTKVIDTLHRHKSEFFEKHGBEGVBAEKKAISLLSKLRNB LQTDRPFIPLVBKFVDTDIWNQYLBYQQSLINBSDGKSRWFYSP WLLV\BCYMYRRIHEAI\TQSPPIDYFWFKESKEQNFYGSQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL SL\SGGESSSQMTNVINSLEDLKPFILLINDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	1 1			DESDIERST. DECLYTHER COUDT, TOTOGRAPH CONTENTS
6694 292 813 SILLHLAPPGAYTPSQPLSSVSTRTASSVRRQARESRQHELPVR EVHSLGQILPQDGITARAGPPRAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\PDEWMPSLFIGDAYAARDKSKLIQLGTTHVV NAAAGKFQVDTGARFYRGMSLEYYGIRADDNPFPDLSVYPLP 6695 292 813 SILLHLAPPGAYTPSQPLSSVSTETASSVRRQARESRQHELPVR EVHSLGQILPQDGITARAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\TDEVWPSLFIGDAYAARDKSKLIQLGITHVV NAAAGKPQVDTGARFYRGMSLEYYGIBADDNPFFDLSVYFLP 6696 1 782 PRVRGRVGERWAPISVPAAMSSEMEPILLAWSYFRRKFQLCAD LCTQMLEKSPYDQAAWILKARALTEMVYIDEIDVDQBGIARMML DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML TSPDGPPINLSRLNILTKYSQKPKLAKALIEYIFHHENDVKTALD LAALSTEHSQYKDWWK/DQIEKCYYRVGMYREABKQIKSS 6697 3 782 PPLFIRRINSRALRPGSRRVWAVVPASISGQDVGSFAYLTIKDR LQTDKPPIPLVBKFVDTDIWNQYLHYQQSILNESDGKSRWFYSP WLLVLSCYMYRRIHEAI\TQSPPIDYFWSKSKEQNFYGSQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLIQISLWGEISVDL SL\SGGESSSQMTNVLNSLEDLKPFILLINDMEHLWSLISNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV				
EVHSLGOILPQDGITARAGPPRAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\PDEVWPSLFIGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYPLP 6695 292 813 SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAABSRQHELPVR EVHSLGQILPQDGLTARAGPPRAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDBVWPSLFIGDAYAARDKSKLIQLGITHVV NAAAGKPQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYPLP 6696 1 782 PRVRGRVGERWAPLSVPAAMSSEMEPLLLAWSYFRRKFQLCAD LCTQMLEKSPYDQAAWILKARALTEMVYIDBIDVDQBGIAEMML DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRBABKQIKSS 6697 3 782 PPLFIRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR LQTDKRPIPLVRKFVDTDIWNQYLKYQQSLLMRSDGKSRWFYSP WLLVLGTLRHKKSEFFEKHGBEGVBAEKKAISLLSKLRNB LQTDKRPIPLVRKFVDTDIWNQYLKYQQSLLMRSDGKSRWFYSP WLLVLGTLRHALAI\IQSPIDYFDVFKESKEQNFYGSQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL SL\SGGESSSQNTNVLNSLEDLKPFILLINDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	6694	292	R13	
LAVGPSGCHTEP\FDEWPSLFLGDAYAARDKSKLIQLGITHVV NAAAGKPQVDTGAKFYRGMSLEYYGIRADDNPFPDLSVYPLP 6695 292 813 SLLLHLAPPGAYTPSQPLSSVSTETASSVRQAAESRQHELPVR EVHSLGQILPQDGLTAKAGPPRAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\TDEWPSLFLGDAYAARDKSKLIQLGITHVV NAAAGKPQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP 6696 1 782 PRVRGRVGERWAPLSVPAAMSSEMEPLLLAWSYFRRKFQLCAD LCTQMLEKSPYDDAAWILKARALTEMVYIDEIDVDQBGIAEMML DENAIAQVPRPGTSIKLPGTNOTGGPSQAVRPITQAGRPITGFL RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML TSPDGPFINLSRLNLTKYSCKPKLAKALIKYIFHHENDVKTALD LAALSTEHSQYKDWWK/DQIEKCYYRVGMYREABKQIKSS 6697 3 782 PPLFIRRINSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR LQTDKPFIPLVBKFVDTDIWNQYLBTQQSLLMESDGKSRWFYSP WLLV\ECYMYRRIHEAI\TQSPPIDYFDVFKSKEQNFYSQQES ULACTHURQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL SL\SGGESSSQMTNVLNSLEDLKPEFILLINDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV			013	PULCICOTI DODCI TARACODERODRACIONAL DA MIZARIA
NAAAGKFQVDTGAKFYRGMSLEYYGIRADDNPFFDLSVYFLP				LANCESCUMPED PREMIUDELET CHAVAARDEST TOT COMPRE
6695 292 613 SILLHLAPPGAYTPSQPLSSVSTETASSVRQAAESRQHELPVR EVHSLGQILPQDGLITARAGPPEAQDPMCSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEWWPSLFIGDAYAARDKSKLIQLGITHVV NAAAGKRVQUTGAAFPRGMSLEYYGIEADDNPFFDLSVYFLP 6696 1 782 PRVRGRVGERWAFLSVPAAMSSEMEPLILIAWSYFRRKFQLCAD LCTQMLEKSPYDQAAWILKARALTEMVYIDEIDVDQBGIAEMML DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL RPSTQSGRPGIMEQAIRTPETAYTARPITSSSGRFVRLGTASML LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRRABKQIKSS 6697 3 782 PPLFIRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR LQTDKRPFIPLVBKRVDTDIWNQYLBYQQSLLMBSDGKSRWFYSP WLLVLGYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQES WLLVLGYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL SL\SGGESSSQMTNVLNSLEDLKPFILLNDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	1 1			MANACEPONTER PERSONAL PROPERTY OF THE PROPERTY
EVHSLGQILPQDGLTARAGPPRAQDPMGSPGISLPANHIGFANA LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGTTHVV NAAAGKPQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYPLP  6696  1 782 PRVRGRVGERWAPLSVPAMMSSEMEPLLLAWSYFRRKFQLCAD LCTQMLEKSPYDQAAWILKARALIEMYYIDEIDVDQBGIARMML DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML TSPDGPPINLSRLNLTKYSQKPKLAKALIEYYHHHENDVKTALD LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYREAEKQIKSS  6697  3 782 PPLFLRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR LQTDKPPIPLVBKFVDTDIWNQYLHYQQSLLNBSDGKSRWFYSP WLLV\CTMYRRIHEAI\TQSPPIDYFDVFKESKEQNFYSSPSPWLLV\CTMYRIHEAI\TQSPPIDYFDVFKESKEQNFYSSPSPWLLV\CTMYRIHEAI\TQSPPIDYFDVFKESKEQNFYSSPSPWLLV\CTMYRIHEAI\TQSPPIDYFDVFKESKEQNFYGSQSSL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	6695	292	873	STATISTICAL AND CONTROL OF THE STATISTICS OF THE
LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV NAAAGKPQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP  6696  1 782 PRVRGRVGERWAPILSVPAAMSSEMEPLILIAWSYFRRKFQLCAD LCTQMLBKSPYDQAAWILKARALTEMVYIDEIDVDGGTARMML DENAIAQVPRGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL RPSTQSGRPGTMRQAIRTPRTAYTARPITSSSGRFVRLGTASML TSPDGPPINLSRLNLTKYSQKPKLAKALIEXTHHENDVKTALD LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYREABKQIKSS  6697  3 782 PPLFLRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR IPQILTKVIDTLHRHKSEFFEKHGBBGVBAEKKAISLLSKLRNE LQTDKPPIPLVBRKYDTDIWNGYLHYQQSLLNESDGKSRWFYSP WLLV\ECYMYRRIHEAI\TQSPPIDYFDVFKBSKEQNFYSSQES IIALCTHLQQLIRTIEDLD\ENQLKDEFPKLLQISLWGEISVDL SL\SGGESSSQNTNVLNSLEDLKPFILLINDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	]			RVHSLGOTT.DODGT.TARACDDRAODDDCCTOCTONAUTCON
NAAAGKPQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP	1 1			LAVCPSCCHTED\ FDRUWDST.FICHAVAADDEUT TOT OTHER
6696  1 782 PRVRGRVGERWAPISVPAAMSSEMEPILLAWSYFRRKFQLCAD LCTQMLEKSPYDQAAWILKARALTEMYVIDEIDVDQBGIAEMML DENAIAQVPRPGTSIKLPGTNQTGGPSQAVRPITQAGRPITGFI RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML TSPDGPPINLSRLNLTKYSQKPKLAKALIEKYIPHHENDVKTALD LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYREABKQIKSS 6697 3 782 PPLFIRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR IPQILTKVIDTLHRHKSEFFEKHGBEGVBAEKKAISLLSKLRNE LQTDKPFIPLVBKFVDTDIWNQYLBYQQSLLNBSDGKSRWFYSP WLLVVECYMYRRIHEAI\IQSPPIDYFDVFKBSKEQNFYSQQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL SL\SGGESSSQNTNVLNSLEDLKPFTILINDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	1			NAAAGKPOUTTGAKFYRGMSI.EVVCTPADDMDEEDT.ODD
LCTQMLBKSPYDOAWILKARALTEMVYIDEIDVDQBGIAEMML DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML TSPDGPFINLSRLNLTKYSQKPKLAKALIBYIFHHENDVKTALD LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYREABKQIKSS  6697 3 782 PPLFIRRINSRALRPGSRRVMAVVPASLSGQDVGSFAYLTIKDR LQTDKPFIPLVBKFVDTDIWNQYLBYQQSLLNESDGKSRWFYSQ LQTDKPFIPLVBKFVDTDIWNQYLBYQQSLLNESDGKSRWFYSQ WLLV\ECYMYRRIHEAI\TQSPPIDYFDVFKESKEQNFYGSQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL SL\SGGESSSQNTNVLNSLEDLKPFILLINDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	6696	i	782	PRINCIPULA PICTURA PIC
DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL RPSTQSGRPGTMRQQAIRTPRTAYTARPITSSSGRFVRLGTASML TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD LAALSTHRSQYKDWWWK/DQIEKCYYRVGMYRBABKQIKSS  6697 3 782 PPLFIRRINSRALRPGSRRVMAVVPASLSGQDVGSFAYLTIKDR IPQILTKVIDTLHRHKSBFFEKHGBBGVBAEKKAISLLSKLRNB LQTDKPFIPLVBKFVDTDIWNQYLBYQQSLLNBSDGKSRWFYSP WLLV\BCYMYRRIHEAI\JQSPPIDYFDVFKESKEQNFYGSQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL SL\SGGESSSQMTNVLNSLEDLKPFILLNDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKBCKCTSCKKSBCRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV		_ [		
RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD LAALSTEHSQYKDWWWK/QIEKCYYRVGMYRRABKQIKSS  6697 3 782 PPLFIRRINSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR IPQILTKVIDTLHRHKSEFFEKHGBEGVEAEKKAISLLSKLRNE LQTDKPFIPLVBKFVDTDIWNQYLBYQQSLLNESDGKSRWFYSP WLLV\RCYMYRRIHEAI\TQSPPIDYFDVFKESKEQNFYGSQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGBISVDL SL\SGGESSSQNTNVLNSLEDLKPFILLINDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKCCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	1 1			DENATAOVDDDCTCI.KT.DCTDCTCCCCCCAADDTTTCAADAAAAA
TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYREABKQIKSS  6697 3 782 PPLFLRRINSRALRPGSRXVMAVVPASLSGQDVGSFAYLTIKDR IPQILTKVIDTLHKKSEFFEKHGBEGVBAEKKAISLLSKLRNE LQTDKPFIPLVBRFVDTDIWNQYLBYQQSLLNESDGKSRWFYSP WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYSGQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL SL\SGGESSSQNTNVLNSLEDLKPFILLINDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	1			
LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYREAEKQIKSS  6697 3 782 PPLFLERLINSRALEPGSRKVMAVVPASLSGQDVGSFAYLTIKDR IPQILTKVIDTLHRHKSEFFEKHGEBGVEAEKKAISLLSKLENE LQTDKPFIPLVBKFVDTDIWNGYLHYQQSLLNESDGKSRWFYSP WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYSGQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL SL\SGGESSSQNTNVLNSLEDLKPFILLINDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	1 1	· .		TCDCCDPTAT.CDI.NI TVVCOVDVI NENT TOUTSUMMING
6697 3 782 PPLFLRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR IPQILTKVIDTLHRHKSBFFEKHGBBGVBAEKKAISLLSKLRNB LQTDKPFIPLVBKFVDTDIWNQYLBYQQSLLNBSDGKSRWFYSP WLLVVEYMYRIHEAI\IQSPPIDYFDVFKBSKEQNFYGSQES IIALCTHLQQLIRTIEDLD\BNQLKDBFPKLLQISLWGBISVDL SL\SGGBSSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKBCKCTSCKKSBCRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV				
IPQILTKVIDTLHRHKSEFFEKHGEBGVEGEKATISTIKDRE  IPQILTKVIDTLHRHKSEFFEKHGEBGVEGEKAISLLSKILRNE LQTDKPFIPLVEKFVDTDIWNQYLBYQQSILNESDGKSRWFYSP WLLV\ECYMYRRIHEAI\IQSPPIDVFDVFKESKEQNFYGSQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK  6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP  6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	6697	- 3	702	DDI DI DDI DDCCDYIMAIRD OF CONTROL
LQTDKPFIPLVBKFVDTDIWNQYLEYQQSLLNESDGKSRWFYSP WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKBSKEQNFYGSQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	/	· 1	104	TRAIT TENTENT HOUSE PROPERTY TO THE TENTE HOUSE PROPERTY TO THE TENTE HOUS
WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKBSKEQNFYGSQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKBCKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV		1		TOTOLOGICA COLORA CONTROL CONT
IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	1			MATERIAL STATES TO THE STATES OF THE STATES
SL\SGGESSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV		i		MDDA /Primikkihryi / IÖZLGIDAŁDAŁKRZKEÓNŁAGZÓGZ
6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	]			TIME THE COMMENT OF THE PROPERTY OF THE PROPER
6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV	6699			
POPPE A LYNCK ADE WANT WORK A GARGA A A A 19 CKH L KCA				
	6679	325	492	
				LLGKRKGSVGAGSFQLPGGHLEFGETWBECAQRETWBEAALHLK
NVHFASVVNSFIBKENYHYVTILMKGEVDVTHDSRPKNVEPEKN				NVHFASVVNSFIBKENYHYVTIIMKGBVDVTHDSBPKNVBPBKN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	-	\=possible nucleotide insertion)
	<del>                                     </del>		ESKRIIYNHAFFFQRSKWSGGILQ
6700	1098	1392	TQCWRSSTPGMRTHFRTQP/RLECGQGFSQQENGHCMDTNECIQ
1			FPFVCPRDKPVCVNTYGSYRCRTNKKCSRGYBPNBDGTACVERT
1		ł	LLLGLCNLLGK
6701	2	1485	AAAGPRTRVRRAAAFEGQPSPSPGLGPTSDKAAAPRTPKRRRLW
			RQRQ/HPAMLCYVTRPDAVLMEVEVEAKANGRDCLNQVCRRLGI
			IEVDYFGLQFTGSKGESLWLNLRNRISQQMDGLAPYRLKLRVKF
[	1	}	FVEPHLILQEQTRHIFFLHIKEALLAGHLLCSPEQAVELSALLA
j			QTKFGDYNONTAKYNYEBLCAKRLSSATLNSIVAKHKELEGTSO
			ASABYQVLQIVSAMENYGIBWHSVRDSEGQKLLIGVGPEGISIC
		1	KDDFSPINRIAYPVVQMATQSGKNVYLTVTKESGNSIVLLFKMI
}	į	1	STRAASGLYRAITETHAFYRCDTVTSAVMMQYSRDLKGHLASLF
1		1	LNENINLGKKYVPDIKRTSKEVYDHARRALYNAGVVDLVSRNNQ
		1	SPSHSPLKSSESSMNCSSCEGLSCQQTRVLQEKLRKLKBAMLCM
l		į.	VCCEREINSTFCPCGHTVCCESCAAQLQVGESAAHFCLQPHLSL
		1	LLTGSRSQVLAR
6702	397	1971	PLAKFLKLDLVNVLCLPMEDVFLFYRTCFCSMGLGSSCHLSLPK
			RARALLCSRKATVVRDLVAVRMAKEQEFTQLCKLPAQPSHPHCV
	1		NNTYRSAQHSQALLRGLLALRDSGILFDVVLVVEGRHIEAHRIL
		ł	LAASCDYFKGMFAGGLKEMEQEEVLIHGVSYNAMCQILHFIYTS
		·	ELELSLSNVQETLVAACQLQIPEIIHFCCDFLMSWVDERNILDV
			YRLABLFDLSRLTBQLDTYILKNFVAFSRTDKYRQLPLEKVYSL
1	1		LSSNRLEVSCETEVYEGALLYHYSLEQVQADQISLHEPPKLLET
!			VRFPLMEAEVLQRLHDKLDPSPLRDTVASALMYHRNESLQPSLQ
l		}	SPQTELRSDFQCVVGFGGIHSTPS\MSSATRPKYLNPLLGEWKH
	1		FTASLAPRMSNQGIAVLNNFVYLIGGDNNVQGFRABSRCWRYDP
i			RHNRWFQIQSLQQEHADLSVCVVGRYIYAVAGRDYHNDLNAVER
			YDPATNSWAYVAPLKREVYAHAGATLEGKMYITCGRKGRIT
6703	45	1244	GVGPRAAAMPLELELCPGRWVGGQHPCFIIAEIGQNHQGDLDVA
		•	KRMIRMAKECGADCAKFQKSELEFKFNRKALERPYTSKHSWGKT
			YGEHKRHLEFSHDOYRELQRYAEEVGIFFTASGMDEMAVEFLHE
ļ			LNVPFFKVGSGDTNNFPYLEKTAK/TRGWHSVLRDVCGVQLNDE
			TSSWDVLGRVRTSKEKVLMVLVLDYSGRPMVISSGMQSMDTMKQ
	1	ł	VYQIVKPLNPNFCFLQCTSAYPLQPEDVNLRVISEYQKLFPDIP
			IGYSGHETGIAISVAAVALGAKVLERHITLDKTWKGSDHSASLE
	I	ļ	PGELABLVRSVRLVERALGSPTKQLLPCEMACNEKLGKSVVAKV
		1	KIPEGTILTMDMLTVKVGEPKGYPPEDIFNLVGKKVLVTVEBDD
	J		TIMEE
6704	82	1007	TMNTRNRVVNSGLGASPASRPTRDPQDPSGRQGBLSPVBDQRBG
	[	1	LEAAPKGPSRESVVHAGQRRTSAYTLIAPNINRRNBIQRIABQB
		]	LANLEKWKEQNRAKPVHLVPRRLGGSQSETEVRQKQQLQLMQSK
			YKQKLKREESVRIKKBABBABLQKMKAIQREKSNKLEBKKRLQB
			NLRREAPREHQQYKTAEFL/RQTEHRIARQKCLSKCCLWPTILM
			MGQKLGLQ\DSLKAEENRKLQKMKDEQHQKSELLELKRQQQBQE
			RAKIHQTEHRRVNNAFLDRLQGKSQPGGLEQSGGCWNMNSGNSW
			GI
6705	2	786	RLCRNSARVPCGWSASRSLGEGAGFIGPLRGPHPRAGGTGTSFT
			SYKRKGGIMSTIAAFYGGKSILITVATGFLGKELMEKLFRTSPD
	1		LKVIYILVRPKAGQTLQHRVPQILDSKLFEKVIEVRPNVHEKIR
		!	AIYADLNQNDFAISKEDMQELLSCTNIIFHCAATVRFDDTLRHA
			VQLNVTATRQLLLMASQMPKLEAFIHISTAYSNCNLKHIDEVIY
			PCPVEPKKIIDSLEW\LDDAIIDEITPKLIRDWPNIYTYTK
6706	130	531	FTHSSSSHSQEMLGKLMMLRNDGHFCDITIRVQDKIFRAHKVVL
			AACSDFFRTKLVGQAEDENKNVLDLHHVTVTGFIPLLEYAYTAT
	]		LSINTENIIDVLAAASYMQMPSVASTCSEPMKSSILWNTPNSQP
			EK
			<b></b>

PCT/US00/34263

		4.7	- 2 36 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, P-Phonylalanine, G-Glycine,
{	location	corresponding	H=Histidine, I=Tsoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
]	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
[	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
)	amino acid	sequence	Codon, /=possible nucleotide deletion,
l .	sequence	·	\=possible nucleotide insertion)
6707	2233	1343	YWSGIGYBLQHFHWRKFHFEKKGPPSTCQBRLYESRSRWPCIS*
1	1		GMVVVGWTAVNGSW*GGQLRCVCVCTSHSSDSTRSSQRASKCHS
Į.	l		FFILSQ*KT*SSWENWVFAKYSRIYSYGHSCSKGRGD*DFK*NV
i	1	1	SQAR*SRFCGLCNPCGHCGLDINLRGGSSPWTDKHSCVHNNLLC
ì	İ	1	NRRVFSLLCEGPGHCYQGAVCRRACAAASPGLDSAAEPHRLCEH
ļ	Į.		TD+LPK+GPGYIQHFHCDSNILCILYNISFNLFSYSF+GVARYA
Ì	1		C*RCHWYFEWLLYNHCGDILVACL*RRQL*SSQ
6708	115 .	1729	TVGSWSRSGRSPPVGRQLLLTGRGAQAAGSPQGGMALQVELVPT
ļ		1	GRIIRVVHPHRPCKLALGSDGVRVTMESALTARDRVGVQDFVLL
	1	1	enftseafienlrrrfrenliytyigpvlvsvnpyrdiqiysr
1	1	1	QHMERYRGVSFYEEPPHLLAVADTVYRALRTERRDQAVMISVES
1		ţ	GAGKTDATKRLLQLYAETCPAPQRGGAVRDRLLQSNPVLEAFGN
ļ	1		AKTLRNDNSSRFGKYMDVQFDFKGADVGGHILSYLLEKSRVVHQ
1	1		NHGERNFHIFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAK
{	ļ	Į.	VSSINDKSDWKVVRKALTVIDFTEDEVEDLLSIAASVLHLGNIH
			Faaneesnaqvttenqlkyltrllsvegstlrbalthrki iakg
.}	1		RELLSPLNLEQAAYARDALAKAVYSRTFTWLVGKINRSLASKOV
1 -	(	į.	ESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFI
1	1	ł	BLTLKSEQEBYEAEGIAWEPVQYPNNKIICDLVREKFKGII\SI
L	l		LDE\ECLRPGE ·
6709	3	894	PPHKHLFPSGERGPFSFLVSRRGLGPGKMGKKGKKEKKGRGAEK
ĺ			TAAKMEKKVSKRSRKEEEDLEALIAHFQTLDAKRTQTVELPCPP
}	j	)	PSPRIMASLSVHPEKDELILFGGEYFNGQKTFLYNELYVYNIRK
l			DTWTKVDIPSPPPRRCAHQAVVVPQGGGQL:WVFGGEFASPNGEQ
1 .			FYHYKDLWVLHLATKTWBQVKSTGGPSGRSGHRMVAWKRQLILF
ł		1	GGFHESTRDYIYYNDVYAFNLDTFTWSKLSPSGTGFTPRSGCQ\
L			IPSLPRAASSVYGGYSKQRVKKDVDKGTRHSDMP
6710	158	980	RHKMTNYRVESSSGRAARKMRLALMGPAFIAAIGYIDPGNFATN
1			IQAGASFGYQLLWVVVWANLMAMLIQILSAKLGIATGKNLAEQI
į .			RDHYPRPVVWFYWVQABIIAMATDLAEFIGAAIGFKLIIGVSLL
Į.			QGAVLTGIATPLILMLQRRGQKPLEKVIGGLLLFVAAAYIVELI
ſ	•	İ	PSQPNLAQLGRGMVIPSLPTSRAVFLAAGVL\GATIMPHVI/YI
l	Į.		WHSSLTQHLHGGSRQQRYSATKWDVAIAMTIAGPVNLAIMATAA
		<del></del>	SELNFYGHTGVA
6711	3	347	VTECKTMICKMSQLKRNI*TMINITHHYSVKLGHPDTLIHGEFK
	Į	l	BLVRTDLHNILMKENKNDQAI+HIMEDLDTNAHMQIIYKELIMI
<u></u>	<u> </u>	ļ <del></del>	MAMLTWSYHDNMHDADYGPGQQHRPG
6712	118	578	PHGQKRTRYPQVRAPGQQPQAQLAMALCLKQVFAKDKTFRPRKR
Į	Į.		FEPGTQRFELYKKAQASLKSGLDLRSVVRLPPGENIDDWIAVHV VDFFNRINLIYGTMABRCS*TSCPVMAGGPRYEYRWQDBRQYRR
1		1	
7===		<del> </del>	PAKLSAPRYMALLMDWIESLI
6713	2485	3	QARGSDSEDGEFEIQAEDDARARKLGPGRPLPTPPTSECTSDVE PDTREMVRAQNKKKKSGGFQSMGLSYPVFKGIMKKGYKVPTPI
1			PDTREMVRAQNKKKKKSGGPQSMGLSYPVFKGIMKKGYKVPTPI ORKTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAQTG
1	1	}	
1			ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF
	1	l	AALHENPDIIIATPGRIVEVAVRMSLKIQSVEYVVYDEADRIFE
1	1		MGFAEQLQEI IARI.PGGHQTVLFSATLPKLLVEFARAGLTEPVL
1	l	Į.	IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV
1	ł		VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKPTL
1	<b>S</b>		GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA
1	]	1	RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA
1			GVDGMLGRVPQSVVDEEDSGLQSTLBASLELRGLARVADNAQQQ
1	1	1	YVRSRPAPSPESIKRAKEMDLVCIGLHPLFSSRPEEERLQRLRL
1	1		VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ
1	1		GOOGROEOOEGPVGPAPSRPALOEKOPEKEERERAGESVEDIFS
Į.	l	<u></u>	EVVGRKRQRSGPNRGAKRRREEARQRDQRFYIPYRPKDFDSBRG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	· ·		LSISGEGGAFEQQAAGAVLDIMGDBAQNLTRGRQQLKWDRKKKR
)	]	1	FVGQSCQEDKKKIKTESGRYISSSYKRDLYQKWKQKQKID+S*L
ł		{	GRRRGILTRRRPRTBEVGEARPLAQAGCIPGPHAPRHPLQAESA LELKTKQQILKQRRRAQKAALSLQRWWPQAALCPQ
6714	169	1416	NNCOELLPPPPAPMAHIPSGGAPAAGAAPMGPQYCVCKVELSVS
6/14	109	1416	GONLLDRDVTSKSDPFCVLPTENNGRWIBYDRTETAINNLNPAF
ł	i	}	SKKFVLDYHFBEVQKLKFALFDQDKSSMRLDRHDFLGQFSCSLG
ł	ļ	l	TIVSSKKITRPLLLLNDKPAGKGLITIAAQKLSDNRVITLSLAG
1			RRLDKKDLFGKSDPFLEFYKPGDDGKWMLVHRTEVIKYTLDPVW
i	j		KPFTVPLVSLCDGDMBKPIQVMCYDYDNDGGHDFIGEFQTSVSQ
	Į.		MCEARDSVPLEFECINPKKQRKKKNYKNSGIIILRSCKINRDYS
			FLDYILGGCQLMFTVGIDFTASNGNPLDPSSLHYINPMGTNEYL
1		1	SAIWAVGQIIQDYDSDKMFPALGFGAQLPPDWKVSHEFAINFNP
<b>,</b>	}	}	TNPPCSGVDGIAQAYSACLP
6715	32	493	GPAGAESGSLHCLPATVQALAGAAHSPHGGQPPRRGPLIGSGMP
	İ		GKPKHLGVPNGRMVLAVSDGELSSTTGPQGQGEGRGSSLSTHSL
	•	İ	PSGPSSPFPTBEQPVASWALSFERLLQDPLGLAYFTEFLKKEFS
			ABNVTFNKACERFQQIPASDT
6716	1	176	GAGGPAPRSFGSEEPRAALERDKMSARAAAKSTAMBETAIWEQ
			HTVTLHRVSLCCSK
6717	115	896	LFAMSGFENLNTDFYQTSYSIDDQSQQSYDYGGSGGPYSKQYAG
			YDYSQQGRFVPPDMMQPQQPYTGQIYQPTQAYTPASPQPFYGNN FBDBPPLLBELGINFDHIWQKTLTVLHPLKVADGSIMNETDLAG
	1	Ì	PMVFCLAFGATLLLAGKIQFGYVYGISAIGCLGMFCILNLMSMT
		<b>{</b>	GVSFGCVASVLGYCLLPMILLSSFAVIFSLQGMVGIILTAGIIG
		l	WCSFSASKIFISALAMEGQQLLVAYPCALLYGVFALISVF
6718	290	599	KOSSTVPGTILPSLKWHNSGLCKPPETGGKMTTFKEGLTFKDVA
}		1	VIFTEELGLLDPVQRNLYQDVMLENFRNLLSVGHHPFRHDVFL
	· ·		LEKEKKLDIMKTATQ
6719	1	691	PTRPKRQDREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET
!	<b>]</b>	}	DLDSDDDKIRKPNNFMKDSASQDNGLSRKISRKRVCSSDSDSSL
		<b>,</b>	QVVKKSSKARTGLLRITRRCAATAANKIKLMSDVBDVSLBNVHT
	1	l	RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP
	]		DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK
	<u> </u>		RKSSSVTSSG
6720	3	B22	HEVAREAGGTVYPQRGTMPGTKRFQHVIBTPBPGKWELTGYRAA
	1	1	VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY
	}	ĺ	QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF
	{	ł	LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IRELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP
	1	1	VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM
}	ì		SVVTLISE
6721	3	822	HEVAREAGGTVYPORGTMPGTKRFOHVIETPEPGKWELTGYEAA
	1 "	1	VPITEKSNPLTODLDKADARNIVRLLGQCDAEIPQEEGQALSTY
	İ	1	ORLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF
		ì	1MSVSPNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG
	Į.		IBELKKVAAGKKRVIVIGISVGLSAPPVAGQMDCCMNNTAVFLP
Ì	1	ĺ	VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM
	1	1	SVVTLISE
6722	1	390	RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQATYVALGEAVE
			LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK
	1	]	PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGOHHNYONW
6723	173	659	VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT
•	1		GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSABIL
	1		ABIARILRPGGCLFLKEPVETAVONNSKVKTASKLCSALTLSGL
		<del></del>	<u></u>

Degiming coation corresponding to first anto acid and acid residue of anto acid residue of anto acid equence corresponding to first anto acid anto acid equence corresponding to first anto acid anto acid equence corresponding to first anto acid anto acid equence corresponding to first anto acid acquence corresponding to first anto acid acquence corresponding to first anto acid equence corresponding to first anto acid acquence corresponding to first anto acid equence corresponding to first anto acid corresponding to first anto acid equence corresponding to first anto acid equence corresponding to the first anto acid equence corresponding to the first anto acid equence corresponding to the first anto acid equence corresponding to the first anto acid equence corresponding to the first anto acid expenses to the first anto acid expenses to the first anto acid expenses to the first acid expenses to the fir	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Docation   Corresponding				
location   corresponding to first   antho acid   antho acid   residue of   antho acid   residue of   antho acid   residue of   antho acid   sequence   s	1			
to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence  6724  173  655  173  657  173  658  720  6724  173  659  720  6724  173  659  720  6725  356  721  6726  722  6726  722  6727  723  724  725  726  727  727  727  728  728  728  728				
to first anion acid residue of amino acid anion acid anion acid control residue of anion acid anion acid anion acid anion acid sequence sequence sequence (anion acid sequence) sequence (but to the sequence) sequence (but to the sequence) (but	Ì			
amino acid ceidue of amino acid sequence  amino acid sequence  Codon, /-possible nucleotide deletion,	1			
residue of amino acid sequence (amino acid sequence) sequence (amino acid sequence) sequence (amino acid sequence) sequence (amino acid sequence) (amino a				
Codon, /-possible nucleotide deletion,   Possible nucleotide				<u> </u>
Sequence			ł	
SPANKLOREPLITPREVGSVREHLEHESIDNL	}	1	Sequence	
6724 173 659 VCQYCTARMDREISAGQVAVWONDKSSPVALKALUDVKOQJA GNEARSVEWNIK (LQLQARIKASSPYTLISGLIVPGCSTTHERARIL APIARILAPGGCLPLKEPVBTAVDNNSKYKTASKLCSALTLSGL VERKELRPGGCLPLKEPVBTAVDNNSKYKTASKLCSALTLSGL VERKELRPGGCLPLKEPVBTAVDNNSKYKTASKLCSALTLSGL VERKELRPGGCLPLKEPVBTAVDNNSKYKTASKLCSALTLSGL VERKELRPGGCLPLKEPVBTAVDNNSKYKTASKLCSALTLSGL TOSSEKAGGCS LIRLSSPLLALBERRGLVEVPPG 6726 98 714 HLQKMERK IBREKRKEYSKGRINSLEDTDQCNRCCSSTLWTLNA GYLITTOKQTLIKKPUPTPLBGIVGKILCPPDADGHYY IDRIGL LFRHVINFLRINGELLLE BEGIRRENGLVEVPPG GYLITTOKQTLIKKPUPTPLBGIVGKILCPPDADGHYY IDRIGL LFRHVINFLRINGELLLE BEGIRRENGLVEVPPG GYLITTOKQTLIKKPUPTPLBGIVGKILCPPDADGHYY IDRIGL LFRHVINFLRINGELLLE BEGIRRENGLVEVPPG GYLITTOKQTIKKPUPTPLBGIVGKILCPPDADGHYY IDRIGL LFRHVINFLRINGELLLE BEGIRRENGLVEVPPG GYLITTOKQTIKKPUPTPLBGIVGKILCPPDADGHYY IDRIGL LFRHVINFLRINGELLLE BEGIRRENGLVEVPPG GYLITTOKQTIKKPUPTPLBGIVGKILCPPDADGHYY IDRIGL LFRHVINFLRINGELLLE BEGIRRENGLVEVPPG GYLITTOKQTIKKPUPTPLBGIVGKILCPPDADGHYY IDRIGL LFRHVINFLRINGELLLE BEGIRRENGLY PKORTEN THE STANDAR SERVEN SERVE	ļ	acquence	ļ	
GNEGRUSURI KQLLQARIKKISS DTITISGLUPGSTTLEISR BIL  ARTARITA PROGIC PLEXPEPTETAVINGKYTTASKLCSALTISGL  VEVXELQREPLTPERVQSVRRHLGHESIDNL  6725  356  722  RERTTPFVILATNIDDIMILARIGESHNIQBEREDHAGSELSLVID  ASMEKUDETDELQLARVOPINDOPMOGLBAVEKNISVSTMTLCAG  ICSYBENGGICS IRLS EPLIALARPROLUKVEFV  HIGGMERK IMBERKERKFYSGKINGLEDDTOCKNICKSTIMTLINVG  GTILLTOKOTLINKPUTPLBSITVORGILLOPPDADGHYF LORGI  LPRHVANPILNORELLBERGHERRIGLEDDTOCKNICKSTIMTLINVG  GTILLTOKOTLINKPUTPLBSITVORGILLOPPDADGHYF LORGI  LPRHVANPILNORELLBERGHERRIGLAGREF POLICAGLAREVKS  RUKKEOLIPBETTPLEITUNEDRSOGLEIFVANPDFISKIKSRI  ULVSKSRILDGPBERSSISSINI TOPKKYTIK  FROMGDERFHYVGKHOTPOKYDTPFKGPTYNGCTDII CCVFIL  LAIVOFVANOLILARVOCHTOC CUKECHDELITLINARSS  RUPPYTKOPCVPGKENTKOVAEVLERDGICPRVLIESEPLARRONS  KDPPYTKOPCVPGKENTKOVAEVLERDGICPRVLIESEPLARRONS  ROMENTERPTYVSNYMDI I SIGITAMANSLIFI ILLEFILAGIMG  RIMITIGLIULIG.  FRAHKOLIMUNGENTYTYDGHGRSKINITOLVKGRAKANOVLER  ROMENTERPTYVSNYMDI I SIGITAMANSLIFI ILLEFILAGIMG  RIMITIGLIULIG.  FRAHKOLIMUNGHYDFYSDERRIGHARVOGTENLENDIDINKVIJGH  LIFENDPORROLIMATTHPE IRKEMMKEFFKYFILREPRTSPRKK  HIVPSALKERDSISSINGKROPTOKOTROGROPPGGOVENDOCHNONG  GIANGERPVALPKERRORIKGRORPOVERGOCHNOLINKVIJGH  LAVKKFPUVCGGRORPOGPOKRORLOFVERGOCHNOLINKVIJGH  LAVKKFPUVCGGRORPOGPOKRORLOFVERGOCHNOLINKVIJGH  LAVKKFPUVCGGRORPOGPORGROLPOFTOKROUGARVOGPOPOR  GLOGFFELGORKORRORROFUTOKROUGARVOGPOPOGPORGROPPOGPORGPORGPOGPORG  GURSPLIHPILAPTSVYFIPODYKREKGBREGFORGPORGPORGPOPORG  GIPSDTHIPTILAPTSVYFIPODYKREKGBREGFORISLIKKREAE  REPREVABANVEVSKOCKOMERRERAPSVIJKRENTERPTERPLINNDEGS  6730  784  1015  NIMOVYEVIGLORVASSERIKKRERGUNGLINKRYBERGARANTY  MDLQVEYKKOLOMERIKKRERGUNGLINKRYBERGHANDYNNEKEAE  REPREVABANVEVSKOCKOMERRERPROGRESHRIPHDENDPRIKERAE  GRORPAPPPSSPPLICLGPGGSDPOOLITGLINKCISSISHOPTOP  AGRORPPPPSSPPLICLGPGGGSDPOOLITGLINKCISSISHOPTOP  AGRORPPSSPPLICHGPGGGSDPOOLITGLINKCISSISHOPTOP  AGRORPPSSPPLICHGROUBSCOPPLOPSRIPHINGBERGER  GRORPAPPSSCOCKORGREGROPTURGERGERAPSVERDERFRIPHORD  LATARVORMANGARGUNGRAPATURPSERGERFRINKERGERFRINKERGE  GRORPAPSSCOCHORSPROGREGORSPROHERDERFRIPHDPH  AGRORPAPSSCOCHORSPROHE	572A	172	650	L
ARIARILAPGICIPILAR PORTAVONNSKUNTASKICSALTILSGI.  VRVERGÜRBEILTER VOSVREBILDENSOM.  6725 356 722 RRETPFVILATMÖDDEMLALRIQBERNILGBARCHARDESLSIVO. ASMELVIDET POLQALF VQRING PERKOLVEY PER 6726 98 714 HIGGMERK HERREKRIST SKRINSLEDTIGGENECSSTIATITASK. CTYSENGROCH SILLS APPLICATE REPROLVEY PER 6726 98 714 HIGGMERK HERREKRIST SKRINSLEDTIGGENECSSTIATITASK. LPHAVLINI LANGEN LILL PER OF THE VILL SPILLAL REPROLVEY PER 6727 1 831 PERMORDER PIT VILL STREET LILL SPILLAL REPORT SKRINST SKRIN LOPKYPI K.  6727 1 831 PERMORDER PIT VILL STREET PER OF THE VILL SKRING PER OLD FER OLD TIME VILL SKRING PER OLD FER OLD THE VILL SKRING PER OLD TO LEVER PER OLD THE VILL SKRING PER OLD TO LEVER PER OLD THE VILL SKRING PER OLD TO LEVER PER OLD THE VILL SKRING PER OLD T	10,23	1 1/3	1 639	- · · · · · · · · · · · · · · · · · · ·
6725 356 722 RERTPPVILATEMODIALALINGERMILGERENIAGESLISUM ASWELVDPTPDLQALFVQPNDOPPWGQLRAVEVKWSVRMTLCAG ICSYEGKGGWCSIRLSSPLLKURPERDIAVEVPPV 6726 98 714 HIGKMERK INSEREKKEYEGKRENSILEDTORGEKGSTLATINVG GYLYTTORQTLTKYPDTPLGGLURPERDIAVEVPPV 6727 1 HORMER INSEREKKEYEGKRENGLIGENGESTLATINVG GYLYTTORQTLTKYPDTPLEGTUNGKLICPPDADGHY PIDRGL LPRHVINFILKNEGLLIPEGTRONGLIAGEVKS RWKKGLIPERTTFLEITORHDENGGGRIFTGABEVKS RWKKGLIPERTTFLEITORHDENGGGRIFTGABEVFS RWKKGLIPERTTFLEITORHDENGGGRIFTGABEVFS RWKKGLIPERTTFLEITORHDENGGGRIFTGABEVFS RWKKGLIPERTTFLEITORHDENGGGRIFTGABEVFS RWKKGLIPERTTFLEITORHDENGGRIFTGABEVFS RWKKGLIPERTTFLEITORHDENGGGRIFTGABEVFS RWKKGLIPERTTFLEITORHDENGGGRIFTGABEVFS RWKKGLIPERTTFLEITORHDENGGGRIFTGABEVFS RWKKGLIPERTTFLEITORHDENGGGRIFTGABEVFS RWKKGLIPERTTFLEITORHDENGGGRIFTGABEVFS RWKKGLIPERTTFLEITORHDENGGRIFTGABEVFSIKTENGENGGFS RWILMGILLUGS RWEYSKGPCVPGFKRNKGVABVLEIDGGRANGTTLINARGS RWEYSKGPCVPGFKRNKGVABVLEIDGGRANGTTLINARGS RWEYSKGPCVPGFKRNKGVABVLEITGAGSKRNTITULGFTM RGMILMGILLUGS RGMILMGILLUGS RGMILMGILLUGS RGMILMGILLUGS RGMILMGILLUGS RGMILMGILLUGS RGMILMGILLUGS RGMILMGILLUGS RGMILMGILMATTHPELRERMKKETFKYFLREPRTSPRKK HVBSALKRADSALRHOT RGMILMGILMATTHPELRERMGRAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1		•	
6725 356 722 RERTPY LIATMODIALAURIQEENNIQEARCHAGESISUVD ASMELUDET POLOALI-YUPFINOPPROGLARVEWISVEMITLCAG ICS YELGOROGIS IRLS PULLAURIPRIOLEY PFV CONTROL OF THE CONTROL OF T	Į.	Į.	ļ	· ·
ASMELUPITPICALF_VOPPHICOPENGLIANEW/KHSURMTLCAG ICS YESKIGKOSI FILIS BELLAKIP PRICULEVEN FOR THE SECOND PRICULAR PRICULEVEN FOR THE SECOND PRICULAR PRICULARY FOR THE SECOND PRICULAR PRICULARY FOR THE SECOND PRICE TO SECOND	C775		722	I
ICSTERIGGMESTHILERPHILDUREVPFV	0/25	300	122	_ · · · · · · · · · · · · · · · · · · ·
6726  98  714  HLÖMRÖRT INDERERREYSEGUNSLEDTDOCKNICKSTLATLINUS GYLYLTÖKOLTT KYPDTPLEGI VNOKILCPPDADGHYPI DRÖGL LPRIVARTIRINGELLIPSE PRENGILÄGEASEVKS RWEKEGLIPERSTYLEITDNIDERS GOLRIPCHAPDE I SKIKSRI VLUSKSRILÖGP PERS 15 SINT 10 FKYTE UNUSKSRILÖGP PERS 15 SINT 10 FKYTE VLUSKSRILÖGP PERS 15 SINT 10 FKYTE VLUSKSRILÖGP PERS 15 SINT 10 FKYTE LA 1 631  FRÖGGERPHYYGHGF FÖKYDPTFKEP I YNRGCTOLI KCVPLL LA 1 VGVAVAU I LAMTGEDOR FKKYT PTÖRSEGOKGTRINKE YLFYFNI VKCAS PLVILER FÖCPTPQI CVEKCPDRYLTYLNARS RØPEYTKOP CVPG FKRIKGVAEVLERGE COPATITYLNARS RØPEYTKOP CVPG FKRIKGVAEVLERGE COPATITYLNARS RØPEYTKOP CVPG FKRIKGVAEVLERGE COPATITYLNARS RØPEYTKOP CVPG FKRIKGVAEVLERGE COPATITYLANARS RØPEYTKOP CVPG FKRIKGVAEVLERGE COPATITYLANARS RØPEYTKOP CVPG FKRIKGVAEVLERGE COPATITYLANARS RØPEYTKOP CVPG FKRIKGVAEVLERGE COPATITYLANARS RØPEYTKOP CVPG FKRIKGVAEVLERGE COPATITYLANARS RØPEYTKOP CVPG FKRIKGVAEVLERGE COPATITYLANARS RØPEYTKOP CVPG FKRIKGVAEVLERGE COPATITYLANARS RØPEYTKOP CVPG FKRIKGVAEVLERGE COPATITYLANARS RØPEYTKOP CVPT CVPT CVPT CVPT CVPT CVPT CVPT CVP	ļ	1	ļ	
GYLVLTOKOTILEVEDTELGITVEGKILCPPDADGHYPIDROGIL LPRHVLINFLRNGELLLPBOFRENQLLAQEAEFFOLKGLAEBVKS RWEKEQLYPERTTYLBITONIDREGGLAFCPCARDETSKIKSRI  6727 1 831 FROMGEBERPHYVGHOFTPGKVDTPYKKETIVARDETSKIKSRI VLVSKSRILDGFPERFSISSNITORVIFIK RFORGGERPHYVGHOFTPGKVDTPYKKETIVARGCTOLITCCVFLL LAIVGVAVOI LAAFIGOPRKVITYPTDSRGEPCOQGTKNENKE VLLYPANIVKCASPLVLLRFQCPTPQICVEKCPDRYLITYLNARSS RDPEYYKQPCVPGFKRNKSVAEVLREDGCPAVLITPSKPLARRCE PALHAYKGVLAVOKETTYEDGHOSRKNITOLVEGAKRAGVUER RQAMRIERPDYTVSWWOI ISLGCAMMANDLIFIILLRFLAGH RGMIINGILVLGY RGMIINGILVLGY FCSSWIRSLANSSISSKWMPLVULTGGIASGKSSVTQVFQQLGCA VIDVDAMARRWVQPGYPAHRRIVEVPGTEVLLENGDINRKVLGD LIFNOPDERQLIANATHPEIRKEMMETFKYFJRBRTSPROKK HVPSALKENDSLMRNDT GYGSLAGHAPGAGGGCCCYPEKGGGPGVGGCOPGVGGQGPGAGG PKGGKGEPYALPKGGGRDCGGCCYPEKGGGPGVGGCQPVGHOQDVANDP GLQGPFGLQGRKGDKGBRAGPGTGPKGGGPPGVGGQCYNGPD GLQGPFGLQGRKGDKGBRAGPGTGPKGGGPPGRGGFTDFGPGQ PKGGKGEPYALPKERGBYFTGCCCTYGEGGGCPFGCGGPGFGFGGGPG PKGGKGEPYALPKERGBYFTGCCCTYGEGGGPFGRGFGFDGFGQG PKGGKGEPYALPKERGBYFTGCCCTYGEGGGPFGRGFGFGFGGG PKGGKGEPYALPKERGBYFTGCCCTYGEGGGPFGRGFGFGFGGG PKGGKGEPYALPKERGBYFTGCCCTYGEGGGPFGRGFGFGFGGGG PKGGKGEPYALPKERGBYFTGCCCTYGEGGGPFGRGFGFGFGGGG PKGGKGEPYALPKERGBYFTGCCCTYGEGGGPFGRGFGFGGGG PKGGKGEPYALPKERGBYFTGCCCTYGEGGGPFGRGFGFGGGG PKGGKGEPYALPKERGBYFTGCCCTYGEGGGPFGRGFGFGGGG PKGGKGEPYALPKERGBYFTGCCCTYGEGGGPFGRGFGFGGGG PKGGKGEPYALPKERGBYFTGCCCTYGEGGGPFGRGFGFGGGG PKGGKGEPYALPKERGBYFTGCCCTYGEGGGPFGRGFGFGGGGG PKGGKGFAGPFTGCCCTTGCGGPGGGPFGRGFGGGGGGGGGGGGGGGGGGGGGGGGGG			l	
LPHRYLNTFLINGIGLILIPBGPRENGLIAGRAFFFOLEGLAREVKS RWEKEQLTPRETTFLEITDNIDRSQGIRIPCNAPPTSKIKKSRI  6727 1 831 FROMGDERPHYTCKHOTPQKYDPTFKGPTYMRCTJTCCVPLI LATVGVAVOL LANTIGDNIPKJTYTHSEBTYLTCVVKL LATVGVAVOL LANTIGDNIPKJTYTHSEBTYLTGCVFL LATVGVAVOL LANTIGDNIPKJTYTHSEBTYLTGCVFL ROMGDERPHYTCKHOTPQKYDPTFKGPTYMRCTJTCVVKL REPTYKOPCYPGFKNIKVAVEAULBIOCOGGTENISKE VLFYTMIVKCASPLVILLBFQCPTFDICVSKCPDRYLTYLINARSS RDPETYKOPCYPGFKNIKVAVEAULBIOCOGGTENISKE PAIHAYKGVLMVGNETTYEDGHGSRKNITDLVEGAKKANGVLEA RQLAMRI PEDTTVSWWDI ISLGIARAMSLLPITLLRFLAGIM RGMI INGILVIGY GRANITHGILVIGY FCSSMURSLADSSISMKMPLVGLTGGIASGKSSVIQVPQUGCGA VIDDDWAMRHVVOPGYPALMRIVUVEYGTSVLISMGDINKKVLGD LIFNOPDRROLLANTTHPEIRREMMKETFKYFLREPRTSPRGKK HVPSALKRADSLAMRDD LAGVKKFDVPCGGRDCGGCCCVPRKGGRGQPGVGVGGVGUGGG GROFGGGGGRGRGRORGARAGPGTORKGDGAVGVGFDGAGG GROFGGGGGRGRORGARAGPGTORKGDGAVGVGFQGADG GROFGGGGGRGRORGARAGPGTORKGDGAVGVGFDGAGG PRGGKGEPFALPKERDRYRKGENGERCLUGFGGPPGRGHGVGQM GPUGAPGRJCGGKGDKGBRARAGPGTORKGUGGGPPGRGHGVGQM GPUGAPGRJCGGKGDKGBRARAGPGTORKGUGGGPPGRGHGVGQM GPUGAPGRJCGGKGDKGBRARAGPGTORKGUGGGPPGRGHGVGQM GPUGAPGRJCGGKGDKGBRARAGPGTORKGUGGGPPGRGHGVGQM GPUGAPGRJCGGKGDKGBRARAGPGTORKGUGGGPPGRGHGVGQM GPUGAPGRJCGGKGDKGBRARAGPGTORKGUGGGPPGRGHGVGQM GPUGAPGRJCGGKGDKGBRARAGPGTORKGUGGGPPGRGHGVGQM GPUGAPGRJCGGKGDKGBRARAGPGTORKGUGGGPGGGGGGD FRAGKGRPFPAPSFDJKMCLGGGGPGGDFTPGRGHGCG FRAGKRAPGRAFASTSTUMAGGGGRAAGPGTAKRATY NDLQVBYGKCGLQMKSLMKKRKRKIGTQMPSILIRRNGSLKKRIS LIKTJANVSINRKDESI GRGRLAPQNGGSDAPATTPPSRQGRREVRFSDEPSFBYTHGRGR AGRUCYTAATTOAAAPATRNCLPDISGGRPTPPBATRHRQGN LGSIRKSSFSTKATSTTUMAGGRRAAAVBERMUTVTPPATPIRF GRGRLAPQNGGSDAPATRTDCLPDISGGRPTPPBATPIRF GRGRLAPQNGGSDAPATRTDCLPDISGGRPTPPBATPIRF GRGRLAPQNGGSDAPATRTDCLPDISGRPTPPBATRHRQGN LGSIRKSSFSTKATSTTMAGGGRPTAPVBERMUTVTPPATPIRF FRATSVQQVMPSBEGGSTEREDQDSSHSSVTTVKRSRDDSGG DKTTRSSQYIESFW  BGSCGVGRPSRNGGGESAPGGBPTPPBATRIGRGRBSSBB DEASSGTDLSGTTKKTLBFBTSDABGRATAKTRARGROPPAT FRATSVQCWAPSBEGGTEREDQDSSHSSVTTVKRSRDSBGBG DKTRRSSQYIESFW  LLABATSUGGRGGGGGAPGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	6726	98	714	
RWRKEGLTPRETTITLEITONHORSGGIRIFONAPDFISKIKSRI  6727 1 831 FROMGDERBHYTGKHGFPQKYDDTPKGFITNRGCTDITCCVFLL  LAIVGVANGILANTKGDPKUTJPTDSRGEFCGGGGTKNENKP  LAIVGVANGILANTKGDPKUTJPTDSRGEFCGGGGTKNENKP  RDPSYKQPCVPGFKNNKUVARVLRDGDCPAVLIPSKFLARRCF  PAIHAYKGVIMVGNETTYEDGHGSRKNITDLVEGARKANGVLRA  RQLAMRIPSDTTVSWYNDIISIGIAMANSLLPIILLRILAGIMA  RGMIINGIIVLGY  6728 486 935 FCSSWLRSLANSSISSMMPLVGLTGGIASGKSSUTQVFQQLGCA  VIDVDUMARHVUQPGYPAHRRIVEVPGTEVLLENGDIRKVLIGD  LIFNQPBRQLIANAITHPRIRKMKETEKYFLREPRTSPRGKK  HVSSALKENDSLANSSISSMMPLVGLTGGIASGKSSVTQVFQQLGCA  VIDVDUMARHVUQPGYPAHRRIVEVPGTEVLLENGDIRKVLIGD  LAFVKRPVPQCGGRCGGCQCTPSKGGGRGQPPVGPQGYNGPP  GLQGFFGLLGGRGGKGRGAFQTVAFKGRGGGCPPVGPQGYNGPP  GLQGFFGLLGGRGGKGGRGAFQTVAFKGRDQGSGGCQTPSCPQGYNGPP  GLQGFFGLLGGRGGKGGRGAPGTVTVFGLAGSV  GFWGARGRGPPGCGGCQCTPSKGGGGGGGGPPGPGGPQGG  PKGQKGEPYALPKERDRYRGEPGEPGLVGFQGPPGRPGPGQG  GFWGARGRGPPGPGFKGQCGNRGLGFYGVKGKGBUQGPGRN  GFWGARGRGPPGPGFKGQCGNRGLGFYGVKGKGBUQGPGRN  GFWGARGRGPPGPGFKGQCGNRGLGFYGVKGKGBUQGPGRN  GFWGARGRGPPGPGFKGQCGNRGLGFYGVKGKGBUQGPGRN  GFWGARGRGPPGPGFKGQCGNRGLGFYGVKGKBUQGPGRN  GFWGARGRGPPGFFGKGQCGNRGLGFYGVKGRGDPGGGGGG  FKRILAGGAVPFEVEVGCCWKTTRESEGVHLERFTSPLKNNDBGS  GFS31 1 446 GIRKRIHGGAVPFEVEVGCWKTTRESEGVHLERFTSPLKNNDBGS  GFWGARGPPFFFFFFLWCLQPGGGSDPQGLTQLRHCLSHSPQDTPW  ACKNOWLTHANTONALARENGENALTERSHLHENGRN  FKFKVABAYBVLSNCCHLERPFSLAYLENGDLKKNISA  LILTARVEVINRCBEIL  GRGCLAPDNGGSSDAPAYTTPSRGHRFWRSDEVFAVFRFRFRFRFFFFF  VALUVEVSCGLQKWNFSEGGFRENDDGSHISVTTVKARSRGDRGC  PCTEEMKTRRTTRLOQGISRQPFLQPSPWITGLRGDSHSSEB  DEASSGTDLSGTISKTVRS IQBAPAVSEDJVILRRPFPLRYPR  YBATSVQGVNFSEGGFRENDDGSHISVTTVKARSRGDRSC  DKTTRSSGYILSFW  GGGRLAPDNGGSSDAPAYTTPSRGAYTLERRPFLRYPR  YBATSVQGVNFSEGGFRENDDGSHISVTTVKARSRGDBGG  DKTTRSSGYILSFW  GGGRLAPGRRQGGESASDGHISCPKPSIIGRRGKSLEDAK  KKKSRREDDVMASGTVKRHLKTGTCKPULAHTKGSAPPEKVL  VLIRRDALIAAQGKGTGBWYSRFISSTVTTVKARSRGDBGG  DKTTRSSGYTRFW  GGGRLAPGRGFRGCGGGASDGHISCPKPSIIGRGKBGARGLGCAGA  KKKKSRREDDVMASGTVKRHKKTGGCGRKVTKKSLBLSKSCLI  QLLSIMGGRGAAGARDVIHMLKTETTKPEVLEAHTKGABPRFRILEQL  LLABCHRTRTYLEENCHERT  GGGGLAPGVFRFRGCGCGCASDGHISCPKFATHE	1 .		<b>,</b>	
VLUSKSRILOGFPERFSISSMI TOPKYFIK   1 831   FREMGDERPHYYGKHOTPOKYDTYNGCTDTICCVFLL	ļ	1	ļ	
6727 1 831 PREMISERPHYTIGHETPOKYDPTEKGPITNECCTULICCYPILL LAIVGYVAVOILAPTHGDPRKVIPPTDREGEFTOKOGGTKNENKEY YLFYTHTVKCASPLVILBERQCFTPQICCERCEPRILITIANARS RDPEYTKOPCVPGFKNNKGVARVILADGOCPAVILBERGLARRCEP PAHRAYKGVIAVGENETTYBOGHGSKRINTOLVSGARKANGGVIRA RQLAMRIFEDTYTVSHYNDIISLGJAMAMSLLFIILLRFLAGIMG RGMIIMGILVLGY FCSSWLRGIANSSISWKMYLVGLTGGIASGKSSVIQVPQQLGCA VIDVDUMARHVVQPGYPAHRRIVEVFGTBVLLSHODINRKVLGD LIFNQPBRQLIANATTHPBIRTKEMHKEFTKYFLRBERTSPRGKK HVPSALKRADSLMRRDT  6729 259 1191 VGLTGAQSGTTASMGRQAAVAGFALRRWLLLGTVTVGFLAQSV LAGVKKFDVPCGGRDCSGCCQCYPRKGGRGQPGPVSPGGYNGPP GLQGPFGLQGRKGDKGGRGAPGVTGPKGDVGARGVGPPAGDGT PGHEGGGGRGRPGPVGCCNSTCGDSGPGGPFOSPGGYGDPGQ PKGGKGPPYALDKERDRYRGEGGRGQCCNGPGFGFFGPOPQGQ PKGGKGPYALDKERDRYRGEGGRGQCCNGCPGGFGFGFTGPGQG PKGGKGPYALDKERDRYRGEGGRGPGVCFFCKGEKGDVQPGPN GIPSDTLHPILAPTGVTFHPDQYKGEKGSBGBPGRGQCGPPNSPGHQG RGPVALPKERVARAYBVLSNDEKRDIIVDKYGTGGINBF 6730 784 1015 NMUDYTEVLGIQRYASFEDIKKAYHKVALKMHPDKNPENKERAE RKFKEVARAYBVLSNDEKRDIIVDKYGTGGINBF 6731 1 446 GIRRILHGAVVPFUVOVGVCVFWFTTRSEGVHLKRPTSPLKNNDBGS LDTYAGLDSAVSDSASKSCVPSRNCLDLYBRILTREGTAKRATY NDLQVSYGKCQLQMKELMKKPREIQTQNFSLINENGSLKKNISA LIKTARVEINRKDBBI LIKTARVEINRKDBBI LASILRESSSTYTASTTIMAGGGRRARVERGWVYTYRAPIRE GRGFLAPQNGGSSDAPAYTFPPSRGCRREVFFSBRPHHFQB LASILRESSSTYTASTTIMAGGGRRARVERGWVYTYRAPIRE GRGFLAPQNGGSSDAPAYTFPPSRGCRREVFSBRPHHFQB PLVAKERSPVCKKTILLERFFISSSVTLBSFW SAMMFPVFSGCYNFSEGGERGERDDQDSSISSTTTVKARSKDSDRSG DKTTRSSSQYILSFW TRATSYQGCNAFFSEGREDDQDSSISSTSTTVKARSKDSDRSG DKTTRSSSGYTLSFW TRATSYQGCNAFFSERFRIDDGNSSISSTSTTVKARSKDSDRSG DKTTRSSSGYTLSFW TRATSYGGCNAFFORGESASDGHTSCPRFSILGRAGKSLSEDAX KKKGNRREDDVARSTVKRHLKTSGSCERKYKKSLBLSKEDLI QLLSIMEGELQARRDVHHMLKTSTKVEVLEAHLYGSASPEKULI VLIRNDALLAQRKSIGENVYKSPISSLORLEKKKYLTIKRHEPLKYER VLIRNDALLAQRKSIGENVYKSPISSLORLEKKKYLTIKRHEQL LLABCKHRRTYTELENBCHKKHTDYMNRSDDFTNLLEQERGREKKK LLEQERAYQARKE  6734 189 551 SAMMFPVFSGCPGELDEKNKSLELVSPERVAVHFTWEEWQDLDD	l	1	1	
LAIVGYVAVGI LAWTHGDPRKVIYPTDSRGEPCQQKGTKNENKP YLEYPHIVKCASPLVILLEFQCPTPQI CUSKCDRILITILARARS RDPEYYKQPCVPGFKRNKGVAPULRDGDCPAVILLESKPLARRCE PAHHAVKGVIMVGNETTYEDGHGSRKNITOLUGGAKKANGVIRA RQLAMRIPBDYTVSWYMDI ISLGYLAMAMSLLPI ILLRPLAGIMG RGMI IMGILVLGY RGMI IMGILVLGY CTSSWLESIANDSSISWKMYLVGLTGGIASGKSSVIQVPQQLGCA VIDVDWARHVVQPGYPAHRRI UVEVFGTRVLLENGD INRKVLGI LIFNQPDRRQLIMATTHPEI RKEMMKETFKYFLREPRTSPRGKK HVPSALKEADSLMRRDT  6729 259 1191 VGLTGAQSGRTASMGRDQRAVAGPALRRWLLLGTVTVGFLAQSV LAGVKKFDVPCGGRDCSGGCQCYPEKGGGCQPGPGPQGYNGPP GLOGFPGLGGRKGDKGBRGAPGFGDVGLAGRGVGPPGDQGYNGPP GLOGFPGLGGRKGDKGBRGAPGFGDVGLAGRGVGPPGDQGY PKGQKGBPGLGRKGDKGBRGAPGFGDVGLAGFQGPPGDQGY GTPSDTIHPI IAPTGVTPHPDQYKGRKGBSGPGPFGBPGLVGG GFWGARGRGPPGPPGFKGQCKNRGLGPYXVKGKRGDVGQPGN GIPSDTIHPI IAPTGVTPHPDQYKGRKGBSGPGPGFGHCGIN  6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKERAE RKFKBVARAYBVLSNDDKRDI JVKXCTTGGLANBF 6731 1 446 GIRKRILGGAVVPRVWGCPWBTRSSRGVHLREPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYBEI LITEGTARRATY NDLQVEYKGKQLQMKEILMKFRBIQTQNPSLINENGSLKKNI SA LIKTARVBUNKOBBI  6732 102 1205 GRRQRRPPPSPSPLWCLQPGGGSDPQQLTQLKHCLSHSPQDTW AGRQVCYTAATTQAADAPATRNCLDDISGRPPPPBSIRKHHIQRN LGS IKPSSRSTKATSTTMAGDGRRAEAVREGWGVYTPRAPIRE GRGHLAPQNGGSSDAPAYRTPPSRQGRREVRESDPPGVYGDDF PLAKERSPVGKKTILEBEPNSBGAKRVBRSDATYRRRGRROPP PQSTEEMMTNRTTHLQQQHSGPPLQPSPMTRRGLARDSHSSRB DEASSQTDLSQTI SKKTVRS IQBAPAVSBDLVTLKRRPPLRYPR YRATSVQCKVNFSBGSTERDDQDSSHSSVTTVKRRSCDDBSS DKTTRSSGYI HSFW  6733 613 1311 RSCGQWGMRSRNGCGESASDGHTSCPKPSI IGNAGKKSLSEDAK KKKSNRKEDDVMASGTVKRHLKTSGCERKTKKSLBLSKEDLI QLLS IMEGBLQARBUVIHMLKTEKTRPULBLERKKSLLSKEDLI QLLS IMEGBLQARBUVIHMLKTEKTRPULBLERKKSLLSKEDLI QLLS IMEGBLQARBUVIHMLKTEKTRPULBLERKKSLLSKEDLI ULRBCALAQBKGLEDVYNETI SERDHERGKOKSTYRRMI-EQL LLABKCHRTVYELLENEKHKHITDYMNKSDDFTNILLEQERERLKK LLABKCHRTVYELLENEKHKHITDYMNKSDDFTNILLEQERERLKK LLABKCHRTVYELLENEKHKHITDYMNKSDDFTNILLEQERERLKK LLABKCHRTVYELLENEKHKHITDYMNKSDDFTNILLEQERERLKK	L	<u> </u>		
### ### ##############################	6727	1 .	831	_
RDPEYYKQPCVPGFKNNKGNAEVLRDGDCPAVLIPSKPLARRCE PALHAYKGVLWGBETTYEDGHSRRNITUDVGGAKKANGVLEA RQLAMMIFBDYTVSWPDITSLGTAMMSLLFITLLERFLAGIMG RGMIIMGILVLGY  6728 486 935 FCSSWLRSLSWKMFLUGLTGGLASGKSSVIQVPQQLGCA VIDVDUMARHVQPGYPAHRRIVEVPGTEVLLENDGINRKVLGI LIFNQPDRRQLLMATTHPETRKEMMKETFKYFLREPRTSPRGKK HVPSALKBADSLMRRDT  6729 259 1191 VGLTGGAGGGRTASMGRQRAVAGPALERWLLLGTVTVGFLAQSV LAGVKKFDVPCGGRDCGGGCQCYPEKGGGCQPGPGPGDGYNGPP GLQGPPGLQGRCDKGBRGAPGFGDUOGAGGGPPGDGDYGP PCHCQGGPRGRPGYDGCNGTQGDSGPQGPPGPGGYNGPP GROCKGEPYALPKERRDRYRGEPGRPGLYFVCKGEKGDYPGDAGT GPURADCRCPPTADPERKGQCGPRGPGPGPGCGGCGPPGPGPGG PKGQKGEPYALPKERRDRYRGEPGRPGLYFVCKGEKGDWGQPGPN GIPSDTLHPILAPTGVTFHPDQYKGEKGBBGPGTRGISLKGEE GIM  6730 784 1015 NMUDYYEVLGLQRYASPEDLKKAYHKVALKWHPDKNPENKEKAE RKPKEVARAYEVLSNDEKRDIYDKYGTBGLNBP  6731 1 446 GIRKRLHGAVVPRVEVECEPWTRESSRVHLREPTSPLKNNDEGS LDIYAAGLDSAVGBASKSCVPSRNCLDLVEBTLITEGTTAKRATY NDLQVEXYGKCQLQMKELMKKFKBIQTQNPSLLINENQSLKKNISA LIKTARVEINRKOBEI  6732 102 1205 GRRGRRPPPPSPPLWCLQPGGGSDPQOLTQLEHCLSHSPQDTPW AQQCVCTTAATTQAADPATRNCLPDHSGRPPPPRSHRHHRQRN LGSIKPSSRSTKATSTTMAGGGRRAEVRESWYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQCRREVRESDEPEVYGDPE PLVAKERSPUGKRTLLERFRSDAKKEVRESWYVTFRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQCRREVRESDEPEVYGDE PLVAKERSPUGKRTLLERFRSDAKKEVRESWYVTFRAPIRE GRGRLAPQNGGSSDAPAYRTPSRQCPREVRSDEPEVYGDE PLVAKERSPUGKRTLLKFVRSIQERAPVSEDDVIKLRRPPLRYRR YBRTSVQQKVNPSBEGGFTERDDQDSSHSSVTTVKARSRDSRSG DKTTRSSQYIESFW  THATSVQQKVNPSBEGGFTERDDQDSSHSSVTTVKARSRDSBSG DKTTRSSQYIESFW  1311 RSCRQVGMSRRQGGESASDGHISCPKPSIIGNAGKKSLSEDAK KKKKSMRKEDDWASGTVKRHLKTSGECERKYKKSLELSKKDLI QLLSIMBGELQARBDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLRRDALLAQRKSIGEDVYSKPISBLDRLBEKQKETTRRMLEQL LLEQEKAYQARKE LLEQEKAYQARKE  6734 189 551 SAMMFFVFSGCPGGLQEKNKSLELVSFEKVAVHFTWEBEMQDLDD	ļ	ļ	ĺ	1
PATHAYKGYLMYCNETTYEDGRGSERNITDLVEGGAKRANGYLER RQLAMRI FBDYTVSWYMDI ISLGIAMAMSLLFI ILLEPIAGIMG RGMI INSILVLGY  6728 486 935 FCSSWLESIADSSLSWKWIVGLTGGIASGKSSVTÖVFQOLGCA VIDVDWARRHVVQPGYPAHRRIVEVFGTEVILENGD INRKVLGD LIFNQPDRRQLINATTHPE IRREMMKETFKYTJREPRTSPRGKK HVDSALKRADSLMRRDT  6729 259 1191 VGLTGGAGGGFTASMGEDQBAVAGPALRRWLLLGTVTVGFLAGSV LAGVKKFDVPCGGRCDGCGCQCYPEKGGRQPGPVGPQGYNGPP GLGOFPGLGGGGRGDGCGCGCQCYPEKGGRCQPGPVGPQGYNGPP GLGOFPGLGGGGRGDGFGGCGCCGCCAPEKGGRGPGPVGPQGYNGPP GLGOFPGLGGGGRGRGPGFUGCGCGNGGGPGPGCGCGCAPEKGGCGCGCGCCAPEKGGRGPGPVGPQGCPPGPQGCPPGCGCGCGCGCGCCCAPEKGGGGRGPGPGPGCGCGCGCGCCAPEKGGGGGGGGGGCGCCAPEKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	]			
RQLAMRIPBDYTOSWYWDIISLGYAMAMSLLPIILLRPLAGIMG RGMIIMSILVLGY GATINGIIVLGY FCSSWLRSIADSSLSWKWPLVGLTGGIASGKSSVTQVPQQLGCA VIDVDWARRRVVQPGYPAURRIVEGTEVLLEMGDINRKVLGD LIFNQPDERQLINAITHPEIRKEMKERFFFYFYLREPRTSPRGKK HVPSSALKRADSIMERDT  6729 259 1191 VGLTGAGSGRTASMGRQQAVAGPALRRWLLGTVTVGFLAGSV LAGVKKPDVPCGGRDCSGCQCYPKKGGRCQPGPVGPQGYNGPP GLGGFPGLQGRKGDKGBRGAPGVTGFKGDVGAGRGVSGFPGADGI PGHGQGGPRGPCGRKGDKGBRGAPGVTGFKGDVGAGRGVSGFPGADGI PKGKGEPYALPKERDRYRGEPERGLVGFQGPPGRPGHVCQM GPVGABGRGPPCPPGPPCPPCPCCCCMTGCGSGPGGSBGFTGPGPQGP GIPSDTIHPIIAPTGVTPHPDQYKGEKGSGBGPGIRSILKGEE GIM  6730 784 1015 MMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKERAE RKPKEVARAYEVLSNDEKRDIYDKYGTEGIABF  6731 1 446 GIRRILGAVVPRVEVGCPWFTRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYBEILTERGTAKRATY NDLQVEYGKCQLQMKELMKKPREIQTQMPSLINENQSLKRNISA LIKTRAVEINRKDBEI  6732 102 1205 GRRQRPPPPSPPLMCLQPGGGSDPQQLTQLKHCLSHSPQDTPW AQQVCYTAATTQAAPATKNCLPDHSGHRHPQRFNFRHIRQRN LGSIKPSSRSTKATSTIMAGDGRRAKAYREGWGVVTPRAPIRE GRGKLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDPE PLVAKERSPUGKKTILEBFRSDSAKERWFSBAYYHRRIGRD GRGKLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDPE PLVAKERSPUGKKTILEBFRSDSAKERWFSBAYYHRRIRGRN PQFTEEMKTHRTITLQQQHSGPPDPWTRRGLRGHSISSE DEASSQTDLSGTISKKTVRSIQBAPAVSEDLVIRLRRPFLRYPR YBATSVQQKWNFBBGGFTERDDQDSSHSSVTTVKARSRDSDSG DKTTRSSGQYISFW  6733 613 1311 RSCRQVGMRSRRQGGESASDGHISCPKPSIIGNAGKKSLSEDAK KKKKSNRKEDDWARSGTVKRHLKTSGCCERKTKKSLELSKEDLI QLLSIMBGBLQAREDVIHMLKTSKTKPSVLEAHVGSAEPEKVLE VLRRDAILAQEKSIGEDVYEKPISEGLERTKKSSLELSKEDLI VLRRDAILAQEKSIGEDVYEKPISEGLERTKKSSLELSKEDLI LLAEKCHRRTVYELENEKHKHTTDYMNKSDDFTNILLEQERERLKK LLEQEKNYQARKE	1	1	1	
RGMIIMGILVLGY  6728 486 935 FCSSWLSSMKMYLVGLTGGIASGKSSVTQVFQQLGCA VIDVUMARRVVQPGYPAHRRIVEVFGTEVLLBNGDINRKVLGD LIFNQPDRRQLLNAITHPEIRKEMMKETFKYFLREPRTSPRGKK HVDSALKRADSLMRRDT  6729 259 1191 VGLTGAQSGRTASMGEDQRAVAGPALRRWLLIGTVTVGFLAQSV LAGVKKFDVPCGGRCDGCGCQCYPEKGGRQPGPVGPQGYNGPP GLGOFPGLGGRKGDKGBRGAPGVTTGPKGRUDARGVSGFPGADGI PGHEGGGFRGFGPGYDCCMGTGDSGPGGPGSSGFTGNPGPQG PKGQKGEPYALPKERDRYRGEPGBPGLVGFQGPPGRPGVQM GPVGADGRGPPGLDGKGQCGNRGLGFYGVKGKKGDVGQPGNN GIPSDTLHPILAPTGVTFHPDQYKGKGGSBGBPGIRGISLKGEE GIM  6730 784 1015 NMVDYYEVLGLQRYASPEDLKKAYHKVALKWHPDKNPENKERAE RKPKEVAEAYBVLSNDEKRDI YDKKGTEGIMBF  6731 1 446 GIRRRLHGAVVPRVEVGCPWETTRESGVHLERFTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYBEILTEGTTARRATY NDLQVEYGKCQLQMKSLMKKPKRIQTQMPSLINENQSLKKNISA LIKTARVEINRKDEL  6732 102 1205 GRWGRRPPPSPPLWCLQPGGGSDPQOLTDLHCLSHSPQDTPW AQRQVCYTAATTQAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRARAVREXWGVYVTPRAPIRE GRGRLAPQWGSSDAPAYRTPPSGGREVWFSDEPBSVYGDEP PLVAKERSPVGKTRLBEFFSDSAKEVPSAYTLRSRGRRQPR PQSTEEMKTRRTTRLQQHSGQPPPLQPSPWMTRRGLBGISSSE DEASSQTDLSQTISKKTVRSIQBAPAVSEDJVIRLRRPPLRYPR YRATSVQQKNNPSBEGBTERDDQDSSHSSVTTVKARSRDSRSG DKTTRSSSQYISKFW TRATSVQCKNPTSBEGETREDDQDSSHSSVTTVKARSRDSBSG DKTTRSSSQYISKFW VLHRDAILAQEKSIGEDVYEKPISLGRKKKSLKLSKEDLL VLHRDAILAQEKSIGEDVYEKPISLGRKKKSLKLSKEDLK LLEGERKYQARKE  6734 189 551 SAMMFVVFSGCQELGEKNKSLELVVSPRRVAVHFWEBWQDLDD	}		ł	)
6728 486 935 PCSSWLRSLADSSLSWKMFLVGLTGGIASGKSSVTQVFQQLGCA VIDVDWARRIVVOPGYPAHRRIVEVPTBYLLENGDINRKVLGBI LIFNQPRRQLIANATTHPELTRKEMMKETFKYFLREPRTSPRGKK HVPSALKRADSLMRRDT  6729 259 1191 VGLTGAQSGRTASMGRDQRAVAGPAHRRWLLGTVTVGFLAQSV LAGVKKFDVPSGGRCGGGCCYPEKGGGQFGPVGPQGYNGPP GLQGPFGLQGFKGDKGEGCCYPEKGGRGPGGPFGBGGFGPGDGGP PKGQKGBPALPKERDRYRKGEPGEPGLVGFQPFRCPGWGM PPKGQKGBPALPKERDRYRKGEPGEPGLVGFQPFRCPGWCGM GPVGAPGKGPPGPPGPPGPPGPWCGM GPVGAPGRGPPGPPGPPGPPGPPGPWGGM GPVGAPGRGPPGPPGPPGPPGPWGGM GPVGAPGRGPPGPPGPPGPPGPPGPPGPPGPGPGPGPGPGPGP	Į.		Į	I
VIDVDWARRHVVQPGYPAHRRIVENFGTEVLLENGDINKKVLGD LIFNQPDRRQLIMAITHPETRKEMMKETFKYFLREPRTSPRGKK HVPSPALKRADSLMRDT  6729 259 1191 VGLTGAQSGETASMGRDQRAVAGPALRRWLLIGTVTVGFLAQSV LAGVKKFDVPCGGRDCSGGCQCYPEKGGRQCQPOPGQGYNGPP GLQGFPGLQGFRGCKGCKGRGRGAAPGVTGPKGDWGARGVSCFPGADGI PCHRGQGGPRGRRGYDGCNGTQGDSGPQGPPGSEGFTGPPGQG PKGQKGBPYALPKERDRYRGEPGEPGLVGFQCPCPRCPGHVCQM GPVGAPGRPGPPGPPGPKGQQCRRGLGPYGVKGKGKGDWGQPGPN GPSDTHFPLIAPTGVTFHPDQYKGKGKGSGDWGQPGPN GPSDTHFPLIAPTGVTFHPDQYKGKGKGSGBFGIGSLSKGER 6730 784 1015 NMVDYYEVLGLQRYASPEDLKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYEVLSNDEKRDIYDKXGTEGINEF 6731 1 446 GIRKILIGAVVPRVEVVCPWETTRESEGVHLÆRPTSPLKNNDEGS LDTYAGLDSAVSSDASKSCVPSRNCLDLYEELTREGTAKEATY NDLQVEYGKCQLQMKEIMKKPKELQTQNFSLINENQSLKKNISA LIKTARVEINRKDEBI 6732 102 1205 GRØGRPPPPSPPLWCLQPGGGSDPQOLTQLEHCLSHSPQDTPW AQRQCYTAATTOAAAPATRACLPDHSGREPTPPRSHRHHRQRN LGSIKPSSRSTKATSTIMAGDGRRAKAVRESWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGREVWFSDRPPEVYGDPE PLVAKERSPUGKRYTLÆPBPSDSAKBRVRSSAYTLRSRQRRQRR PQSTEEMKTRRTTRLQQUISGQPPLQPSPVMTRRGLRDSHSSRE DEASSGTDLSGTISKKTVRSIQRAPAVSEDLVTRLRRPPLRYPR YRATSVQQKVNPSBEGBTERDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYISSFW  6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPRPSIGNAGKKILSEDAK KKKKSRRKEDDWASGTVKRHLKTSGECERKTKKSLELSKEDLI ULISIMGGELQAREDVIHMLKTRKTREPLEATIVGSAEPEKVLR VLHRDAILAQEKSIGBDVYEKPISBLDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELEWKHKITDYMNSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAMFPVFSGCCQELQEKNKSLELVSPRRVAFFWERWQDLDD				
LIFNOPDRRQLLNAITHPEIRKEMMKETFKYFIRBPRTSPRGKK HVSSALKEADSLMRRDT  G729  25.9  1191  VGLTGAGSGERTASMGTORGRAVAGPALIRRWLLLGTVTVGFILAGSV LAGVKKFDVPCGGRDCEGGCQCYPEKGGRGOPGPVGPQGYNGPP GLOGPPGLOGRKGDKGBRGAPGVTDFKGDVGARGVSGPPGADGI PGHPGQGGPRGPHGLOGRGDKGBRGAPGVTDFKGDVGARGVSGPPGADGI PGHPGQGGPRGPHYDCMGTGTGGDSGPQGPPGSPGFPGPQG PKGQKGBPYALPKERRDRYRGEFGSPGLVGFGGPPGRPGHVCQM GPVGAPGRPGPPGPPGPRGQQCNRGLGPYGVKGKKGDVGQPGPN GIPSDTHIPIIAPTGVTFHPDQYKGEKGBGBGPGISLKGEE GIM  6730  784  1015  NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKGVAEAYEVLSNDKKRDIYDKYGTBGLNSF GIRKILHGAVVPRVEVGCPWFTTESEGVHLRFPTSPLKNNDEGS LDTYAGLDSAVSDSASKSCVPSRNCLDLYEBILITERGTAKRATY NDLQVKYGKCQLQMKELMKKPKBIQTQNFSLLINENQSLKKNISA LIKTARVEINRKDESI GRWGRPPPPSPPLWCLQPGGGSDPQOLTQLRHCLSHSPQDTFW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSTSTKATSTIMAGDGRRAKAVRESWGVVVTPRAPIRE GRGKLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDPB PLVAKERSPVGKKTRLEBFRSDSAKERVRESAYYLKSRGRRQFR PQSTEEMKTRRTTILQQHSEQPPLQPSPWMTRRGLRDSHSSBE DEASSQTDLSQTISKKTVRSIQBAPAVSEDLVIRLRRPPLRYPR YBATSVQQKVMPSBEGGFERDDQDSSHSSVTTVKARSRDSBSSG DKTTRSSQYIESFW  6733  613  1311  RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGKKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLBLSKEDLI QLLSIMBGRLQARBDVIHMLKTEKTKPRFLEAHYGSABPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLABKCHRRTVYTLEMEKHKHTDTMNKSDDFTNLLEQERERLKK LLEGEKAYQARKS LLABKCHRRTVYTLEMEKHKHTDTMNKSDDFTNLLEQERERLKK LLEGEKAYQARKS	6728	486	935	
HVPSALKEADSLMERDT  6729  259  1191  VGLTGAGGERTASMGRDQRAVAGPALIRRWLLLGTVTVGFLAQSV LAGVKKFDVPCGGRDCSGCQCYPKKGGRQPGPVGPQGVNGPP GLQGFPGLQGKKGKKGKGRGAPGVTGPKGDVGARGVGFPGADGI PGHGQGGPRGRPGTGCGGTQGTGGGGDGQGGPGSKGFTGPPGPQG PKGQKGEPYALPKEERDRYRGEDGGPQCDFGSKGFTGPPGPQG PKGQKGEPYALPKEERDRYRGEDGGPQGVGKGKGBUGPGPVGPQGP GFPGADGRPGPCPPGPFKGQQCNRGLGFYGVKGKKGDVGQPGPN GFPGADGRPGPPCPPGFKGQQCNRGLGFYGVKGKKGDVGQPGPN GFPGADGRPGPPCPPGFKGQQCNRGLGFYGVKGKKGDVGQPGPN GFPGADGRPGPPCPPGFKGQQCNRGLGFYGVKGKKGDVGQPGPN GFPGADGRPGPPCPPGFKGQQCNRGLGFYGVKGKKGDVGQPGPN GFPGADGRPGPPCPPGFKGQQCNRGLGFYGVKGKKGDVGQPGPN GFPGADGRPGPPCPPGFKGQQCNRGLGFYGVKGKKGDVGQPGPN GFPGADGRPGPPCPFKGQQCNRGLGFYGVKGKKGDVGQPGPN GFPGADGRPGPPCPFFKGCQCNRGLGFYGVKGKKADFKKEAE RKPKEVABAYEVLSNDEKRD I YDKYGTEGLNEF FRAFKATARAYE INRKDEBI GFRALMGAVVPRVEVGCPWFTTRESGGVHLKEPFTSPLKNNDEGS LLYTARVE INRKDEBI GROWRFPPPSPPFLWCLQPGGGSDPQQLTQLRHCLSHSPQDTFW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQBN LGSIKPSSRSTKATSTINAGGGRRARAVREGKVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPBVYGDFE PLVAKERSPUSKRTRLEBFSDSAKEEVRESAYYIKSRQRQFQFR PQETEEMKTRRTTRLQQHGSQFPLQPSPWTTKRGLRDSHSSEB DEASSQTDLGGTISKKTVRSIQGABAYSTTVKARSRDSDKSG DKTTRSSQYIESFW GTATASSQVIESFW GTATASSQVIESFW GTATASSQVIESFW UKHDAILAQEKSIGEBVYEKPISELGRLEKKKLELSKEDLI ULLSKKCHRRTVYSLENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEGEKAYQARKB LLABKCHRRTVYTLENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEGEKAYQARKB GT34  189  551  SAMMFPVFSGCPQELQEKNKSLELVSPRRVAFFTWEEWQDLDD	ļ		<b>(</b>	
1191 VGLTGAQSGRTASMGRDQRAVAGPALRRWLLLGTVTVGFLAQSV LAGVKKPTVPCGGGRCGGGCQCYPEKGGRCQPGPVGPQGYNGPP GLQGPPGLQGRKGDKGBRGAPGVTGPKGDVGARGVSGFPGADCI PGHPGQGSPRGREPGPGCCKGTQCDSGPQGBPGSKGFTGPPGPQG PKGQKGBPYALPKERRDRYRGEEGEPGLVGFQGPPGREGHVCQM GPVGAPGRPGPPGPCPGKGQQCNRGLGFYGVKGEKGDVGQPGPN GIPSDTLHP11APTGVTFHPDQVKGEKGSBGBPGFRGISLKGEE GIM  6730 784 1015 NMVDYYEVLGLQRYASPEDLKKAYHKVALKMHPDKNPENKEEAE RKFKEVAEAYBVLSNDEKRD1YDKYGTEGLNEF 6731 1 446 GIRRILHGAVVPRVEVGCWETTESBGVHLERPTSPLKNNDEGS LDYAGLDSAVSDSASKSCVPSRNCLDLYBEILTREGTAKEATY NDLQVBYGKCQLQMKELMKKPKELQTQNFSLLINENQSLKKNISA LIKTARVEINRKDBEI LDYAGLDSAVSDSASKSCVPSRNCLDLYBEILTREGTAKEATY NDLQVBYGKCQLQMKELMKKPKELQTQNFSLLINENQSLKKNISA LIKTARVEINRKDBEI GRGRLAPQINGGSDAPATROCLDHSGHPPTPPRSHRHHRQBN LGSIKPSSRSTKATSTIMAGDGRRAKAVREGWGVYVTPRAPIRK GRGRLAPQINGGSDAPATRTPSRQGRREVFFSDEPPBVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKERVRESBEPPBVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKERVRESBEPPBVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKERVRESBEPPBVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKERVRESBEPBPBVGPR YBATSVQQKVMFSEEGETEEDDQDSSISSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSBNQGGESASDGHISCPKPSIIGNAGKKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLBLSKEDLI QLLSIMBGRLQARBDVIHMIKTEKTKSECERKTKKSLBLSKEDLI QLLSIMBGRLQARBDVIHMIKTEKTKSECERKTKKSLBLSKEDLI ULLBGEKAYQARGE ULLBGEKAYQARGE LLABKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEGERBLKK LLEGEKAYQARGE 6734 189 551 SAMMFPVFSGCPQELQEKNKSLELVSPRVAVHFTWEEWQDLDD			ł	
LAGVKKPDVPCGGRDCGGCQCYPEKGGRGQPGPVGPQGYNGPP GLQGYPGLQGRKGDKGBRGAPGVTGPKGDVGARGVSGPPGADGI PGHPGQGGPPGLQGRKGDKGBRGAPGVTGPKGDVGARGVSGPPGADGI PGHPGQGGPRGRPGYDGCKGTQGDSGPQGPPGSBGFTGPPGPQG PKGQKGBPYALPKEERDRYRGEPGEPGLVGFQGPPGRPGHVGM GPVGAPGRPGPPGPPGPGPGPGPGRGQQCRRGLGFYGVKGRKGDVQPGPN GIPSDTLHPIIAPTGVTFHPDQVKGBKGSBGBPGIRGISLKGEE GIM  6730 784 1015 NMVDYYEVLGLQRYASPEDLKKAYHKVALKMHPDKNPENKEEAE RKPKEVAEAYBVLSNDEKRDIYDKYGTEGLNBF 6731 1 446 GIRRILHGAVVPBVEVGCVWETTRSEGVHLÆRPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYBBILTBEGTAKEATY NDLQVBYGKCQLQMKELMKKPRBIQTONPSLINKNQSLKKNISA LIKTARVEINRKDEBI 6732 102 1205 GRØGRPPPPFSPPLMCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTINAGDGRRAKAVRESWGVVVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQCRREVRFSDEPPEVYDDFB PLVAKERSPUCKKTRLEBFRSDSAKBBVRESAYYLASRQRQFR PQETEEMKTRRTTRLQQUBSQPPLQPSPVMTRRGLRDSHSSEB DEASSQTDLSGTISKKTVRSIQBAPAVSEDLVIKLRRPPLRYPR YBATSVQQKVNFSBEGSTEEDDQDSSHSSVTTVKARSRDSDSG DKTTRSSSQYIESFW 6733 613 1311 RSCCWGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLBISKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLRRDAILAQEKSIGGDVYEKPISBLDRLEKKOKETYRRMLÆQL LLSQEKAYQARKB 6734 189 551 SAAMFPVFSGCPQELQEKNKSLELVSPERVAVHFTWEBWQDLDD				
GLQGPPGLQGRKGDKGERGAPGVTGPKGDVGARGVSGPPGADGI PGHPGQGGPRGRPGYDCCNGTYGDGSGPQGPGSEGFTGPPGPGG PKGQKGEPYALPKERDRYRGEPGEPGLVGPQGPPGFRHVGQM GPVGAPGRPGPPCPKGQQCRRGLGFYGVKGEKGDVGQPGPN GIPSDTLHP!LAPTGVTFHPDQYKGEKGSBGBPGIRGISLKGER GIM  784  1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYBVLSNDEKRD!YDKXGTEGINBF  6731  1 446 GIRKILHGAVVPRVEVGCPWETRESBGVHLRRPTSPLKNNDEGS LDTYAGLDSAVSDSASKSCVPSRNCLDLYBBILTEEGTAKRATY NDLQVEVSKCQLQMKELMKKPREIQTQNPSLINKNQSLKKN!SA LIKTARVEINRKDEBI  6732  102  1205 GRWGRPPPPSSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATKNCLPDHSGHRPTPPRSHRHHRQBN LGSIKPSSGSTKATSTIMAGDGRRAEAVREGWGVVYTRAPTRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVKFSDEPPEVYGDFB PLVAKERSPVGKRTHLREPRSDSAKERVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSES DKTTRSSSQYIRSFW  78ATSVQQKVNFSBEGETERDDQDSSHSSVTTVKARSRDSGG DKTTRSSSQYIRSFW  6733  613  1311 RSCRQVGMSRRQGGESASDGHISCPKPSIIGNAGKKSLSDDAK KKKKSNRKEDDVMASGTVKRHLKTSGECRKKTKKSLBLSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLRRDATLAQEKSIGEDVYSKPISBLDRLBEKGKETYRRMLEQL LLABKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQBKAYQARKE  6734  189  551 SAMMFPVFSGCPQELQEKNKSLELVSFERVAVHFTWEEWQDLDD	6729	259	1191	
PGHPGQGGPRGRPGYDGCNGTCGDSGPQGPGSEGFTGPPGPQG PKGQKGBPYALPKERDRYRGEPGBPGLUGFQGPPGRPGHVGQM GPVGAPGRPGPPCPPGPKGQQGNRGLGFYGVKGKGDVGQPGPN GIPSDTLHPILAPTGVTFHPDQYKGEKGBVGQPGPN GIPSDTLHPILAPTGVTFHPDQYKGEKGBVGGPGRGLSLKGER GIM  6730 784 1015 NMVDYYEVLGLQRYASSPEDLKKAYHKVALKWHPDKNPENKERAE RKPKEVAEAYBVLSNDEKRDIYDKYGTEGLNBF 6731 1 446 GIRKTLHGGAVVPRVEVGCPWRTTRESGVHLKRPTSPLKNNDEGS LDTYAGLDSANSDSASKSCVPSRNCLDLYBRITTERGTAKRATY NDLQVEYGKCQLQMKELMKKPKBIQTQNPSLINKNQSLKKNISA LIKTARVEINIKDBI  6732 102 1205 GRWQRPPPPSPLUCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATKNCLPDHSGRRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPSRQCRREVRSDEPPSVYGDFB PLVAKERSPUGKRTRLEBPRSDSAKEBVRESAYYLRSRQRRQPR PQSTEEMKTRRTTRLQQUHSEQPPLQPSPWMTRRGLADSHSSBE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YBATSVQQKVMPSBEGGBTERDDQDSSHSSVTTVKARSRDSDBSG DKTTRSSQYIBSFW  6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGKKSLSEDAK KKKANKENEDDWASGTVKRHLKTSGECRKYTKKSLELSEDAK KKKSNKREDDWASGTVKRHLKTSGECRKYTKKSLELSEDAK VLKRDATLAQEKSIGBDVYBKPISBLDRLBEKQKETTRRMLEQL LLABEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLABEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQBKAYQARKE  6734 189 551 SAAMFPVFSGCPQELQEKNKSLELVSPERVAVHFTWEEWQDLDD	1	1	Į.	
PKGQKGEPYALPKEERDRYRGEPGEPGLVGFQGPPGRPGHVGQM GPVGAPGRPGPPGPPGPRGQQGRRGLGFYGVKGEKGDVGQPGPN GIPSDTLHPI LAPTGVTFHPDQYKGEKGBEGBFGIRGISLKGEB GIM  6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVABAYBVLSNDLKRGI YDKYGTEGLNRF 6731 1 446 GIRKRLHGAVVPRVEVGCPWETREBGVHLERPTSPLKNNDEGS LDLYAGLDSAVSDSASKSCVPSRNCLDLYBBILTREGTAKRATY NDLQVEYGKCQLQMKELMKKPKBIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEBI 6732 102 1205 GRWQRPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTOAAAPATKNCLPDHSGHRPTPPRSHRHHQBN LGSIKPSSRSTKATSTIMAGDGRRAKAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRESDEPPSVYGDFB PLVAKERSPUGKKTRLEEFRSDSAKEBVRESAYYLARGQRRQOPR PQETEEMKTRRITTRLQQQHSEQPPLQPSPVMTRRGLGDSHSSBE DEASSQTDLSQTISKKTVRS IQBAPAVSEDLVIRLRRPPLRYPR YBATSVQQKVNPSBEGETERDDQDSSHSSVTTVKARSRCRQFR PRETSSSQYISSFW 6733 613 1311 RSCRQVGMSRNQGGESASDGHISCPRPSIIGNAGKKSLELSKEDLI QLLSIMEGBLQAREDVIHMLKTEGECERKTKKSLELSKEDLI QLLSIMEGBLQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLARDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLSCHAYQAKKB 6734 189 551 SAMMFPVFSGCPQELQEKNKSLELVSPREVAVHFTWEEWQDLDD	[			
GPVGAPGRPGPPGPPGPKGQQGNRGLGFYYGVKGEKGDVGQPGPN GIPSDTLHP1IAPTGVTFHPDQYKGEKGSBGBPGIRGISLKGEE GIM  6730 784 1015 NMVDYYEVLGLQRYASPEDLKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYBVLSINDEKRDIYDKYGTEGLNEF RKFKEVAEAYBVLSINDEKRDIYDKYGTEGLNEF 6731 1 446 GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDTYAGLDSAVSDEASKSCVPSRNCLDLYBEILTEEGTAKRATY NDLQVBYGKCQLQMKELMKKFKEIQTQNPSLINENQSLKKNISA LIKTARVEINNKDBEI 6732 102 1205 GRWQRPPPPSPPLWCLQPGGGSDPQLTQLKHCLSHSPQDTPW AQRQVCYTAATTQAAAPATKNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAKAVRESWGVVVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVFSBEPPEVYGDFE PLYAKERSPUGKRTRLEEFRSDSAKEBVRESAYYLBSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YBATSVQQKVNFSEBGBTERDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 ESCRQVGMSSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLBLSKEDLI QLLSIMEGBLQARBDVIHMLKTEKTRPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVZKKPISELDRLEEKQKETYRRMLEQL LLABKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLABKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLABKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK	l		1 .	
GIPSDTLHPILAPTGVTFHPDQYKGEKGSBGEPGIRGISLKGEE GIM  6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKPKEVAEAYBVLSNDEKRDIYDKYGTEGLNEF 6731 1 446 GIRKRLHGAVVPRVEVGCPWRTRESEGVHLERPTSPLKNNDEGS LDTYAGLDSAVSDSASKSCVPSRNCLDLYBEILTEEGTAKEATY NDLQVEYGKCQLQMKELMKKFREIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEBI 6732 102 1205 GRWQRPPPPSPPLWCLQPGGGSDPQOLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATKNCLPDHSGHRPTPPRSHRHHRQBN LGSIKPSSRSTKATSTIMAGDGRRAEAVRESWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFB PLVAKERSPVGKRTRLEEPRSDSAKEBVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQRSGPPLQPSPWHTRRGLRDSHSSBE DEASSQTDLSGTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YBATSVQQKVNFSBEGETEEDDQDSHSSVTTVKARSRDSDESG DKTTRSSSQYIBSFW 6733 613 1311 ESCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLBLSKEDLI QLLSIMEGGLQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLABKCHRRTVYELENEKHKHITDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCPQELQEKNKSLELVSFREVAVHFTWEBWQDLDD		1	}	
GIM  6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYBVLGNDEKRDIYDKVGTEGLNEF  6731 1 446 GIRKRIHGAVVPRVEVGCPWETTESEGVHLEFFTSPIKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYBEILTEEGTAKRATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEBI  6732 102 1205 GRWGRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATKNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREEWGVVTVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVKFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEPRSDSAKEBVRESAYYLRSRQRRQPR PQSTEEMKTRRTTHLQQQHSEQPPLQPSPWMTRGLRDSHSSEE DEASSQTDLSQTISKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YBATSVQQKVNFSBEGSTEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYISSFW  6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLBLSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLABKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLABCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLABCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLABCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK	ļ	į.	ļ	
6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKPKEVAEAYBVLSNDEKRDIYDKYGTEGLNEF 6731 1 446 GIRKRIHGAVVPRVEVGCWETTRESECVHLERPTSPIKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYBEILTREGTAKEATY NDLQVEYGKCQLQMKELMKKPKEIQTQNPSLINRNQSLKKNISA LIKTARVEINRKDEBI 6732 102 1205 GRWQRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAPATKNCLPDHSGREPTPPRSHRHHQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRGKLAPQWGSSDAPAYRTPPSRQGRREVKFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSBE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPPLRYPR YBATSVQQKVNPSEEGSTEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYLBSFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGKKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLBLSKEDLI QLLSIMEGGLQARBVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLABKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLABCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLABCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLABCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK				_ ;
RKPKEVABAYBULSNDEKRD I YDKYGTEGLNEF  6731 1 446 GIRKRLHGAVUPRVEVGCPWRTRESEGVHLERPTSPLKNNDEGS LDTYAGLDSAVSDASAKSCVPSRNCLDLYBE ILTEGTAKRATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEBI  6732 102 1205 GRWQRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATKNCLPDHSGHPPTPPRSHRHHQEN LGSIKPSSRSTKATSTIMAGDGRRAKAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGREVFSDEPPEVYGDFE PLVAKERSPUGKRTRLEEFFRSDSAKEEVRESAYYLKSRQORQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEB DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLERPPLRYPR YBATSVQQKVNPSEEGETEKDDQDSSHSSVTTVKARSRDSDRSG DKTTRSSQYIESFW  6733 613 1311 BECRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQARBOVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VUHRDAILAQEKSIGEDVYSKPISELDRLEEKQKETYRRMLEQL LLABKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLABCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLABCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK	2770	704	1015	
6731 1 446 GIRKRLHGAVVPRVEVGCPWRTRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYBEILTREGTAKEATY NDLQVBYGKCQLQMKEIMKKPKEIQTQNFSLINKNQSLKKNISA LIKTARVEINRKDEBI 6732 102 1205 GRWQRPPPPPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATKNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAKAVREGWGVVVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGREVRFSDEPPEVYGDFB PLVAKERSPUGKTTRLEEFRSDSAKEBVRSSAYYLBSRQRRQPR PQETEEMKTRRTTRLQQUSSQPPLQPSPVMTRRGLRDSHSSEB DEASSQTDLSQTISKKTVRSIQEAPAVSPDLVIRLRRPPLRYPR YBATSVQQKVNPSBEGBTERDDQDSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLBLSKEDLI QLLSIMEGELQAREDVIHMLKTBKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLABCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFRRVAVHFTWEBWQDLDD	0/30	/84	1012	No. 1 Control of the
LDIYAGLDSAVSDSASKSCVPSRNCLDLYBEILTBEGTAKEATY NDLQVEYGKCQLQMKELMKKPKEIQTQNPSLINENQSLKENISA LIKTARVEINENDEBI  6732 102 1205 GEWQRRPPPSPPLWCLQPGGGSDPQQLTQLEHCLSHSPQDTPW AQRQVCYTAATTQAAAPATKNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAKAVRESWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGREVRFSDEPPEVYGDFB PLVAKERSPVGKRTRLEEPRSDSAKEBVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPWHTRGLEDSHSSES DEASSQTDLSGTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVMPSEEGSTEEDDQDSHSSVTTVKARSRDSDESG DKTTRSSSQYIBSFW  6733 613 1311 ESCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLBLSKEDLI QLLSIMEGGLQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLABKCHRRTVYELENEKHKHITDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCPQELQEKNKSLELVSFREVAVHFTWEEWQDLDD		<del> </del>	l	L
MDLQVEYGKCQLQMKELMKKPKEIQTQNPSLINENQSLKKNISA LIKTARVEINRKDEBI 6732 102 1205 GRWGRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATKNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRARAVRESWGVVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEPRSDSAKEBVRESAYYLRSRQRRQPR PQSTEEMKTRRTTRLQQQHSGQPPLQPSPWHTRGLRDSHSSEE DEASSQTDLSQTISKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YBATSVQQKVNPSBEGSTERDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIBSFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSISEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLBLSKEDLI QLLSIMEGGLQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLABKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLSQEKAYQAKKS 6734 189 551 SAAMFPVFSGCPQELQEKNKSLELVSFREVAVHFTWEBWQDLDD	0/31	1 1	440	
LIKTARVEINKÜBEI  6732 102 1205 GRWQRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATKNCLPDHSGHRPTPPRSHRHHIQEN LGSIKPSSRSTKATSTIMAGDGRRAKAVREGWGVYVTPRAPIRE GRGRLAPQMGGSDAPAYRTPPSRQGRREVRFSDRPPEVYGDFE PLVAKERSPVGKRTRLEEPRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSBE DEASSQTDLSQTISKKTVKSIQBAPAVSEDLVIRLKRPPLRYPR YBATSVQQKVNPSEEGSTEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIBSFW  6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGKKSLSEDAK KKKKSNRKEDDVMASGTVKRLLKTSGECERKTKKSLBLSKEDLI QLLSIMEGGLQARBVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLABKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLSQEKAYQARKS 6734 189 551 SAAMFPVFSGCPQELQEKNKSLELVSFRRVAVHFTWEBWQDLDD	1	1	1	
6732 102 1205 GRWORRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPPHSGHRPTPPRSHRHHIQEN LGSIKPSSRSTKATSTIMAGDGRRAKAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAAPAYRTPPSRQGREVFSDEPPEVYGDFE PLVAKERSPUGKRTHLEFFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YBATSVQQKVNPSEEBFEEDDQDSSHSSVTTVKARSRDSDRSG DKTTRSSSQYIESFW 6733 613 1311 BSCRQVGMSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVZEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKB 6734 189 551 SAAMFPVFSGCPQELQEKNKSLELVSFRRVAVHFTWEEWQDLDD	{	<b>f</b>		
AQRQVCYTAATTQAAAPATKNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAKAVRESWGVYVTPRAPIRE GRGKLAPQWGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLKSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLKDSHSSEB DEASSQTDLSGTISKKTVRSIQEAPAVSEDLVIRLKRPPLRYPR YBATSVQQKVNPSEGBTEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW  6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRREDDVMASGTVKRHLKTSGECERKTKKSLBLSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHVGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE  6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWQDLDD	<u> </u>		1 1525	
LGSIKPSSRSTKATSTIMAGDGRRAKAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGREVRFSDEPPEVYGDFE PLVAKERSPUGKRTTRLEEFRSDSAKERVRSAYYLASRQRRQPR PQETEEMKTRRTTRLQQQHSQPPLQPSPVMTRGLKDSHSSEE DEASSQTDLSGTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YBATSVQQKVNPSBEGBTERDDQDSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW  6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLBLSKEDLI QLLSIMEGELQAREDVIHMLKTBKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLABKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWQDLDD	6/32	102	1302	
GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEPRSDSAKEBVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQRISEQPPLQPSPWMTRGLRDSHSSBE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNPSBEGSTERDDQDSHSSVTTVKARSRDSDESG DKTTRSSSQYIBSFW  6733 613 1311 ESCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLBLSKEDLI QLLSIMEGRIQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLABKCHRRTVYELENEKHKHITDYMNKSDDFTNLLEQERERLKK LLSQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWQDLDD		1		
PLVAKERSPUGKRTRLEEPRSDAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRGLRDSHSSBE DEASSQTDLSQTISKKTVRSIQBAPAVSEDLVIRLRRPPLRYPR YBATSVQQKVNPSBEGETEKDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIBSFW  6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLBLSKEDLI QLLSIMEGGLQARBVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLABKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLSQEKAYQARKB 6734 189 551 SAAMFPVFSGCPQELQEKNKSLELVSFRRVAVHFTWEBWQDLDD		ļ		t i
PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEB DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YBATSVQQKVNPSEBEGETERDDQDSSHSSVTTVKARSRDSDRSG DKTTRSSSQYIESFW  6733 613 1311 BSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLABKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKB  6734 189 551 SAAMFPVFSGCPQELQEKNKSLELVSPRRVAVHFTWEEWQDLDD	1	I		· · · · · · · · · · · · · · · · · · ·
DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNPSBEGETERDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIBSFW  6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLBLSKEDLI QLLSIMEGBLQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISBLDRLBEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKB  6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFREVAVHFTWEBWQDLDD	1	1	}	
YBATSVQQKVNPSEEGETERDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLBLSKEDLI QLLSIMEGRLQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLABKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWQDLDD	5	}	ļ	
DKTTRSSQYIESFW  6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTGGECERKTKKSLBLSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE  6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFRRVAVHFTWEEWQDLDD		1		
6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSISEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLISIMEGELQAREDVIHMIKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKB 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFRRVAVHFTWEEWQDLDD	i			
KKKKSNRKEDDVMASGTVRHLKTSGECERKTKKSLBLSKEDLI QLLSIMEGELQAREDVIHMIKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLABKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFREVAVHFTWEEWQDLDD		1		
QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCPQELQEKNKSLELVSFREVAVHFTWEEWQDLDD	6733	613	1311	
VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCPQELQEKNKSLELVSFREVAVHFTWEEWQDLDD		l		
LLABKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFRRVAVHFTWERWQDLDD		1		
LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFRRVAVHFTWERWQDLDD	l	1	}	
6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFRRVAVHFTWREWQDLDD	1	<b>!</b>		
	L			
AQRTLYRDVMLRTYSSLVSLGHCITKPEMIFKLEQGAEPWIVEE	6734	189	551	
	L	1		AQRTLYRDVMLETYSSLVSLGHCITKPEMIFKLEQGAEPWIVEE

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
]	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	веquence		\=possible nucleotide insertion)
			TLNLRLSGGSKKQVFSGICHRSLVELQEVHLV
6735	280	558	KSRRAGVTKMSNPFLKQVFNKDKTFRPKRKFEPGTQRFEIHKKA
	ł.	ļ	QASLNAGLDLRLAVQLPPGEDLNDWVAVHVVDFFNRVNLIYGTI XDGCT
6736	195	808	
6/36	195	""	MNYELNPKREMPNIKSLGLTNLNPLLKRLSSVLPLITDYVYPKN SSSNPYLIRRIEELNKTASGNVEAKVVCPYRRRDISNTLIMLAD
İ	1	ì	KHAKEIEBESETTVKADLTDKOKHQLKHRELFLSRQYBSLPATH
ŀ	j	ļ	IRGKCSVALLNETESVLSYLDKEDTFYYSLVYDPSLKTLLADKG
	1	ì	BIRVGPRYQADIPEMLLEGTFFCVFAVL
6737	150	1209	PVIMPLHESPGDIVRPSCCVSSSPKLRRNAHSRLESYRPDTDLS
1	1	1	REDTGCNLQHISDRENIDDLNMEFNPSDHPRASTIFLSKSQTDV
l	1		REKRKSLPINHHPPGQIARKYSSCSTIFLDDSTVSQPNLKYTIK
1	1	1	CVALAIYYHIKNRDPDGRMLLDIFDENLHPLSKSEVPPDYDKHN
	]	J	PEQKQIYRFVRTLFSAAQLTAECAIVTLVYLERLLTYAEIDICP
<b>,</b>	•		ANWKRIVLGAILLASKVWDDQAVWNVDYCQILKDITVEDMNELE
	İ		ROFLELLOPNINVPSSVYAKYYFDLRSLARANNLSFPLEPLSRE
			RAHKLEAISRLCEDKYKDLRRSARKRSASADNLTLPRWSPAIIS
6738	148	653	CACAEQPARARVGAATALPVRWASGEMAPSGSLAVPLAVLVLLL
į	].		WGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACONI, OPEWESFAEWGEDLEVNIAKVDVTEOPGLSGRYIITALPTIYHC
	İ	f	KDGBFRRYQGPRTKKDFINFISDKEWKSIEPVSSWF
6739	3	631	SWPDMARREVAKLEKHLMLLROBYVKLQKKLARTEKRCALLAAQ
1	1	1 032	ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF
j			VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
1	<b>,</b>		REDDVFLTELMKLANRPQLQLLRERCEKGVMSLVNVRNCIRPYQ
			TABELNASTLMNYCABI LASHWVSBVEGVNKAL
6740	3	631	SWPDMAEERVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ
l			ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF
<b>.</b> .			VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
ł	ł	ĺ	REDDVFLTBLMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ
	744	0.25	TAEBLNASTLMNYCARI IASHWYSEVEGVNKAL
6741	141	960	PLTLPPSSRARAGHTMNT&PGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM
Į			YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI
			WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW
	<b>]</b> '		DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
}			PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTO
			LIPKTKIP
6742	141	960	PLTLPPSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA
1			HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM
	1		YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGKDCTARI
ļ	İ		WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW
1			DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
		ł	PLAIGILQEGRFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ
6743	ļ	435	LIPKTKIP
6743	1 -	412	MHSTODKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKOLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDILOTOFRN
1			PABGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL
1	1		LONIR '
6744	95	1343	RTPARNRCAGCEVLSRFSSPNKASSPALQSAGGGLPAVRALRRD
J 77.22	] "	,,,,,	RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQBELT
			DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILLLSRT
1	i ·		LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPBFQESVEBFPE
ŀ			VTVIBPLDEEARPSHIPAGDCSEHWKTQRSEEYBAEGQLRFWNP
}			DDLNASQSGSSPPQDWIERKLQEVCEDLGITRDGHLNRKKLVSI
	<u> </u>	L—	· · · · · · · · · · · · · · · · · · ·

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			CEQYGLQNVDGEMLEEVFHNLDPDGTMSVEDFFYGLFKNGKSLT
		1	PSASTPYRQLKRHLSMQSFDESGRRTTTSSAMTSTIGFRVFSCL
			DDGMGHASVERILDTWQEEGIENSQRILKALDFGLDGNINLTEL
			TLALKNELLVTKNSIHQACI
6745	1	588	TFRDQGWAQRRRWILLGCASWESWEAAIAAGPGLPSSTARQQNNP
			AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERRRDP
		ļ	ELPVTSFDCAVCLEVLHQPVRTRCGHVFCRSCIATSLKNNKWTC
	ł	i	PYCRAYLPSEGVPATDVAKRMKSEYKNCAECDTLVCLSEMRAHI
		1	RTCQKYIDKYGPLQELEETA
6746	110	492	GATGAMAKSAPARHRRKRRSTPLTSSTLPSQATEKSSYPQTTEI
1	l	1	SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCEKMA
l	1		VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN
6747	247	484	BAVTFKDVAVVFTBEELGLLDLAQRKLYRDVMLENFRNLLSVGH
l • • • • • • • • • • • • • • • • • • •	<u></u> :		QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC
6748	201	665	MTTFKEAVTFKDVAVVFTEBBLGLLDPAQRKLYRDVMLENFRNL
""	1	1	LSVGNOPFHODTFHFLGKEKFWKMKTTSQREGNSGGKIQIEMET
j	1	ì	VPEAGPHEEWSCOOLWEQLASDLTRSQNS1RNSSQFPKEGDVPC
ł	i		OIRARLSISXVOOXPYRCNECKO
6749	95	719	RREVKGGDGVCPRARGSPOSQOFPSCAGGGEGLQQSGEALDGAM
1 0,45	1	1 ~~	SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFDKAF
	<b>{</b>	1	VDVDLLLGE IDPDQADITYEGRQKMTSLSSCFAQLCHKAQSVSQ
1	[ -		INHKLEAGLVDLKSKLTETQAEKVVLEKEVHDQLLQLHSIQLQL
ļ	1	1	HAKTGQSADSGTIKAKLSGPSVEBLERELKAN
6750	3	428	SCESRRPGAKWVWASGALPROTTGLGSEQPSGDVAQSNRATMGT
0/50	1	***	TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEAERMFTR
		ł	EPSKEPKIMPKTPSQKNRRKKRRISYVQDKNRDPIRRRLSRRKS
1	!	1	RSSOLSSRR
6751	152	1417	PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIV
0/54	132	1 ****	NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGEEML
Ì	J		QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLCEDL
1			FSRINDTINDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE
1	1		HPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETS
ſ	1		SRSHAVFNIIFTQKRHDAETNITTEKVSKISLVDLAGSERADST
		1.	GAKGTRLKEGANINKSLTTLGKVISALAEMDSGPNKNKKKKKTD
1	1 .	1	PIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLR
		1	YADRAKQIRCNAVINEDPNINKLIRELKDEVTRLRDLLYAQGLGD
		1	ITDMTNALVGMSPSSSLSALSSRNV
6752	24	1834	RNCVPPLGCYRSRVKFHSDIKMQYSHHCEHLLERLNKQREAGFL
0/52		1	CDCTIVIGEFQFKAHRNVLASFSBYFGAIYRSTSENNVFLDQSQ
1	1		VKADGFQKLLEFIYTGTLNLDSWNVKEIHQAADYLKVEEVVTKC
			KIKMEDFAFIANPSSTEISSITGNIELNQQTCLLTLRDYNNREK
		1	SEVSTDLIQANPKQGALAKKSSQTKKKKKAFNSPKTGQNKTVQY
	i	<b>§</b>	PSDILENASVELFLDANKLPTPVVEQVAQINDNSELELTSVVEN
		1	TPPAQDIVHTVTVKRKRGKSQPNCALKEHSMSNIASVKSPYBAE
	1		NSGERLDORYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVKPYV
		1	CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAQKCQLVF
		1	HSRMHHGEBKPYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR
1	1		CGORFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR
1		1	KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED
			HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV
		1	TDTOSPTSDTLLRSTVNGYSEPQLIFLQQLY
	<u> </u>	I	
	1 2	1305	VPSLPYPPOKVVAHTEFTTSSDSETANGIAKPDPVMPGGEBKAS
6753	1 ~	ī	
6753	-	İ	PFGIKLRRTNYSLRFNCDQQABQKKKKRHSSTGDSADAGPPAAG
6753			PFGIKLRRTNYSLRFNCDQQABQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSABPSSSRSVPV AHPGPPPASSQTPAPEHDKAAMKMPLAQKPALAPKPTSQTPPAS

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=beucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	beganice	\=possible nucleotide insertion)
<del></del>	Begacace	<del> </del>	PLSKLSRPYLVELLSRRAGRPDPEPSEPSKEDQESSDRRPPSPP
Į.	Į.	[	GPEERKGOKRDEEERATERKPASPPLPATOOEKPSOTPEAGRKE
		ĺ	KPMLQSRHSLDGSKLTEKVETAQPLWITLALQKQKGYREQOATR
			EERKOAREAKOAEKISKENVSVSVOPGSSSVSRAGSIHKSTALP
ŀ			EEKRPETAVSRLERREOLKKANTLPTSVTVEISYSSPAAPLVKE
<b>!</b>		ļ	VSKRFSSPDDAPVSSEPAWLALAKRKAKAWSDCPLIIK
6754	2	413	FVRRRRRRLGGPEVNTMSSLHKSRTADFODVLKEPSIALEKLRE
. 6734	1	11.3	LSPSGIPCEGGLRCLCWKILLNYLPLERASWTSILAKORELYAO
1	<b>S</b>	ļ	PLREMIIOPGIAKANMGVSREDVTFEDHPLNPNPDSRWNTYPKD
			NEALT THE THE THE THE THE THE THE THE THE TH
6755	298	1343	PGLOLOVALEADWFLDMPGGRRGPSRQQLSRSALPSLQTLVGGG
","	1	1020	CGNGTGLRNRNGSAIGLPVPPITALITPGPVRHCQIPDLPVDGS
	1		LLFRFLFFIYLLVALFIQYINIYKTVWWYPYNHPASCTSLNFHL
1	1	1	IDYHLAAFITVMLARRLVWALISEATKAGAASMIHYMVLISARI,
1	1		VLLTLCGWVLCWTLVNLFRSHSVLNLLFLGYPFGVYVPLCCPHQ
ţ.	,		DSRAHLLLTDYNYVVOHKAVERSASTVGGLAKSKDFLSLLLESL
			KEQFNNATPIPTHSCPLSPDLIRNEVECLKADFNHRIKEVLFNS
i		ļ	LFSAYYVAFLPLCFVKVSGYLTFMCFLDLCVNYINWVFLV
6756	180	754	IERALGSLPLSIPVSWGSLRTLKYOOOPLRPKVLLCOTRVOCHD
1 ****			LRSLOPOPPGLKQSFCLRVLGLOTGATTPGLRDLTCKELIILTE
ì	1		REAQKRKKRKEKESCMALTQGPLTFRDVAIEFSQEEWKSLDPVO
	İ		KALYWDVMLENYRNLVPLGKDNFALEVKICPRVFLYFLCCLSWE
•	1	}	PPHYLTETRALLTHK
6757	2	459	NSRVEAPEAHSRESOGSDAMRKHLSWWWLATVCMLLFSHLSAVO
		,	TRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRKLDID
i	i e		FGAEGNRYYEANYWOFPDGIHYNGCSEANVTKEAFVTGCINATO
Į.	1		AANQGRFQKPDNKLHQQVLW
6758	1	1008	ASGPELPGRRPRDRAPWLPARLLRGVLAVWVSLSALGPGSFCRR
l			RVPSLAQLGHSBAAPSPDDVRWSRVPDRCPEERDRAWPPPPPPPS
}	1		LPPSFRRNMANNSPALTGNSQPQHQAAAAAAQQQQQQCGGGGATK
l	1		PAVSGKQGNVLPLWGNEKTMNLNPMILTNILSSPYFKVQLYELK
Į.			TYHEVVDEIYFKVTHVEPWEKGSRKTAGQTGMCGGVRGVGTGGI
I			VSTAFCLLYKLFTLKLTRKQVMGLITHTDSPYIRALGFMYIRYT
l			QPPTDLWDWFESFLDDEEDLDVKAGGGCVMTIGEMLRSFLTKLE
			WFSTLFPRIPVPVQKNIDQQIKTRPRKI
6759	1	513	RKHNFHSLDGTSTRAFHPQTGLPLLSSPVPQRKTQSGCFDLDSS
1			LLHLKSFSSRSPRPCLNIEDDPDIHEKPFLSSSAPPITSLSLIG
l	1		nfresvlnyrfdplgivdgptaevgasgafcpthltlpvevsfy
1			SVSDDNAPSPYMGVITLESLGKRGYRVPPSGTIQVVCVL
6760	239	606	VLSKKKGLSABEKRTRMMEIFSBTKDVFQLKDLEKIAPKEKGIT
1	[		AMSVKEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLE
ľ	[		VLESQLSEGSQKHASLQKSIBKAKIGRCETEERT
6761	29	1733	ERTLRGLREVAAPSDVADAAVSRRGRCCCCLHCTQTQVAQDCPS
1	}		SSSSVQRCELSLFQSLHTMTSKKLVNSVAGCADDALAGLVACNP
ł	j .		NLQLLQGHRVALRSDLDSLKGRVALLSGGGSGHEPAHAGFIGKG
1	<b>{</b>		MLTGVLAGAVFTSPAVGSILAAIRAVAQAGTVGTLLIVKNYTGD
1	1		rlnfglareqaraegipvemvvigddsaftvlkkagrrglcgtv
Į			LIHKVAGALAKAGVGLKEIAKQVNVVTKAMGTLGVSLSSCSVPG
ļ			skptfelsadevelglgihgeagvrrikmatadeivklmldhmt
1		*	nttnashvpvqpgssvvmmvnnlgglsflelgiiadatvrsleg
			RGVKIARALVGTFMSALEMPGISLTLLLVDEPLLKLIDARTTAA
			AMPNVAAVSITGRKRSRVAPARPQEAPDSTAAGGSASKRMALVL
}			ERVCSTLLGLEEHLNALDRAAGDGDCGTTHSRAARAIQEWLKEG
]			PPPASPAQLLSKLSVLLLEKMGGSSGALYGLFLTAAAQPLKAKT
Ι,		1	SLPANSAAMDAGLEAMQKYGKAAPGDRTMLDSLNAAGQBL
	L	<del></del>	

Predicted   Predicted   Predicted   Incation   Incleotide   Incation   Incleotide   Incation   Incorresponding   Incation   Incation   Incorresponding   Incation				
Incitation   Cortesponding	SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide
location   corresponding to first   safine acid   safine			1	
Louine, Marchionine, Narganine, amino acid residue of amino acid residue of amino acid sequence   Seserine, T-Threonine, Narganine, Percidue of amino acid sequence   Narghophan, Yafyropine, Nardhanown, *=Stop (Codon, /=possible nucleotide deletion, Napossible nucleotide, Napossible nucleo	NO:	I .		
to first anion acid aresidue of anion acid aresidue of seeine, T-Threndine, N-Valine, anion acid anion acid anion acid anion acid sequence (Sectine, T-Threndine, N-Valine, N-Threndine, N-Valine, Sequence (Sequence) (Sequ				
amino acid residue of amino acid sequence  6762  3				
residue of amino acid sequence (Codon, #=possible nucleotide deletion, #=possible nucleotide deletion, #=possible nucleotide deletion, #=possible nucleotide deletion, #=possible nucleotide innertion)  613		to first	1	P=Proline, Q=Glutamine, R=Arginine,
amino acid		amino acid		S=Serine, T=Threonine, V=Valine,
Sequence   Sequence		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
6762 3 613 ASTIGNRIC VAGRARAFPYEVAGERAGGANWEWILLSHIGE OF APPTITUANAGICYTALRIL REY VATASIL IXEMINESTAVICI LYVEREPTSMIGVCLETIALVY FOLLOTIPP IMLISENT LIGGA INVENIMILA OF A CONTINUAL PROPERTY OF THE ACT OF A CONTINUAL PROPERTY OF THE ACT OF THE A		amino acid	sequence	Codon, /=possible nucleotide deletion,
G763 2 760 SGDPFGREFERS COUNTPRACEMBELISHED HISTORY FLOCE LVVVNHYLAROPPRALETY PPSKYLAYTTYCLIKI I DPAFFYSLSA GRBVLPENTHOLOGY CHIPTANY PERKYLAYTTYCLIKI I DPAFFYSLSA GRBVLPENTHOLOGY COUNTPRACEMBELISHEDINGSAPELLYSTAE REGEOCITERARADSGAVGARRELLCTJIGGELLLGYSTWIVE LLSHAWRICLASPTVAGIUSSY SUILGJESTILVGCHSDWUGRE SSLLACILLSALGYLLLGAANIVELVILAGUPAGH FRIETIS ISR ALLSDWUPRERSPYLVGIUSTYLLGAANIVELVILAGUPAGH FRIETIS ISR ALLSDWUPRERSPYLVGIUSTYLLGAANIVELVALARUPAG FRIETIS ISR ALLSDWUPRERSPYLVGIUSTYLLGAANIVELVALARUPAG FRIETIS ISR ALLSDWUPRERSPYLVGIUSTYLLGAANIVELVALARUPAG FRIETIS ISR ALLSDWUPRERSPYLVGIUSTYLGAANIPAG FRIETIS ISR ALLSDWUPRERSPYLVGIUSTYLGAANIPAG FRIETIS ISR ALLSDWUPRERSPYLVGIUSTYLGAANIPAG FRIETIS ISR KROOPTOMIRGYKYNDLIMKARTERSALDVAKRHARNIVOVELKR DQRARADCELLSGELIGGOLOG ISRUMANUTARGUS (OLI IRBUMANUTARGUS) G765 3 550 ARYSKVEHYCRRCRAVAKAPRFILQPPSOPSERHIJAACVASHI RGSVLVERILAGSAMOLI VYRVAVOKARGUSELLISGSKVESPIN RGSVLVERILAGSAMOLI VYRVAVOKARGUSELLISGSKVESPIN RGSVLVERILAGSAMOLI VYRVAVOKARGUSELLISGSKVESPIN RGSVLVERILAGSAMOLI VYRVAVOKARGUSELLISGSKVESPIN RGSVLVERILAGGAR FROEDRAM FRIEDRATINGRYYSAVT PHLINN RGYLVERING FROEDRAL FRIEDRAM FRIEDRATINGRYYSAVT PHLINN  1287 BGGFFKASILVALIM LIGEMKI LICEVEVI SRIHLARIGKEVETE VILLELBAN  6766 1 1287 BGGFFKASILVALIM LIGEMKI LICEVEVI SRIHLARIGKEVER FRIEDRATINGRYYSAVT RVYDBRAKATVRLKERPYD LCLSKAMSSSL KOFLSMILLARIGKOFFT RVYDBRAKATVRLKERPYD LCLSKAMSSSL KOFLSMILLARIGKOFFT RVYDBRAKATVRLKERPYD LCLSKAMSSSL KOFLSMILLARIGKOFFT RVYDBRAKATVRLKERPYD LCLSKAMSSSL KOFLSMILLARIGKOFFT RVYDBRAKATVRLKERPYD LCLSKAMSSSL KOFLSMILLARIGKOFFT RVYDBRAKATVRLKERPYD LCLSKAMSSSL KOFLSMILLARIGKOFFT RVYDBRAKATVRLKERPYD LTSTALDERSHKIKKLIPATIGOPT RVYDBRAKATVRLKERPYD LTSTALDERSHKIKKLIPATIGN THE AVISABLY TRENDERSH TRANDARKATUR LICEVEVI SRHILARIGKOFFT RVYDBRAKATRIKERPYD LTSKAMSKLARIGHTERIARIGKOFT RVYDBRAKATRIKERPYD LAGANTY L		sequence		\≃possible nucleotide insertion)
LIVVPRREPTSMIGVGLETIM.VFELLQIFEPSIMLISENPILLGUVVMINITARQPERSERVYPESSULAPTECUMI IDPAPYVSLSA GENVLESTMOPGDDVUSNYETKGRGK  5763 2 760 SGDDPFEGRERGCCCVREPPAGRGRIGGSHWDMSAPRLVSETAE REGEORTSTEARADSGAVGARREILGSHWDMSAPRLVSETAE REGEORTSTEARADSGAVGARREILGLYIGGGILLGRYSMVVP LLSLHVRSLGASETVAGIVGSSYGILQIFSSTLVGCKSDVVGHV LLSLHVRSLGASETVAGIVGSSYGILQIFSSTLVGCKSDVVGHV LLSLHVRSLGASETVAGIVGSSYGILQIFSSTLVGCKSDVVGHV LLSLHVRSLGASETVAGIVGSSYGILQIFSSTLVGCKSDVVGHV LLSLHVRSLGASETVAGIVGSSYGILQIFSSTLVGCKSDVVGHV LLSLHVRSLGASETVAGIVGSSYGILQIFSSTLVGCKSDVVGHV LLSLHVRSLGASETVAGIVGSSYGILQIFSSTLVGCKSDVVGHV LLSLHVRSLGASETVAGIVGSSYGILQIFSSTLVGCKSDVGHVGF SSLLAGATILLGANDERVGFILGPVGGYITELEDGG VLTATE CICLUPT LINGLGAVAGATER REGEORTER LANGLUS LA	6762	3	613	ASTISWRLCVAGABARRPVPVAGBRAGGGAMWFMYLLSWLSLFI
INVVNNITIAROPFRAERY IPPSKVLAYFTECHMI IPPAFYVSLSA   GRBVLPSTMOREDDWSNYFTERKEK   GRBVLPSTMOREDDWSNYFTERKEK   GRBVLPSTMOREDDWSNYFTERKEK   GRBVLPSTMOREDSWSTMORKES   CREEK   GRBVETTSTARAADSGAVGARRILLGTJAGOTLDLGGYSMVLV   LUSLAVISLASETVLGIGNSTUCKOSBOVUGRR   RKEGROTTSTARAADSGAVGARRILLGTJAGOTLDLGGYSMVLV   LUSLAVISLASETVLGIGNSTUCKOSBOVUGRR   SSLIACTLLGAGGATVLJUGHSTALVGOSBOVUGRR   SSLIACTLLGAGGATVLJUGHSTALVGOSBOVUGRR   ALLSDVUPEKRERVLJUGHPTALSGAVEVPGAGGATIJCHERDGW   SSLIACTLLGAGGATVLJUGHTALVGOSTE   KREGOTDBIRGGYKNDLIMKRATERSALDVLKRERNDKOVDERFOR   RUSUDTWELKER KREGOTDBIRGGYKNDLIMKRATERSALDVLKRERNDKOVDERFOR   RUSUDTWELKER RORRABOCELIKERGENGOLGLERHINDEDGSTE   KREGOTDBIRGGYKNDLIMKRATERSALDVLKRERNDKOVDERFOR   RUSULVERLANGSANDGALTERVAGAVGRASDBLLGSSVLSSENS   RUSUNDERLANGSANDGALTERVAGAVGRASDBLLGSSVLSSENS   RUSUNDERLANGSANDGALTERVAGAVGRASDBLLGSSVLSSENS   RUSUNDERLANGSANDGALTERVAGAVGRASDBLLGSSVLSSENS   RUSUNDERLANGSANDGALTERVAGAVGRASDBLLGSSVLSSENS   RUSUNDERLANGSANDGALTERVAGAVGRASDBLLGSSVLSSENS   RUSUNDERLANGSANDGALTERVAGAVGRASDBLLGSSVLSSENS   RUSUNDERLANGSANDGALTERVAGAVGRASDBLLGSSVLSSENS   RUSUNDERLANGSANDGALTERVAGAVGRASDBLLGSSVLSSENS   RUSUNDERLANGSANDGALTERVAGAVGARD   RUSUNDERLANGSANDGALTERVAGAVGANDGALTERVAGAVGANDGALTERVAGAVGAND   RUSUNDERLANGSANDGALTERVAGAVGANDGALTERVAGAVGANDGALTERVAGAVGAND   RUSUNDERLANGSANDGALTERVAGAVGANDGALTERVAGAVGANDGALTERVAGAVGAND   RUSUNDERLANGSANDGALTERVAGAVGAND   RUSUNDERLANGSANDGALTERVAGATA   RUSUNDERLANGSANDGALTERVAGATA   RUSUNDERLANGSANDGALTERVAGATA   RUSUNDERLANGSANDGALTARA   RUSUNDERLA				QVAFITLAVAAGLYYLAKLIEBYTVATSRIIKYMIWFSTAVLIG
GRIVLESTMOPGIDIVUSNYFTKICHEKIK  2 760 SESPEPPERER PERCOCCUPE PROAGMIZIGENDANSAPELUSETAE RKQBQKTGTEABAADSGAVGARRFILCLYLIGGFLOFSSTLVGCKSDVOVER SLAGALLISAGYLILGARITVIFTAARVPAGFFRITISISK ALLSDAVVERERRELVIGESTITASGVGET LIGPESTLVGCKSDVOVER SLAGALLISAGYLILGARITVIFTAARVPAGFFRITISISK ALLSDAVVERERRELVIGEFTTASGVGET LIGPEVGGYTITZEBOGF TLTAPTCTLVFT LINAGILWPFPERRERKCST  6764 80 438 LKKODTWALSKYNLLIAMKAETERSALDVALKHARNOVDVETKR RORABADCEKLERQIQLIREMUMCOTSGSIQ  6765 3 550 ARYSEVEHYCREKCRAVARAFRETIJOPPSGPSEHFLAACVASHL RGSVLVEBALISGARMOITTEVAVOVKRGSDBLLSGSVLSSPNS MYSSHVTANGNOSKKFGGBORNIGARSFRUHIRELIGGEVTETE VILLGLEPPGKVTHILMLIGKORGAFLEATERAALTNANTYSAVT PHLENQ  6766 1 1287 BEGSFFASLIMLMPLGERKLHCEVEVISRHLFALGLÄNRGKOVR AVISLCQTGRSQPEVRAFILLISTLKOKRGTEYELREN IRGFT KEVENGRKATURLESPEVNICLESKANSSLIGHARLIAHRGKOVR AVISLCQTGRSQPEVRAFILLISTLKOKRGTEYELREN IRGFT KEVENGRKATURLESPEVNICLESKANSSLIGHARLIAHRGKOVR OTTOPUSTLITPVIKTSERFRFTKINVITSKONTELSKINKLEPEPSE RINISLEYLDLEGNTFEQDEVLEVITLORUSTILISSARFILHING LLAHANINHLISSPEVALCHSTLOKSISSLIDLSRIKKIRLIPUPGCQ LQELKMIKHLDDINELIQPPCKIGGLINLEPLSARRIKLEPLPSEF RINISLEYLDLEGNTFEQDEVLEVITLORUSTILISSARFILHING GRIGGSDNSTKOPARASGOGGARSGOGLASDUMY RQPLEQPTCOPEGIGLIREAGKARIGLIGGARRGARGARGARGHAR  6767 336 919 APMICICSSDLOPPKKRAFIRENTERGRATHLING GRIGGSDNSTKOPARASGOGLARSOQUARSOQUASDUMY RQPLEQPTCOPEGIGLIREAGKARIGLIGGARRGARGARGARGARGA HAMVULVINLIGAREAGLIAGARGARGARGARGARGARGARGARGARGARGARGARGAR				LYVFERFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCG
2 760 SGPDPPGGREFECCCURPFAGAMELICAGHNDMSAPELVSETAE REGRORTGERERADGGCCOURPFAGAMELICLISCAGELD-GOVAVORR REGRORTGERERADGGCCOURPFAGAMELICLISCAGELD-GOVAVORR SSLLACTLLISALGYLLIGATHNYF, FYLARVPAGFFERTH-LISTS ALLSDVYPERERREPLVIGHERITAGGGTE LIGHTLISTS ALLSDVYPERERREPLVIGHERITAGGGTE LIGHTLISTS ALLSDVYPERERREPLVIGHERITAGGGTE LIGHTLISTS ALLSDVYPERERREPLVIGHERITAGGGTE LIGHTLISTS ALLSDVYPERERREPLVIGHERITAGGGTE LIGHTLISTS ALLSDVYPERERREPLVIGHERITAGGGTE LIGHTLISTS ALLSDVYPERERREPLVIGHERITAGGGTE LIGHTLISTS ALLSDVYPERERREPLVIGHERITAGGGTE LIGHTLISTS ARGORITHMEN CONTROL AND ARGORITHMEN CONTROL AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICATE AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CO				LVVVNHYLAFOFFABBYYPFSBVLAYFTFCLWIIDFAFFVSLSA
2 760 SGPDPPGGREFECCCURPFAGAMELICAGHNDMSAPELVSETAE REGRORTGERERADGGCCOURPFAGAMELICLISCAGELD-GOVAVORR REGRORTGERERADGGCCOURPFAGAMELICLISCAGELD-GOVAVORR SSLLACTLLISALGYLLIGATHNYF, FYLARVPAGFFERTH-LISTS ALLSDVYPERERREPLVIGHERITAGGGTE LIGHTLISTS ALLSDVYPERERREPLVIGHERITAGGGTE LIGHTLISTS ALLSDVYPERERREPLVIGHERITAGGGTE LIGHTLISTS ALLSDVYPERERREPLVIGHERITAGGGTE LIGHTLISTS ALLSDVYPERERREPLVIGHERITAGGGTE LIGHTLISTS ALLSDVYPERERREPLVIGHERITAGGGTE LIGHTLISTS ALLSDVYPERERREPLVIGHERITAGGGTE LIGHTLISTS ALLSDVYPERERREPLVIGHERITAGGGTE LIGHTLISTS ARGORITHMEN CONTROL AND ARGORITHMEN CONTROL AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICITATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICATE AND ARGORITHMEN CONTROL REGSVILVERALGGGAPLICATE AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CONTROL REGGER AND ARGORITHMEN CO			ł	GENVLPSTMOPGDDVVSNYFTKGKRGK
LIJSHHVISICASETVAGIVGSSTGILOJESTIVGKR SSILACILISANTVIFJVARVEGIFFHTISISK ALISDVVPBKERPLVIGHENTASGVGFILOPVCGYITTELEDGE YLTAPICCINFILMAGIVMPPPREBARGSTE  6764 80 438 LKKMOTTMISUSKINDEPURSKUGSTE KKMORTDIBLGKYKDILJKABETERSALDVKLKHARNQVDVBLKR RQRABADENKERGOJQLIERMIKOTTSGGIU  6765 3 550 ARYSKVDBFCRRCGAVARAPRILOPSSGESRHELANCVANIL RCSYLVSRIASGOMERICOJGSTED SINGKANGAVANIL RCSYLVSRIASGOMERICOJGSTED SINGKANGAVANIL RCSYLVSRIASGOMERICOJGSTED SINGKANGAVANIL RCSYLVSRIASGOMERICATERAATTMANYYSAVT PHLBRING  6766 1 1287 BEGISPFRASI/MLMPLGEMKLHCEVEVISHLEPALGIAKNEGAVA PHLBRING  6766 1 1287 BEGISPFRASI/MLMPLGEMKLHCEVEVISHLEPALGIAKNEGAVA VILLELBPGKVTHILMAGINGAFLELATERAATTMANYYSAVT PHLBRING  6766 1 1287 BEGISPFRASI/MLMPLGEMKLHCEVEVISHLEPALGIAKNEGAVA VILLELBPGKVTHILMAGINGAFLELATERAATTMANYYSAVT PHLBRING  6766 1 1287 BEGISPFRASI/MLMPLGEMKLHCEVEVISHLEPALGIAKNEGAVA VILLELBPGKVTHILMAGINGAFLELATERAATTMANYYSAVT PHLBRING  6766 1 1287 BEGISPFRASI/MLMPLGEMKLHCEVEVISHLEPALGIAKNEGAVA VILLELBRANG PHLBRINGAVA VILLELBRANG VILLELBRANG VILLELB	6763	2	760	
LIJSHHVISICASETVAGIVGSSTGILOJESTIVGKR SSILACILISANTVIFJVARVEGIFFHTISISK ALISDVVPBKERPLVIGHENTASGVGFILOPVCGYITTELEDGE YLTAPICCINFILMAGIVMPPPREBARGSTE  6764 80 438 LKKMOTTMISUSKINDEPURSKUGSTE KKMORTDIBLGKYKDILJKABETERSALDVKLKHARNQVDVBLKR RQRABADENKERGOJQLIERMIKOTTSGGIU  6765 3 550 ARYSKVDBFCRRCGAVARAPRILOPSSGESRHELANCVANIL RCSYLVSRIASGOMERICOJGSTED SINGKANGAVANIL RCSYLVSRIASGOMERICOJGSTED SINGKANGAVANIL RCSYLVSRIASGOMERICOJGSTED SINGKANGAVANIL RCSYLVSRIASGOMERICATERAATTMANYYSAVT PHLBRING  6766 1 1287 BEGISPFRASI/MLMPLGEMKLHCEVEVISHLEPALGIAKNEGAVA PHLBRING  6766 1 1287 BEGISPFRASI/MLMPLGEMKLHCEVEVISHLEPALGIAKNEGAVA VILLELBPGKVTHILMAGINGAFLELATERAATTMANYYSAVT PHLBRING  6766 1 1287 BEGISPFRASI/MLMPLGEMKLHCEVEVISHLEPALGIAKNEGAVA VILLELBPGKVTHILMAGINGAFLELATERAATTMANYYSAVT PHLBRING  6766 1 1287 BEGISPFRASI/MLMPLGEMKLHCEVEVISHLEPALGIAKNEGAVA VILLELBPGKVTHILMAGINGAFLELATERAATTMANYYSAVT PHLBRING  6766 1 1287 BEGISPFRASI/MLMPLGEMKLHCEVEVISHLEPALGIAKNEGAVA VILLELBRANG PHLBRINGAVA VILLELBRANG VILLELBRANG VILLELB				
SSILACILLSALGYILLIGAATNVILGULARVPAGITERTILS ISE ALLSDVVPBKBRPLVIGHPITASGUGFILDVUGGYITELBODG YLTAPICCIVFILMGLUWFFPRERARGSTE  6764 80 438 LKKMDTWHISVRILFBQLVRRUELLSEGBEVQFYQGALDFBEFF KRORTDBIELGKYROLLMARTERSALDVUKKHARNOVDVBIKR RQRABDCEKLERQIQLIRRHLMCDTSGGIQ  6765 3 550 ARYSKVBRCBRCBARAPEPFLIQFSGSERRHLARCVARML RGSVLVSEALSGSAMDGIVTEVAVGVKRGSDELLSGSVLSSPNS MISSMVTANGNDSKRFKGBIRHIGAPSKVLHITEKLERGVTETTS VLAIGLPBEVKTVILLMEKGRAPERLATERBALTKANNYSAVT PHLENQ  6766 1 1287 EGGSPFASSITHLMBIGEMKLHCEVEVISRHLPALGIRNRGKVR AVISLCQOTSBSQD PVRAPILLISTIADKRGTRYBLERN TROPFT KYVDBCKATVGLRSPVDICTSKANSSSLFLSMRELAMRCN VDTPVSTLTPVKTSEPENFKTRMVITSKRDYPLSKRHRQCH LGISKRILLODNISLLGSFVCKTGQLINLRRIGAMRHARCN VDTPVSTLTPVKTSEPENFKTRMVITSKRDYPLSKRHPYSLEHL CTSYCGLWRVDMRMICLKSLBKLDLSHNHIKKDPATIGDLHILQ KIALBINNILSSFSVALCHSTLQSFLSGLISMRELAMRCN VDTPVSTLTPVKTSEPENFKTRMVITSKRDYPLSKRHPYSLEHL CTSYCGLWRVDMRMICLKSLBKLDLSHNHIKKDPATIGDLHILD KIALBONNILSSFSVALCHSTLQSFLSGLISMRELAMRCN VDTPVSTLTPVKTSEPENFKTRMVITSKRDYPLSKRHFLNDFLOSE RNISLEYLDLGSGTPFTGDVLJPVKLQAPITLLSSGAPTILBNR IPYGSILTPPHLCODLDTAKLCVCGRCLASSFIGGTTTNILHSV AHTVULVINDLGGTPALITSYFCSLGCVULPVKLQAPITLLSSGAPTILBNR IPYGSILTPPHLCODLDTAKLCVCGRCLASSFIGGTTTNILHSV AHTVULVINDLGGTPALITSYFCSLGCVULPVKLQAPITLLSSGAPTILBNR IPYGSILTPPHLCODLDTAKLCVCGRCLASSFIGGTTNINLSV APTULIVNDLGGTPALITSYFCSLGCVULPVKLQAPITLLSSGAPTILBNC GRQSBNSYKRDPAKSRSQFFISSTDQPGLAARKSQOTLASDUHY RQPLEOPPCDPEGLGLRARGXAHGLGDVKYKSDLAILTRGVWT PGSSYKVBMARRABLANARGLGLGGAYRGABAVEAGDRIQSGEV NPDATBILLWKKKALLL  6767 336 919 APHICLCSSDLQPRYKBAPLRDRGTGCAGNGKSDERLLQAV RNDAPRVAALLARKSLVPYTLDDFKGSARFH  6768 2 363 PGST1SCYLLSGGLDLCRQVACGERKHRAPTMSTTRABPKKTE LRLSPTDLGSCCPPCDPCPIPKPARGRRQCADGMGSGEV NPDATBILLWKKKALLL  6769 284 396 MSTFDFSTARKNOGLANKVSCLKAMMITIMLQAMGQAD  6769 284 396 MSTFDFSTARKNOGLANKVSCLKAMMITIMLQAMGQAD  6770 1 397 ORMVQVIWSTANALGDVTROPVKNOGRADGADGAG  FRANGKARNARIVYBATLPTFRPROPIPOTLYBTKSUMG  FRANGKARNARIVYBATLPTFRPROPIPOTLYBTKSUMG  FRANGKARNARIVYBATLPTFRPROPIPOTLYBTKSUMG  P**GWKLDAGVRTOPANRSPPROPIPOTLYPHSNUMG  RGGSMKAKARNIVYBATLDFTRANGFUNGSVVANDFALGPAMTETHV		ŀ	1	
ALLSDWYPEKRPLYTGHENTASCWOFTLGPVVGGYIJTELEDGF YLTAPICPLYFILMGLYWFPRREARGSTE 6764 80 438 TAKMDTWMLSVRTLEEGGRBVQFIQLAKDFEDFR KRORTDHELGKYKDLIMKAETEBSALDVUKKHARNQVDVEIKR RQRARADCEKLERQIQLIKERMIQLTSEGMBVQFIQLAKDFEDFR KRORTDHELGKYKDLIMKAETEBSALDVUKKHARNQVDVEIKR RQRARADCEKLERQIQLIKERMIGLOFFGGSERHFLARCVARHL RGSVLVSBALSGSAMDGIVTBVAVGVVKRGDELLGSVLSSPINS NMSSMVTANGNDSKUFKGERKHDGAPSRVLHITEKLPGEVTFTE VILLGLPFGKVTWILMLKGKOQRIELATERAATTKANYSAVT PHLENQ 6766 1 1287 EGSFFASLITHIMLGEMKLHCEVEVISRHLPALGIGIRRRGKVR AVISLCQUTESGOP PVRAFALLSTLLOKRGTYFLERNINGSVF KYDDGKATVRLKEPPVDICLSKANSSSLKGFLSAMRLAHRGCN VDTPVSTLITPVKTSBFBMFKTKNV 1TSKODYFLSKRYFSLEHL CTSYCGLWVDMRMLCLKSLERKDLSHMIKKLPATIGDLHILD EIMINDNHIRSFSVALCHSTLOKRGTYFLIRBNINGSPT KYDDGKATVRLKEPPVDICLSKANSSSLKGFLSAMRLAHRGCN VDTPVSTLITPVKTSBFBMFKTKNV 1TSKODYFLSKRYFSLEHL CTSYCGLWVDMRMICLKSLERKDLSHMIKKLPATIGDLHILD EIMINDNHIRSFSVALCHSTLOKRGTYFLIRBNINGSPT KYDDGKATVRLKEPPVDICLSKANSSSLKGFLSAMRLAHRGCN VDTPVSTLITPVKTSBFBMFKTKNV 1TSKODYFLSKRYFSLEHL CTSYCGLGVUDMRMICLKSLERKDLSHMIKKLPATIGDLHHLD EIMINDNHIRSFSVALCHSTLOKRGTYLLERSARNKLPPUPGC LORIKAIKLADDNELOGPPCKTGOLINIKLSARNKLPPUPGEP RNISLEYLDLSGGILFYLCQVLCOFFCLMSFIGGTTMNNIHSV ARTVVLVNDLGGTBAP ILSYCGLIGCHVKSSDLJIKNG FPGSTXKWBARRABALDNARCJGJGGSVDDDFRMHFILNV RQPLPGCKTKKDPAKSRSSPFISTDQGGELJARKSQDLASSDUHY RQPLLPGPTCDPBCJGLRHAQXAHDJGSDWKYKSDLAILTRGVWT PPGSYXVEMARRABALDARGLGJGGVCSVDDDBFRMHFILNV RQPLPGGSPKYKEMRRABALDARGLGJGGVSVDDDFRMHFILOV RNDATKILHVKKKRALLI  6769 284 396 MSTEPFSTAENNQELARMSCJLARMFKTET LRISPTDIGGSPPCGGSCPTPLAGGRRGQDMGKSDBRILQAV ENNDAPKULANDADLAAISGCOPPLTKARRSVAGF KRQGYPTGCKVVILGENKWEPPRILTTAPPRTRDFRGLSAKS KRQGYPTGCKVVILGENKWEPPRILTTAPPRTRDFRGLSAKS KRQGYPTGCKVVILGENKWEPPRILTTAPPRTRDFRGLSAKS KRQGYPTGCKVVILGENKWEPPRILTTAPPRTRDFRGLSAKS CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC			ŀ	· · · · · · · · · · · · · · · · · · ·
STOCK   SO   438   LIKKMDTYMILSVENILPEQLVRRVEILISEGNEVOFIQLAKOPEDER   KRKORTDHELISKYRDLIMKAETERSALDVKIKKBARNOVDVSIIR   RORARADCEKLERQIQLIREMIMCITGGGIQ   RKRORTDHELISKYRDLIMKAETERSALDVKIKKBARNOVDVSIIR   RORARADCEKLERQIQLIREMIMCITGGGIQ   RKSIKVUHERLIGSAMMGIVTEVAGVKASDELLISSSVILSSENS   NMSSMVTANDRIDNSKEK REGNERMGAPERSELISKSVILSSENS   NMSSMVTANDRIDNSKEK REGNERMGAPERSELISKSVILSSENS   NMSSMVTANDRIDNSKEK REGNERMGAPERSELISKSVILSSENS   NMSSMVTANDRIDNSKEK REGNERMGAPERSELISKSVILSSENS   NMSSMVTANDRIDNSKEK REGNERMGAPERSELISKSVILSSENS   NMSSMVTANDRIDNSKEK REGNERMGAPERSELISKSVILSSENS   NMSSMVTANDRIDNSKEK REGNERMGAPERSELISKSVILSSENS   NMSSMVTANDRIDNSKEK REGNERMGAPERSENTERFET   VIALGLIPPEGEVATILLISKILPSLIPSLIJESKER REGNERM   VIALGLIPPEGEVATILLISKILPSLIPSLIPSLIPSLIPSLIPSLIPSLIPSLIPSLIPS			ł	
6764  6765  6765  6765  6765  6765  6766  6766  6766  6766  6766  6766  6766  6766  6766  6766  6766  6766  6766  6766  6766  6766  6766  6766  10  1287  6766  11  1287  6766  11  1287  6766  12  1287  6766  12  1287  6766  13  1287  6766  14  1287  6766  14  1287  6766  15  1287  6766  10  1287  6766  10  1287  6766  10  1287  6766  10  1287  6766  10  1287  6766  10  1287  6766  10  1287  6766  10  1287  6766  10  1287  6766  10  1287  6766  10  1287  6766  10  1287  6766  10  1287  6766  10  1287  6767  10  1287  6767  10  1287  6767  10  1287  6767  10  10  10  10  10  10  10  10  10  1		Į	ł	
KKWORTDHELGEYKULLMKRAETERSALDVKLKHARNQVDVBIKR RQARADCEKLERQIQLIREMLMCDTSGSIG:  ARTSKVÜHFCERRCRAVARAPRETLIGPPSGPSEHFLÄACVARMI. RGSVLVSRALSGSAMDGIVTEVAVGVKRGSDEHLEGSVLSSENS NMSSMVYTANGNDSK KRKGEDKNEGAPSRVLHTEKLEGKEVTETE VIALGLPFGKVTNILMLKGKNQAFLELATERAAITNGNYYSAVT PHLBNQ  6766  1 1287 BGGSFRASLTWIMFLGEMKLHCEVEVISRHLPALGLRNEGKGVR AVLSLCQQTSRSQPPVRAFLLISTLKOKRGTRYELREN RGFFT KYVDGKARVAVLKSEPPVDICLSKANSLAFISAMRLAHRGCN VDTPVSTLTPVKTSEFENFKTKWITSKKÖYPLSKNFPYSLEHL QTSYCGLWKVDMRHLCKSLRKLDLSHHHIKKLPATIGDLHHLD GTSYCGLWKVDMRHLGKSTLKLDLSHHHIKKLPATIGDLHHLD GTSYCGLWKVDMRHLGPSVKLPUTLLESSARPTILHNR IPYGSHIIPFHLCQDLDTAKICVCGFTCLNSFIQGTTTMNIHSV AHTVVLVINDLGGTEAPLISTLFSCLSKWIKTALPTLGSHHIK IPYGSHIIPFHLCQDLDTAKICVCGFTCLNSFIQGTTTMNIHSV AHTVVLVINDLGGTEAPLISTYFCSLACVVNSSDI 6767 336 919 APHICLCSSDLQFFYKREFIRDRGGJGTGYCSVDDDPRWKHFLNV GRIGSDNRYKKDFAKSBSOPHSSTODPELLQARRSQOLASDHY RQPLPQPTCDPRQLGLRHAQXAHQLGSDVKYKSDLAILTRGVGWT PPGSYXVEMARRABALBANRGGGJGAYRGARAVERGDHQSGEV NPDATFILHVKKKALLL 6769 284 396 MSTPDFSTAKNNQELANBVSCLKARHITJMLGAMGQAD 6770 1 397 ORNYQVINSSTNAKLHDYKDBVVKKMTERNYNSYMOVFRVEK KIRGYFIGCKVTLRGERNWEPFERLITLAVPRIRDFRGLSAK 6771 3 378 APAGTLANTGKSVKDVDRYQAVJARLLLEBENRFCADCQSKGPR KIRGYFIGCKVTLRGERNWEPFERLITLAVPRIRDFRGLSAK 6771 1 1400 AAAFLQGHTVNGFINTVITSL\ERRYDLESYGGLTASSYDIAA CLCLITYSYFCGSG\HKPRMLGMGR\VLMGTGSLVASSYDIAA CLCLITYSYFCGSG\HKPRMLGMGR\VLMGTGSLVASSYDIAA CLCLITYSYFCGSG\HKPRMLGMGR\VLMGTGSLVASSYDIAA CLCLITYSYFCGSG\HKPRMLGMGR\VLMGTGSLVASSYDIAA CLCLITYSYFCGSG\HKPRMLGMGR\VLMGTGSLVASSYDIAA CLCLITYSYFCGSG\HKPRMLGMGR\VLMGTGSLVASSYDIAA CLCLITYSYFCGSG\HKPRMLGMGR\VLMGTGSLVASSYDIAA CLCLITYSYFCGSG\HKPRMLGMGR\VLMGTGSLVASSYDIAA CLCLITYSYFCGSG\HKPRMLGMGR\VLMGTGSLVASSYDIAA CLCLITYSYFCGSGGTFTLLCCRAFTATLITEMSTFSSFKLES QFSLSASRAPITGGYLUVPAGGGGFFTLGCFFVNKLELRGSAVIK FCLECTVVSLIGILVPSLKCPSVPMAGVTASGCSLLPEGHINL TAPCNAACSCQPHIYSSVCGSDGLMYFSLCHAGCPAATETNVDG	5764	l	450	L
RQRARADCEKLERQIQLIERMILMCOTESGIIQ	0.104		430	
6765  3 550 ARYSRVDHYCRRCRAVARABRETILQFPSGBSRHFLARCVARMI. RGSVLUSRALGSSANDGIVTEVAVGVKKUDSDLLGGSVLSSPNS NMSSMVVTANGBDSKKYRGBRNADGAPSRVLHIRILDGKVTETS VIALGLPFGKVTNILMLKGKMQAFLELATERAAITMGNYYSAVT PHLENQ  6766 1 1287 EGGSFKASLTWLMPLGEMKLHCEVEVISRHLPALGLRNRGKGVR AVISLCQQTSRSQPFVRAFILLISTLADRKRTYBLERNIRGFFT KYPDGBKATVELKEPPVDICLSKANSSSLKGFLSANKLAHEGGN VDTPVSTLTPVKTSEFRBFKTKMVITSKKDYPLSKNFFYSLEHL QTSYCGLVRVDNRMLCLKSLEKJLDISHNHIKKLPPTISEBH KLININNHLRSPSVALCHSTLQKSLWSLDISKNKIKALPVQFCQ LQBLKMLKLIDDNELLQFFCKLGQLINLRFLGSARRKLPFUPSEF RNISLSYLDLFGNTTEPQFKVLPVLAPPLIGDLTHLBSV AHTVVLVDALGGTEAPIISYFCSLGGVYNSSDI  6767 336 919 APMICLCSSDLQFFXKRAFLRDRGLQIGTCSVDDDPRMKHPLNV GRIQSDNBYKKDFAKSRSQPHSSTDQPGLLQAKRSQQLASDVHY RQDLPQPTCDPBOLGHRIAKAHQDSVHYKSDLINLTRGUSWT PPGSYLVBMARRAAKLANARGLGLQGAYRGARAVEAGDHQSGEV NPDATRILHVKKKKALLL  6768 2 363 PGSTISCYLLSRGSLFLCMQVACGBERHRAPTMRTLRARFKKTE LRISPTDLGSCPCOPCPIPRPAARGRRGSQDWGKSDBRLLQAV ENDLAPRAVALLARRGLYPTKLDFGSAPHL  6769 284 396 MSTFDFSTARNQELARROXGLGKGRAFHL 6769 284 396 MSTFDFSTARNQELARROXGLGKAFKTKAKETE LRISPTDLGSCPCOPCPIPRPAARGRRGSQDWGKSDBRLLQAV ENDLAPRAVALLARRGLYPTKLDFGKAPH  6770 1 397 QRNYQVIWSSTMAKLEDYYKDEVVKKULTEFRYNSVMQVPRVEK LITLMWQGBALDAKKLINAAADLAGGGKPLTKARKSVAGF KLRQGYPIGCKVTLRGERMWFPFRLITLAVGRIBDFRGLASKS 6771 3 378 APAGTLANTGSVKDVURYQAVLANLLLEEDNKFCADCQSKGFR MASMNIGVFICTRCAGIHRNIGVHISRVKSVMLDQWGDGQGKFR MASMNIGVFICTRCAGIHRNIGVHISRVKSVMLDQWGDGQGKFR MASMNIGVFICTRCAGIHRNIGVHISRVKSVMLDQWGDQGCGRFR MASMNIGVFICTRCAGIHRNIGVHISRVKSVMLDQWGDQGCAAPFT AVPILGYPRQDBGSQRYAVMRAARMIQLKDSRGEANPIDEGKT LIGGALLNIYTEMGRRTELITESPLWGAMWVGFLGSGAAAFFT AVPILGYPRQDBGSGRYAVMRAARMIQLKDSRGSAAAFFT AVPILGYPRQDBGSGRYAVMRAARMIQLKDSRGSAAAFFT AVPILGYPRQDBGSGRYAVMRAARMIQLKDSRGSAAAFFT AVPILGYPRQLBGSGGTFILGGFFVNKLRLRGSAVIK PCLFCTVVSLLGILVFSLHCFSVPMAGVTASYGGSLLPEGHINL TAPCNAACSCQPBHYSPVCGSGLMYFSJCGSLLPEGHINL TAPCNAACSCQPBHYSPVCGSGLMYFSJCGSLLPEAHLINL				
RCSVLVSEALSGSAMDGIVTEVAVGVERGSDELLSGSVLSSPNS NMSSMVVTANGADSKKFKGBDKMDGAPSEVLHIRILIGEGEVTETE VILIGILPFGKVTNI LINLKGKNQAPELLATHERAJTYKGNYYSAVT PHLENQ  6766  1 1287 BEGSFKASI-TWLMPIGEMKLHCEVEVISRHLPALGIRNRGKGVR AVISLCQGTBRSQPFVRAFLLISTLKDKRGTRYBLERNIRGFFT KFVDEGKATVRLKEPPVDICLSKANSSSLEGFLSAMRLAHAGCN VDTPVSTLTPVKTISSFRMPKTKMVTISKKDYPLSKRHL QTSYCGLVRVDMRMLCLKSLRKLDLSHNHIKKLPATIGDLIHLQ KLAININDHLBFSVALCHSTLQRSLUSLGISLBKLKLALPVQFCQ LQELKRILKLDDNELQFPCKLGGLJINLRFLSAARKLPFLSEEF RNISLEYLDLFGNTFEQPKVLPVIKLQAPITLLBSSARTILHNR IPYGSHIIPFHLQDLDTAKLCVCGFCLSFFJGGTTTMNIHSV AHTVULVDNLGGTBAPIISYFCSLGCVVNSSDI APHICLCSSDLQFRYKRAFLEDRGLQGYCVNSSDI GRIGSDNKYKKDFAKSRSOPHSSTCVDDDPRMKHFLNV RQPLPQPTCDPEQLGLRHAQXAHQLQSDVKYKSDLNLTRGVGWT PPGSYKVEMARRABALLANARGLGLQGYKGABAVEAGHOGGEV NDDATKILLBVKKKALLL 6768 2 363 PGSTISCYLLSBGBLPLCMQVACGBRKHRAPTMKTLRGVKKTF PROSYKVEMARRABALLANARGLGLQGAYRGABAVEAGHOGGEV NDDATKILLBVKKKALLL 6769 284 396 MSTFDFSTARNOQELANRVSCLKAMITILMJCAKGAD 6770 1 397 QRNYQVIWSSTNAKLHDYKDEVKKAMITILMJCAKGAD 6770 1 397 QRNYQVIWSSTNAKLHDYKDEVKKAMITILMJCANGAD 6771 3 378 APAGTLANGKSVLOVDRYQAVLAHEFNYNSVMQVPRVEK ITLMMVGRALDKKLLDNAAADLAALSQCPLITKARKSVAGF KIRQGYPIGCKVTLRGRRMMEFPERLITLAVPRIRDFRGLSAKS 6771 3 378 APAGTLANGKSVLOVDRYQAVLALLERBNKFCADQCSKGPR 6772 1 1400 AAAFLGGATVONTYQAVLAHLERBNKFCADQCSKGP 6772 1 1400 AAAFLGGATVONTYGAVLAHLERBNKFCADQCSKGP 6772 1 1400 AAAFLGGATVONTYGAVLAHLERBNKFCADQCSKGP 6772 1 1400 AAAFLGGATVONTYGAVLAHLERBNKFCADQCSKGP 6774 AAPIGGTVNGFITUTUTSLALBERDKFCADQGSGAASYDIAA CLCLTFVSYPGGSG\HRNLGWGR\VLMGTGSLVFALPHFTAG F**GWELDAGWTCPANFR, VCAG\HTSBLSRYQLVFMLGQFL HGGATTYLTGGTVTLDENVKASSCTYLTALFYRALGGGAAAPFT AVPILGYPRQLPGSGGYAVMRABEMIGLGSGAAAFFT ALGGALLAHLYTEMGRRTELITESPLWGGAMWGPLGSGAAAFFT ALGGALLAHLYTEMGRRTELITESPLWGGAMWGPLGSGAAAFFT ALGGALLAHLYTEMGRRTELITESPLWGGAMWGPLGGGAAAFFT AVPILGYPRQLPGSGGTFLLGGFFVNKLRIRGSSAVIK FCLFCTVVSLLGILVPSLHCFSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDCMYTSYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDCMYTSYGGSLLPEGHLNL	Cace	ļ	550	
MMSSMVYTANGIDSKKPFGGROMDGAPSRVLHTRKLDGEVTETE VILIGLEPFGKVTNIIMLKGKNQAFLELATREAAITKRAYYSAVT PHLENQ 6766  1 1287 EGGSFKASLTHLMPLGEMKLHCEVEVISRHLPALGLRNEGGVR AVLSLCQQTSRSQPPVRAFLLISTLKDKRGTRYELRENIKQFFT KYVDEGKATVELKESPVDICLSKANSSSLKGFLSAMKLAHBGCN VDTPVSTLTPVKTSEFMBFKTKMVITSKDVPLSKNFFYSLEHL QTSYCGLVRVDMRMLCLKSLKKLDLSHNHIKKLPATIGDLIHLQ KLMINDNHLRSFSVALCHSTLQKSLWSLDISKNKKLALPVQFCQ LQBLKBLKLDDDBELQFFCKLGQLINLRFLSAARKLPFLPSEF RNISLSFYLDLFGNTFEQPKVLPPVLAQPILLISSAARKLPFLPSEF RNISLSFYLDLFGNTFEQPKVLPPVLAQPILTLESSAARKLPFLPSEF RNISLSFYLDLFGNTFEQPKVLPPVLAQPILTLESSAARKLPFLPSEF RNISLSFYLDLFGNTFEQPKVLPPVLAQPILTLESSAARKLPFLPSEF RNISLSFYLDLFGNTFEQPKVLPPVLAQPILTLESSAARKLPFLPSEF RNISLSFYLDLFGNTFEQPKVLPPVLAQPILTLESSAARKLPFLPSEF RNISLSFYLDLFGNTFEQPKVLPPVLAQPILTLESSAARKLPFQFSEF RNISLSFYLDLFGNTFEQPKVLPPVLAQPILTLESSAARKLPTQFSEF RNISLSFYLDLFGNTFEQPKVLPPVLAQPILTLESSAARKLPTQFSEF RNISLSFYLDLFGNTFAQFVLAGTURGFTTMNLHSV AHTVVLNDNLGGTEAPILTSFCSILGCYWSSDSD  4 PMGTLCSSDLQFTKRAFPLGAGLGGVKYSDLDDFMKHFLNV GRLQSDNEYKKDFAKSRQFHSSTDQPGLLQAKRSQQLASDVHY RQPLPQFTCDPEQLSLRHAQXAGLQGSDVKYSDLNLTRGVGWT PGSTXVKMARRAARLANARGLGLGGAVKRGARVEAGDHQSGVV NPDATHILHVKKKKALLL  6768 2 363 PGSTISCYLLSGSGLPLCQAVCGEBKHRAPTMKTLRARFKKTE* LRLSFYDLGSCPPCOPCPIPKPAARGRRGSQDWGSDBRLLQAV ENNDAPRVAALIARRGLVPKLDAWKSCABHL 6770 1 397 QRNYQVIWSSTMAKLHDYTKLDPGGSAAPHL 6769 284 396 MSTTDFSTARNQELANKVSCLKAMI/THLQAMGQAD 6770 1 397 QRNYQVIWSSTMAKLHDYTKDBVVKKUMTRFNYNSVMOVPRVEK ITLMWGGRAIDKKKKALLU 6771 3 397 QRNYQVIWSSTMAKLHDYTKDBVVKKUMTRFNYNSVMOVPRVEK ITLMWGGRAIDKKKALLU 6771 3 398 APAGTLAMTGKSVKDVDRYQAVLANALLEEDMKFCADCQSKGFR MASWNIGVFICIRCGHRMWFPFERNLESPANGAWMOFHLGSGAAAFFT 6772 1 1400 AAAFLQGMTVAGFINTUTTSL\ERRYDLISYQSGLASSYDIAA CLCLITFVSYFGGSG\HKPRMLGMSR\VILSTGLSKYQLVFMLQGFL HGVGATPLVTLGVTVLDENVKSSCSPIYILATYTAALLGPAAGY LIGGALLNIYTHMGRRTFLITTSPLWYGGGGAAAFFT AVPILGYPRQLPGSGYAVMRAAEMIQLGDSSRGEANPDFGKT IRDLPLSIMLLLKWPTFILLCLAGATEATLINGGSGAAAFFT AVPILGYPRQLPGSGYAVMRAAEMIQLKDSSSTPDFKLES QFSLSASRAATLFGYLVVPLGGGGGTFIGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVPSLHYSSLCHAGCPAATEINVIG	0/05	, ,	220	-
VIALGLPPGKVTNILMLKGKNQAFLELATERAAITAKNYYSAVT PHLENQ  G766  1 1287 EGGSPKASITWLMPLGEMKIHCEVEVISRHLPALGLKNRGKGVR AVISLCQQTSRSQPVRAFILLSTILDKKGTRYSLRENISGFFT KFVDEGKATVRLKEPPVDICLSKANSSLKGFLSAMRLAHRGCN VDTPVSTLTPVKTSEFEMPKTKNVITSKOVPLSKNFYSLEHL QTSYCGLVRVDMRMLCLKSLRKIDLSHNHIKLPATIGDLTHLQ KLHINDHILESSVALCHSTLGKUSLJSHNHIKKLPATIGDLTHLQ KLHINDHILESSVALCHSTLGKUSLJSLSKIKJKLAPUVPGE RNISLEYLDLFGNTFRQPKVLEVIKLQAPUTLSSARTILHNR 1PYGSHITPPHLGODLDTAKLGVCGRFCINSFIGGTTTMNLHSV AHTVVLVDNLGGTEAPIISYFCSLGCYVMSSDI 6767 336 919 APMICLCSSDLQFVXKBFLRDRGLQTGYSVDDDPRMKHFLNV GRIQSDNEVKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY RQPLPQPTCDPROLGLRHQKAHOLQSDVKXSDLNITRGVGWT PPGSYKVEMARRABLANARGLGLQGAVGSDKKKSDLNITRGVGWT PPGSYKVEMARRABLANARGLGLQGAVGSDKKKSDLNITRGVGWT PPGSYKVEMARRABLANARGLGLQGAVGSBKHRAPTMKTLRARFKKTE 6768 2 363 PGSTISCYLISBSSLPLCMQVACGBSKHRAPTMKTLRARFKKTE PPGSYKVEMARRABLANARGLGLQGAVGSBCHRAPTMKTLRARFKKTE LRLSPTDLGSCPPCOPCPIPKAARGRRQSQDWGKSDBRLLQAV ENNDAPRVAALIARKGLVPTKLDPBGKSAFHL 6769 284 396 MSTPDFSTAENQGLANBVSCLKAMITHLQAMGQAD 6770 1 397 QRNQVINSSTMALHDYXKDEVVKLMTFBNYSVMOVPRVEK KIRQGYPICKVTLRGERNWBPFBRLITTAVPRIRDFRGLSARS 6771 3 378 APAGTLAMTGKSVAVDDRVQVIABILLEEDNKFCADCOSGRS 6771 3 378 APAGTLAMTGKSVAVDDRVQVIABILLEEDNKFCADCOSGRS 6772 1 1400 AAAFLQGMTVNGFINVITSL LERRYDLHSVGSLASSYDIAA CLCLTFVSVEGGSG\KKPRMLCHGR\VLMATSSLVPALPHFTAG P**GWKLDAGVRTCPANPR\PVCAS(HTSGLSRYQLVFMLGQFL HGWGATFLITLGVTYLDRNVKSSCSPITIAIPTTAALLGPAACY LIGGALLNIYTEMGRRTEUTTSPLMVGSRSVLPFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAS(HTSGLSRYQLVFMLGQFL LIGGALLNIYTEMGRRTEUTTSPLMVGRSANPGRASAPPT AVPILGYPRQLPGGRGYAVMRAAEMHQLKDSSRGEASNPDGKT IRDLPLSIMLLKNPTPTLLCLAGATEATLITGMSTTSPKRLES QFSLSASRAATLFGYLVVBAGGGGFTLGGFFVNKLBLRGSAVIK PCLFCTVVSLLGILVFSLCGSDGLMYSSLCHBGCPAATETNVDG	ľ			
6766 1 1287 BEGSPRASLTWLMPLGBMKLHCEVEYISRHLPALGLRNRGKGVR AVISLCQOTSRSOPPVRAFILLISTLKDKRGTRYBLRENIRGFFT KEYUDEGKATVELAERPEVDICLSKANSSSLKGFLSAMKLAHRGCN VUTPVSTLITPVKTSEPENFKTKMVITSKKDYPLSKENFYSLSHL CTSYCGLVRVDMRMLCLKSLRKIDLSHMHIKKLPATIGDLTHLL ELMINDNHLRSPSVALCHSTLQKSLWSLDLSKNIKIALPVQFCQ LQBLKNLKLDDNELIQFPCKIGQLINLRFLSAARNKLPFLPSEF RNISLEYLDLFGNTFEQPKVLPVIKLQAPLTILBSSARTILHNR IPYGSHITPHHLCQDLDTAKICVCGRFCLNSFIGGTTTMNLHSV AHTVVLVDNLGGTEAPIJSTCLGGYVMSSDI  6767 336 919 APMICLCSSDLGFRYKBRFLRDRGLQGYGSVDDDPRMKHFLNV GRIQSDNBYKKDPAKSRSGFHSSTDOPELLQAKRSQQLASDVHY RQPLPQPTCDPBQLGLRHAQKAHQLQSDVKKKSDLAIDTRGGWY RQPLPQPTCDPBQLGLRHAQKAHQLQSDVKKKSDLAIDTRGGWY RQPLPQPTCDPBGLGLRHAQKAHQLQSDVKKKSDLAIDTRGGWY RQPLPQPTCDPBGLGLRHAQKAHQLQSDVKKKSDLAIDTRGGWY RQPLPQPTCDPBGLGLRHAQKAHQLQSDVKKKSDLAIDTRGGWY RQPLPQPTCDPBGLGLRHAGKAHQLQSDVKKKSDLAIDTRGGWY RQPLPQPTCDPBGLGLRHAGKAHQLQADWKKTERAFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDBRLLQAV ENNDARTKLAHLANKKKKALLL  6768 2 363 FGSTLSCYLLSSGSLPLCHQVACGEBKHRAPFMKTLRARFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDBRLLQAV ENNDARFRAALLARKGLUPTKLDPBGKSSHFL  6769 284 396 MSTPDESTABRNGGLANRVSCLARMITIMLQAMGGAD  6770 1 397 QRNYQVIWSSTHAKLHDYYKDEVVKKLWTFFNYNSVMQVPRVEK ITLNMGVGBAIDAKKLLDNAADLAAIGSQRPLTKARKSVAGF KIRQGYPIGCKVTLKGRRNWBFPBELTTLAPRTRDFRGLSAKS  6771 3 378 APAGTLAMTGKSVKDVDRYQAVIANLLLEEDNKFCADCQSKGPR MASMNIGVFICTRCAGIHRNLCVHISRVKSVNLDQWTQBQIQCM ORKGNGKANRLVBATVJRSTWGTDPPLIFFSNLRG  6772 1 1400 AARFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLYASSYDIAA CLCLITVSYFGGSG\HKRMLCWGR\VLMMTGSLVFALUPHFTAG P++GWLDAGVRTCPANPR\PVCAG\HTSGLSRVQLVFMLQPIL HGVGATPLYTLGVTYLDRNVKSSCSPIYLAITYTAAILGPAAGY LIGGALLNIYTBMGRRTELITTSPLWGGRANFDLLGGRAAPFT AVFILCYPRQLPGSQRYAWRARHGQLKDSSRGEASNPDPGKT IRDLPLSIWLLKNPTFTLLCLAGATEATLITGMSTFSDKFLES QFSLSASRAATLFGYLVVBAGGGGTFLGGFFVNLRLRGGSAVIK FCLFCTVVSLLGILVFSLCGSDGGGGFFVONKLRLRGSAVIK FCLFCTVVSLLGILVFSLCGSDGGGGFFLAGGFFANTBKRGSAVIK FCLFCTVVSLLGILVFSLCGSDGGGGFFLAGGFFANTBKRUNGG FCLFCTVVSLLGILVFSLCGSDGGGGFFLAGGFFANTBKRUNGG			i	
1287   BGGSPRASLTWLMPLGEMKLHCEVEVISRHLPALGLRNRGKGVR		į		
AVI.SLCQQTSRSQPPVRAPILLISTLKDKRGTRYBLRENIEQFFT KRYDEGKATURLERPPUDICLSKANSSLRGFISAMRIAHRGCN VDTPVSTITIPVKTSEPKBRFYTKMVITSKKDYPLSKYPFYSLEHL QTSYCGLVRUDMRHICLKSLRKLDLSHNHIKKLPATIGDLIHLQ ELMININHESFSVALCHSTLQKSLWSLDLSKNKIKALPVQFCQ LQEIKNIKLDDNELIQPFCCHGQLINLRFISAARNKLPPLPSSE RNISLEYLDLFGNTFGPKVLPVIKLQAPLTILESSARTILHNR IPYGSHIIPFHLCQDLDTAKICVCGRFCLNSFIQGTTMNLHSV AHTVVLVDNLIGGTEAPIISYFCSLGCYVNSSDI  6767 336 919 APMICLCSSDLQFRYKRAFIRDRGLQIGYCSVDDDPBMKHFLNV RQPLPQPTCDPBQLGLRHAQXAHQLQSDVXYKSDLMLTRGVGWY PPGSYKVMARRABKLANARGLGLQGAYRGAEAVEAGDHQSGV NPDATRILHVKKKALLL  6768 2 363 PGSTISCYLLSEGSLPLCMQVACGEBKHRAPTMKTLRARFKKTE LRISPTDLGSCPPCGPCPIPKPAARGRQSQDMGKSDBRLLQAV ENNDAPRVAALIARKGLUPTKLDPBGKSAFHL  6769 284 396 MSTFDESTARNDCLANBVSCLKAMNTHMQAMGQAD  6769 1 397 QRNYQVINSSTNAKLHDYYKDEVVKKLMTEFNYNSWQVPRVEK KIRQSYPIGCKVTLRGERMWEPFERLITLAVPRINDFRGSAKS  6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR KIRQSYPIGCKVTLRGERMWEPFERLITLAVPRINDFRGSAKS  6772 1 1400 AAAFLQGMTUNGFINTVITSL\ERRYDLHSYQSGLTASSYDIAA  CLCLITVSYFGGSG\HRPRHLGMGKYCVMGMYDBQIQCM QRNGGKARNLYRAYLYBAYTLFTRRPQIDPYLLWSNLEG  6772 1 1400 AAAFLQGMTUNGFINTVITSL\ERRYDLHSYQSGLTASSYDIAA  CLCLITVSYFGGSG\HRPRHLGMGKYCVMGMYDBQIQCM PP+GWKLDAGAYRCTPANPRF,PVCSG\GSRGPANPTT MSGWRIAGNYTCPANPR PVCCSG\GSRGPANPTT MSGWRIAGNYTCPANPR PVCCSG\GSRGPANPTT MSGWRIAGNYTCPANPR PVCCSG\GSRGPANPTT MSGWRIAGNYTCPANPR PVCCSGTRYGLSKYQLVFNLGQFI. HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAALLGPAAGY LIGGALLNIYTENGRRTELTTESPLWGAWWUGFLOSGAAAFTT MSGWRIAGNYTCPANPR PVCCSGTRYGLSKYQLVFNLGQFI. HGVGATPLYTLGVTYLLGRGGGTFLGGFFVNKLLRIRGSAVIK MSWRIAGTLIAVPSLLCHGGGGTFLGGFFVNKLLRIRGSAVIK PCLFCTVVSLLGILVPSLHCPSWMAWARARMILLKGSAVIK PCLFCTVVSLLGILVPSLHCPSWPAGVTLAYGGGSLTPRGGFLINL TAPCNAACSCQPSHYSBVCGSDGLMYFSLCHAGCPAATETNVDG	7872			
KEVDEGKATVRLÆBPPVDICLSKANSSSLKGFLSAMRLAHRGCN VDTPVSTLTPVKTSEPSNFTCTKVITISKKDYPLSAMRLAHRGCN VDTPVSTLTPVKTSEPSNFTCTKVITISKKDYPLSAMPYSLEHL CTSYCGLVRVDMRHLCKSLRKLDLSINHHKKLPATIGDLIHLQ ELNLNDHHLBSFSVALCHSTLQKSLÜSLDLSKNKKALPUQPCQ LQBLKBLKLDDNBLLQPPCKIGGLINRFLSAARNKLPPLPSBEP RNISLEVLDLGKGNTFPGDRVLPVIKLQAPLTLLBSSARTILHNR IPYGSHIIPPHLCQDLDTAKICVCGRFCLNSFIQGTTTMNLHSV AHTVVLVDRLGGTEAPTISTFCSLGCVINSSDI 6767 336 919 APMICLCSSDLQFYKKBFLRDRGIQIGYCSVDDDPRMKHFLNV GRLQSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQOLASDVHY RQPLPQPTCDPEQLGLRHAQXAHGLQSDVKYKSDLANLTRGVGWT PPGSYKVEMARRAAKLANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATBILHWKKKKALLL 6768 2 363 PGSTISCYLLSEGSLPLCMQVACGBBKHRAPTMKTLGARFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDBRLLQAV ENNDAPRVAALIARKGLVPTKLDPEGKSAHL 6769 284 396 MSTEDESTAKNOQLABREVSCLKAMITIMLQAMXQAD 6770 1 397 QRNYQVIWSSTNAKLHDYYKDEVVKKLMTEPNYNSVMQVPRVEK ITLNMGVGRALADKYKLDDYKADEVKKLMTEPNYNSVMQVPRVEK ITLNMGVGRALADKKLLDNAADALAALGGKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEPPERLITTAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEBDNKFCADCQSKGFR MASMNIGVETCIR CAGIHRNYLHISRVKSVNIDQWTQBQIQCM QRMGKARRLYEAYLPETFRRQIDPYLFWSNLEG 6772 1 1400 AAAFLQGWTUNGFINTVITSL\BRRYDLHSYQSGLJASSVDIAA CLCLTFVSYFGGSG\HKFRWLGRR\VLMGTCSLVFALPHFTAG PF+GWKLDAGVRTCPANPR\PVCAG\HTSGLSXPQLVPMLGQFI. HGWGATPLYTLGVTYLDENVKSCSPIYIAIFYTAALLGBAAGFT AVPILCYFRGLPGSGKYAVMRAARMHQLKDSSRGEASNDPIGGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITCMSTFSPKFLES QPSLSASRAATLFGYLVVPRAGGGSTFLGGFVWKLELRGSAVIK FCLFCTVVSLLGILVPSLHCSVPMAGVTASYGGSLLPKGEINLI. TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	6766	1	1287	
VDTPVSTLTPVKTSEPENFKTKMVITSKKDYPLSKNFPYSLEHL QTSYCGLVRVDMRNLCLESLRKLDLSHNIIKKLIPATIGDLIHLQ KLIMINDHILESPSVALICHSTLQKSLWSLDLSKNKIKALPVQFCQ LQELKNLKLDDNELIQFPCKIGQLINLRPLSAARNKLPFLPSEP RNISLEVILDEGNITEQPKVLFVIKLQAPLITLLESSARTILHNR IPYGSHIIPPHLCQDLDTAKICVCGFFCINSFIQGTTTMNLHSV AHTVVLVDNLGGTEAPIISYFCSLGCYWSSDI 6767 336 919 APMICLCSSDLQFFXKEAFLRDRGLQIGKTSVDDPRMKHFLWV GRLQSDNEYKKDFAKRSRSQFHSSTDQGLLQARRSQOLASDUHY RQPLPQPTCDPEQIGLIRHAQXAHQLQSDWKKSDLMLTRGVGWT PPGSYKVEMARRAABLANARGLGLQGAYRGAEAVEAGDHYSGEV NPPATRILHWKKKKALLL 6768 2 363 FGSTISCYLLSEGSLPLCMQVACGEBKHRAPTMKTLRAFFKKTE LRISPTDLGSCPPCGPCFIPKPAARGRRQSQDWGKSDBRLLQAV ENNDAPRVAALIARKGLVPTKLDPBGKSAFHL 6769 284 396 MSTPDFSTAENNQELANEVSCILKAMITLMLQAMGQAD 6769 1 397 QRNYQVIWSSTMAKLHDYKDEVVKKLMTEFFNNSVMQVPRVEK ITLNMGVURALADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEPFERLITTLAVPRIRDFFRGLSARS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVANALLLEEDNKFCADCQSKGPR MASWNIGVFICIRCAGHRNLSVHSTVSTVSUDDWTQSGLQCK GRKCNGKANRLYBAYLPBTPRRPQDPYLFMSNLBG 6772 1 1400 AAAFLGGMTUNGFINTVITSLJERRYDLHSYQSGLXSSYDIAA 6771 6 AAAFLGGMTUNGFINTVITSLJERRYDLHSYQSGLXSSYDIAA 6772 1 1400 AAAFLGGMTUNGFINTVITSLJERRYDLHSYQSGLXSSYDIAA CLCLITYSYSTEGSG\HRPMLGWGR\UMGTGSLDYFNLGQPL HGGGATLNIYTEMGRRTELTTESPLWYGSGLXSSYDIAA 6772 1 1400 AAAFLGGMTUNGFINTVITSLJERRYDLHSYQSGLXSSYDIAA 6772 1 1400 AAAFLGGMTUNGFINTVITSLJERRYNDLHSYQSGLXASSYDIAA 6772 1 1400 AAAFLGGMTUNGFINTVITSLJERRYNDLHSYQSGLXASSYDIAA 6772 1 1400 AAAFLGGMTUNGFINTVITSLJERRYNDLHSYQSGLXASSYDIAA 6772 1 1400 AAAFLGGMTUNGFINTVITSLJERRYNDLHSYQSGLXASSYDIAA 6772 1 1400 AAAFLGGMTUNGFINTVITSLJERRYNDLHSYQSGLXASSYDIAA 6772 1 1400 AAAFLGGMTUNGFINTVITSLJERRYNDLHSYQSGLXASSYDIAA 6772 1 1400 AAAFLGGMTUNGFINTVITSLJERRYNDLHSYGSGLASSPDFGKT 6772 1 1400 AAAFLGGMTUNGFINTVITSLJERRYNDLHSYGSGLASSPDFGKT 6772 1 1400 AAAFLGGMTUNGFINTVITSLJERRYNDLHSYGSAGLASSPDFGKT 677			i	
QTSYCGLVRVDMRMLCLKSLRKLDLSHNHIKKLPATIGDLIHLQ KLININDHLESFSVALCHSTLQKSLMSLDLSKNKIKALPVQPCQ LQRIKNIKLDDNRLLQPPCKIGQLINLRPLSSARNKLPDLPSEBF RMLSLEYLDLFGNTFBQPKVLPVIKLQAPLTLLESSARTILHNR IPYGSHIIPPHILCQDLDTAKICVCGRFCLNSFIQGTTTMNLHSV AHTVVLVDNLGGTERPIISYPCGLGCYWSSDI  6767 336 919 APMICLCSSDLQPRYKERFLRDRGLQIGYCSVDDDPRMKHFLNV GRIQSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY RQPLPQPTCDPEQLGLRHAQKAHQLQSDVKYKSDLANLTRGVGWT PPGSYKVEMARRAARLANARGLGLQGAYRGARAVEAGDHQSGEV NPDATKILHVKKKKALLL  6768 2 363 PGSTISCYLLSEGSLPLCMQVACGBEKHRAPTMKTLRAFKKTE LRISPTDLGSCPPCOPCPIPKPAARGRRGSQDWGKSDERILQAV ENNDAPRVAALIARKGLVPTKLDPBGKSAFHL  6769 284 396 MSTFDESTAKNNQELANEVSCLKAMITIMLQAWGQAD 6770 1 397 QRNYQVIWSSTNAKLHDYYKDEVVKKUMTEFNYNSVMQVPRVEK ITILMGVGRALADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRGGYPIGCKVTLRGERNWBEPFERLITTLAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR MASWNIGVFICIRCAGIHRNLSVHISRVKSVNLDQWTQRQIQCM QRMGNGKANRLYBAYLPETFRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSILERRYDLBSYGSGLASSYDIAA CLCLTFVSYPGGSG\HKPRWLCWGR\VLWGTGSLVFMLGQPL HGGGALLNIYTEMGRRTELTTESPLWGTSLVFALLGFBAAGY LIGGALLNIYTEMGRRTELTTESPLWGTSLVFALLGFBAAGY LIGGALLNIYTEMGRRTELTTESPLWGTSLVFALLGFBAAGY IRDLPLSIWLLLKNPTFILLCLAGATBATLITGMSTFSPKFLES QPSLSASRAATLFGYLVVPAGGGGTLGGFFVNKKLEKGSAVIK FCLFCTVVGLIGLILVFSLICPSVPMAGYTSSYGSGSANPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATBATLITGMSTFSPKFLES QPSLSASRAATLFGYLVVPAGGGGTLGGFFVNKKLERGSAVIK FCLFCTVVGLIGLILVFSLICPSVPMAGYTSSYGSGSANPDFGKT FCLFCTVGLIGLILVFSLICPSVPMAGYTSSYGSGSANPDFGKT FCLFCTVGLIGLILVFSLICPSVPMAGYTSSYGSGSANPDFGKT TAPCNAACSCQPBHYSPCGSDGLMYFSLCHAGCPAATETNVDG				
ELNLNDNHLESFSVALCHSTLQKSLWSLDLSKNKIKALPVQFCQ LQEIKKNLKIDDNELQFPCKIGGLINLEFISAARNKLPPLPSEF RNISLEYLDLFGNTFEQPKVLPVIKLQAPLTILESSARTILHNR IPYGSHIIPFHILCQDLDTAKICVGEFCLASFIGGTTTNNHSV AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI  6767 336 919 APMICLCSSDLQFRYKEAFLRDRGLQIGYCSVDDDPRMKHFLNV GRIQSDNEYKKDFARSSQFHSSTDQPGLLQAKRSQOLASDVHY RQPLPQPTCDPEQLGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT PROSYKVWMARRAARLANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATRILHVKKKKALLL  6768 2 363 PGSTISCYLLSBGSLPICMQVACGBEKHRAPTMKTLRARFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRQSQDWGKSDKRLLQAV ENNDAPRVAALIARKSLVPTKLDPBGKSAFHIL  6769 284 396 MSTPDFSTARNQELANBVSCLKAMITJMLQAMGQAD  6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVKKKMTFFNYNSVMQVPRVEK ITLNMGVGRATADKKLLDNAADLAALSGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERNWEPPERLITIAVPRIRDFRGLSAKS  6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLBEDNKFCADCQSKGFR WASWNIGVFICIRCAGIHRNLGVHYSRVKSVNLDQWTQBQLQCM QRMGNGKANRLYBAYLPBTFRRRQIDPYLFWSNLEG  6772 1 1400 AAAFLQGMTUNGFINTVITSL\ERRYDLHSYQSGLASSYDLAA CLCLITFVSYFGGSG\HKRNLGMGR\VIMOTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGWGATFLYTLGUTYLDRBNVKSCSPITIALFYTAALLGPAAGY LIGGALLNIYTEMGRRTELITESSTYDLSGAAAFFT APPILGTPROLPGGGRYAWMRAARMHQLKDSSKGEASNPDFGKT IRDLPLSINLLLKRPPPILLCLAGATEATLTGMSTFSBKFLES QFSLASKAATLFYSLLGFSVPMAGYTASYGGSLLPRGHINL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG		Į	ļ	
LQBLKNI_KLDDNBLIQFPCKIGQLINLRFISAARNKLPFIPSEF RNISLEYI.DLFGNTFFQPXVLPVIKLQAPITILBSSARTILHNR IPYGSHIIPFHLCQDLDTAKICVCGRFCLNSFIQGTTTMNLHSV AHTVULVDNLGGTEAPIISYFCSLGCYVNSSDI 6767 336 919 APMICLCSSDLQFRYKEAFIRDRGLQIGYCSVDDDPRMKHFLNV GRIQSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY RQPLPQPTCDPEQLGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT PPGSYKVEMARRAARLANARGLGLQGAYRGABAVEAGDHQSGEV NPDATRILHVKKKKALLL 6768 2 363 PGSTISCYLISBGBLPLCMQVACGBEKHRAPTMKTLRARFKKTE LRISPTDLGSCPPCGPCPIP FKPAARGRRQSQDWGKSDBRLLQAV ENNDAPRVAALIARNGLVPTKLDPEGKSAFHL 6769 284 396 MSTFDFSTAENNQELANEVSCLKAMITIMLQAMGQAD 6770 1 397 QRNYQVIWSSTMAKLEDYYKLDPEGKSAFHL KIRGSYPIGCKVTLRGERNWEFPERLTTLAVPRIRDFRGLSAKS KIRGSYPIGCKVTLRGERNWEFPERLTTLAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR MASWNIGVFICIRCAGIHENLGWHISRVKSVNLDQWTQEQIQCM QRMCNGKANRLYEAYLPEFTRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGWTVMGFINTVITSL\GRRYDLBSYGSGLASSYDLAA CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P++GWKLDAGVRTCPANPR\PVCAG\BTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVCSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTFELTTESPLWGAWWGFIGSGAAAFFT AVPILGYPRQLPGSQRYAWMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSINLLLKNPTFILLCLAGATEATLITGMSTFSSKFLES QFSLSASRAATLFGYLVVPBAGGGGTFLGGFFVNKLERLGSAVIK FCLFCTVVSLLGILVFSLEGFSVPNAGYTASYGGSLLPRGHINL TAPCNAACSCQPBHYSPCGSGGLMYFSLCHAGCPAATETINVDG				
RILSLEYLDLFGNTFEQPXVLPVIKLQAPLTILLESSARTILHNR IPYGSHIIPFHLCQDLDTAKICVCGRFCLMSFIGGTTIMNLHSV AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI  6767 336 919 APMICLCSSDLQFRYKEAFLRDRGLQIGYCSVDDDPRMKHFLNV GRLQSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY RQPLPQPTCDEPQLGLRHAQAKHQLQSDVKYKSDLNLTRGVGMT PPGGSYKVMMARRABLANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATKILHVKKKKALLL  6768 2 363 PGSTISCYLLSESBLPLCMQVACGEBKHRAPTMKTLRARFKKTE LRLSPTDLGSCPPCGPCTIPKPAARGRQQSQWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPEGKSAPHL  6769 284 396 MSTPDFSTAENNQELANEVSCLKAMITLMLQAMGQAD  6770 1 397 QRNYQVINSSTMAKLHDYXDDEVVKKLMTEPNYMSVMQVPRVEK KIRQGYPIGGKVTLAGERMWEPFERLITTAVPRIRDFRGLSAKS KIRQGYPIGGKVTLAGERMWEPFERLITTAVPRIRDFRGLSAKS  6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR MASWNIGYPICIRCAGIHRNLGVHISRVKSVNLDQWTQBQIQCM QRMGNGKANRLYBAYLPEFFRRQIDPYLFMSNLEG  6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLJASSYDIAA CCLCLTFVSYPGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P*+GWKLDAGWTCPANPR\PVCAG\HTSGLSRYQLVFMIGQFL HGVGATPLYTLGVTYLLDENVKSSCSPIYIAFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAMWVGFLGSGAAAFFT AVPILGYPRQLPGSGRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLIKNPTFILLCLAGATEATLITCMSTFSDKFLES QPSLSASRAATLFGYLVLVPSLAGGGSTFFLGGFFVNKLELRGSAVIK FCLFCTVVGLLGILVPSLHCPSVPMAGVTASYGGSLLPEGHINL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATEINVDG		· ·		
IPYGSHIIPFHLCQDLDTAKICVCGRFCLNSFIQGTTTMNLHSV AHTVULVDNLGGTEAPIISYFCSLGCYVNSSDI 6767 336 919 APMICLCSSDLQFRYKEBAFLRDRGLQIGYCSVDDDPRMKHFLNV GRIQSDNEYKKDFAKSRSQFHSSTOPGGLIQARRSQDLASDVHY RQPLPQPTCDPEQLGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT PPGSYKVEMARRAABLANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATKILHVKKKKALLL 6768 2 363 PGSTISCYLLSBSBLPLCMQVACGEBKHRAPTMKTLRARFKKTE LRLSPTDLGSCPPC9PCPIPKPAARGRRQSQDWGKSDBRLLQAV ENNDAPRVAALIAR KGLVPTKLDPBGKSAPHL 6769 284 396 MSTPDFSTARNQELANBUSCLKANLTLMLQAMGQAD 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK ITLNMGVGRAILAKKLLDNAAADLAAISGGKPLTTKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVIANLLLEEDNKFCADCQSKGFR WASMNIGVFICIRCAGHRANLSHISKVKSVNLDQWTQBQIQCM QRMCNGKANRLYEAYLDFSTERRPQDDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLTASSYDIAA CLCLTFVSYFGGSG\HKPRMLGWGR\VLMGTGSLVFALDFHTAG P**GWKLDAGWTCPANPRP\PVCAG\HTSGLSRYQLVFMLGGFL HGWGATPLYTLGVTYLDENVKSCSPIYIAIFYTAAILGPAAGY LLGGALLNIYTEMGRRTELTTESPLWVGANWUGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAARMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITCMSTFSPKFLES QFSLSASRAATLFGYLVPALGGGGTFFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVPSLHCPSVPMAGVTASYGGSLLPRGHINL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATEINVDG			•	
AHTVULVDNLGGTEAPI 13YFCSLGCYVNSSDI  6767 336 919 APMICLCSSDLQFRYKRAPIRDRGLQIGYCSVDDDPRMKHFLNV GRLQSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY RQPLPQPYCDPRQLGLRHAQKAHQLQSDVKYKSDLANLTRGVGMT PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATRILHVKKKKALLL  6768 2 363 PGSTISCYLLSEGSLPLCMQVACGEBKHRAPTMKTLRARFKKTE LRISPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDBRLLQAV ENNDAPRVAALIARKGLVPTKLDPBGKSAFHL  6769 284 396 MSTPDFSTABNNQELANBVSCLKAMITIMLQAMGQAD 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLWTEFNYNSVMQVPRVEK LITLINMGVGRAIADKKLLDNAAADLAAISGQKPLITKARKSVAGP KIRQGYPIGCKVTLRGERNWEPPERLITIAVPRIRDFRGLSAKS 6771 3 378 APAGTLANTGKSVKDVDRYQAVLANLLLEEDMKFCADCQSKGPR WASWNIGVFICIRCAGHRHLGYHISRVKSVNLDQWTQBQIQCM QRMCNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLXASSYDIAA CLCLTFVSYFGGSG\HKPRWLGWGR\VIMGTGSLVFALPHFTAG PP+GWKLDAGVRTCPANPR\PVCAG\TTSGLSRYQLVFMLGGFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTENGRRTELITTESPLWGAMWUGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWILLKNPTFTLLCLAGATEATLITGMSTFSPKFLES QPSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGGTASTGGSLLPEGHINL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATEINVDG				1
6767 336 919 APMICLCSSDLQFRYKBAFLRDRGLQIGYCSVDDDPRMKHFLNV GRLQSDNBYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY RQPLPQPTCDPRQLGLRHAQXAHQLQSDVKYKDLNLTRGVGWT PPGSYKVEMARRAABLANARGLGLQGAYRGABAVEAGDHQSGEV NPDATKILHVKKKRALLL 6768 2 363 PGSTISCYLLSEGBLPLCMQVACGBEKHRAPTMKTLRARFKKTE LRISPTDLGSCPP COPCP1 PKPARGRRQSQDWGKSDBRLLQAV ENNDAPRVAALIARKGLVPTKLDPBGKSAFHL 6769 284 396 MSTPDFSTAENNQELANBVSICLKAMITIMLQAMGQAD 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK ITLNMGVGRALADKKLLDNAAADLAAISGQKPLITKARKSVAGP KIRQGYPIGCKVTLRGERMWEFFBRLITTLAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHTSRVKSVNLDQWTQBQIQCM QBMCNGKANRLYBAYLPETPRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQGGLASSYDIAA CLCLITFVSYFGGSG\HKPRWLGWGR\VIMOTGSLVFALPHFTAG P**GWKLDAGVRTCYPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGGGATPLYTLDRNVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWGAWWGFLGSGAAAFFT AVPILGYPRQLPGGQRYAWWRARHQLKDSSRGEASNPDKKT IRDLPLSIWLLERNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLPLRGSAVIK TRDLPLSIWLLERNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLPLRGSAVIK TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATEINVDG				
GRIQSDNEYKKDFAKSRSQFHSSTDQPGLIQAKRSQQLASDVHY RQPLPQPTCDPEQLIGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT PPGSYKVEMARRAARLANARGLIGLQGAYRGABAVEAGDHQSGEV NPDATRILHVKKKALLL  6768 2 363 PGSTISCYLLSEGGILPICMQVACGEBKHRAPTMKTLRARFKKTE LRLSPTDLGSCPPCGPCP1PKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARKSLVPTKLDPBGKSAFHL  6769 284 396 MSTPDFSTAENNQELANBVSCLKAMITIMLQAMGQAD  6760 1 397 QRNYQVIWSSTMAKLHDYKDEVVKKLMTERYNSVWQVPRVEK LTLNMGVGRALADKKLLDNAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERNWEFFERLITLAVPRIRDFRGLSAKS  6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QRMGNGKANRLYBAYLPBTTRRPQLDPYLFWSNLRG  6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLXASSYDIAA CLCLITFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG PP+GWKLDAQVRTCPANPR\PVCAG\HTSGLSTYQLVFMLGGFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWYGAWWGFLGSGAAAFFT AVPILGYPRQLPGSGRYAVMRAARMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSDKFLES QFSLSASKAATLFGYLVVPAGGGGTFLGGFFVNKLELRGSAVIK FCLFCTVVSLLGILVFSLRCPSVPMAGVTASYGGSLLPBGHINL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATEINVDG			<u> </u>	
RQPLPQPTCDPEQLGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATEILHVKKKKALLL  6768 2 363 PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTT.RARFKKTE LRISPTDLGSCPPCGPCPI PKPAARGRRQSQDWGKSDBRLLQAV ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL  6769 284 396 MSTPDFSTAENNQELANEVSCLKAMI/TLMLQAMGQAD  6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLWTEFNYNSVMQVPRVEK KIRQGYPIGCKVTLRGERMWEFPERLITTAVPRIRDFRGLSAKS  6771 3 378 APAGTLAMTGKSVKDVDRYQAVIANLLLEEDNKFCADCQSKGPR WASWNIGVPICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QRMCNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG  6772 1 1400 AAAFLQGWTVNGFINTVITSL BERYYDLASSYDIAA CLCLTFVSYFGGSG\HKPRWLGWGR\VLWGTGSLVFALPHFTAG P*+GWKLDAGVRTCPANPR\PVCAG\HT3GLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGANWVGFLGSGAAAFFT AVPILGYPRQLPGSGRYAVMRAARMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSILIGILVFSLHCPSVPMAGYTTASYGGSLLPEGHINL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	6767	336	919	
PPGSYKVEMARRAAELANARGIGIQGAYRGAEAVEAGDHQSGEV NPDATRILHVKKKKALIL  6768 2 363 PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTTRARFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPBGKSAFHL  6769 284 396 MSTPDFSTAENNQELANEVSCLKAMIJTLMLQAMGQAD  6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK ITLDMGVGERIADKKLLDNAAADLAAISGQKPLLTKARKSVAGF KIRQGYPIGCKVTLRGERNWEFPERLITLAVPRIRDFRGLSAKS  6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLEEDNKFCADCQSKGPR WASWNIGVPICIRCAGIHRNLGVHISRVKSVNLDQWTQBQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG  6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLTASSYDIAA CLCLTFVSYPGGSGHKRRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTGGLSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTGGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGANWVGFIGSGAAAFFT AVPILGYPQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSILIGILVFSLHCPSVFMAGYTASYGGSLLPEGHINL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG				
NPDATKILHVKKKRALLI.  6768 2 363 PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE LRISPTDLGSCPPCGPCPIPKPAARGRRGSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL  6769 284 396 MSTPDFSTAENNQELANBVSCLKAMI/TLMLQAMGQAD  6770 1 397 QRMYQVIWSSTMAKLBDYKDEVVKKLMTEFNYNSVMQVPRVEK ITLNMGVGEALADKKLLDNAAADLAAISGQKPLITKARKSVAGP KIRQGYPIGCKVTLRGERMWEPFERLITIAVPRIRDFRGLSAKS  6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGWHISRVKSVNLDQWTQEQIQCM QRMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG  6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLTASSYDIAA CLCLITFVSYFGGSG\HKPRWLGKGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGANWVGFIGSGAAAFFT AVPILGYPRQLPGSGRYAVMRAAEMHQLKDSRGEASNPDFGKT IRDLPLSIWLLKNPTFILLCLAGATEATLITGMSTFSDKFLES QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLRELRGSAVIK FCLFCTVVSLIGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG				
6768 2 363 PGSTISCYLLSEGSLPLCMQVACGEBKHRAPTMKTLRARFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPBGKSAFHL 6769 284 396 MSTPDFSTAENNQELANEVSCLKAMI/TLIQAMGQAD 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK LITLNMGVGERIADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWBPPERLITLAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR MASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLTASSYDLAA CLCLITFVSYFGGSG\HKPRWLGMGR\VLMGTGSLVFALPHFTAG P+*GWKLDAGVRTCPANPR\PVCAG\HT3GLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGANWVGFLGSGAAAFFT AVPILGYPQLPGSGRYAVMRAABMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSDKFLES QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGYTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG			İ	
LRLSPTDLGSCPPCGPCP1PKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPBGKSAFHL 6769 284 396 MSTEDFSTAENNQELANEVSCLKAMLITUMLQAMGQAD 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK 1TLNMGVGBALADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITTAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQBQIQCM QRMCNGKANRLYBAYLPETFRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGWTVNGFINTVITSL_KERYDLHSYQSGLTASSYDIAA CLCLITFVSYFGGSG\HKPRWLGWGR\VLMGTCSLVFALPHFTAG P*+GWKLDAGVRTCPANPR\PVCAG\HT3GLSRYQLVFMLQGFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGANWVGFLGSGAAAFFT AVPILGYPRQLPGSGRYAVMRAABMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSSKFLES QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG			ļ <u>.</u>	I
ENNDAPRVAALIARKGLVPTKLDPBGKSAFHL  6769 284 396 MSTFDFSTAENNQELANEVSCLKANIJTLMLQAMGQAD  6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK LITLMMGVGBALADKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFPERLITTAVPRIRDFRGLSAKS  6771 3 378 APAGTLANTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QRMCNGKANRLYEAYLDETFRRPQIDPYLFWSNLEG  6772 1 1400 AAAFLQGMTVNGFINTVITSL BERYDLHSYQSGLLASSYDIAA CLCITFVSYFGGSG\HKPRWLGWGR\VIMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HT3GLSRYQLVFMLQGFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGANWVGFLGSGAAAFFT AVPILGYPRQLPGSGRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSILIGILVFSLHCPSVPMAGYTASYGGSLLPEGHINL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	6768	2	363	
6769 284 396 MSTPDFSTAENNQELANEVSCLKAMI/TLMLQAMGQAD 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEPNYNSVMQVPRVEK ITLMMGVGEALADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERNWEPFERLITIAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMIGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVPICIRCAGIHRNLGVHISRVKSVNLDQWTQBQIQCM QEMCNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLTASSYDIAA CLCLITFVSYPGGSGHKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGANWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGYTASYGGSLLPEGHINL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG		i	1	
6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK ITLNMGVGBALADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVPICIRCAGHRNILGVHISRVKSVNLDQWTQBQIQCM QEMCNGKANRLYEAYLPETPRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSL\GRRYDLHSYQSGLTASSYDIAA CLCLITFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGANWVGFLGSGAAAFFT AVPILGYPRQLPGSGRYAVMRAAEMHQLKDSRGEASNPDFGKT IRDLPLSIWLLKNPTFILLCLAGATEATLITGMSTFSDKFLES QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLIGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG				
ITLNMGVGRAIADKKILDNAAADLAAISGQKPLITKARKSVAGP KIRQGYPIGCKVTLRGERMWEPPERLITIAVPRIRDFRGLSAKS 6771 3 378 APAGTIAMTGKSVKDVDRYQAVIANLLEEDNKFCADCQSKGPR WASWNIGVPICIRCAGIHRNIGVHISRVKSVNLDQWTQBQIQCM QRMGNGKANRLYEAYLPETPRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCIITFVSYPGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGANWVGFLGSGAAAFFT AVPILGYPRQLPGSGRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSDKFLES QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLIGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG				
KIRQGYPIGCKVTLRGERNWEPPERLITIAVPRIRDFRGLSAKS  6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR MASWNIGWFICIRCAGIHRNLGWHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG  6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLXASSYDIAA CLCLITFVSYFGGSG\HKPRWLGMGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HT3GLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGANWVGFLGSGAAAFFT AVPILGYPRQLPGSGRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSDKFLES QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLELRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGYTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	6770	1	397	)
APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASMNIGVPICIRCAGIHRNLGVHISRVKSVNLDQWTQBQIQCM QRMCNGKANRLYBAYLDETFRRPQIDPYLFWSNLEG  AAAFLQGMTVNGFINTVITSLLERRYDLHSYQSGLIASSYDIAA CLCILTFVSYFGGSG\HKPRWLGWGR\VIMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HT3GLSRYQLVFMLQGFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGANWVGFLGSGAAAFFT AVPILGYPRQLPGSGRYAVMRAABMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSDKFLES QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSILIGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG			1	1 ···
WASWNIGVPICIRCAGIHRNIGVHISRVKSVNLDQWTQBQIQCM QRMGNGKANRLYBAYLDBTFFRRPQIDPYLFWSNLEG 6772  1 1400 AAAFLQGMTVNGFINTVITSLERRYDLHSYQSGLIASSYDIAA CLCLITFVSYPGGSG\HKPRWLGWGR\VLWGTGSLVFALDHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HT3GLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDBNVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGANWVGFIGSGAAAFFT AVPILGYPRQLPGSGRYAVMRAARMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASRAATLFGYLVVPAGGGGTFGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG			1	1 = -
QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG  6772  1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGL\ASSYDIAA CLCITFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HT3GLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSGCSPIYLAFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGANWVGPLGSGAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNDDFGKT IRDLPLSIWLLIKNPTFILLCLAGATEATLITGMSTFSPKRIGS QFSLSASRATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVFMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	6771	3	378	APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR
QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG  6772  1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGL\ASSYDIAA CLCITFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HT3GLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSGCSPIYLAFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGANWVGPLGSGAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNDDFGKT IRDLPLSIWLLIKNPTFILLCLAGATEATLITGMSTFSPKRIGS QFSLSASRATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVFMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG		i	1	WASWNIGVFICIRCAGIHRNIGVHISRVKSVNLDQWTQBQIQCM
CLCITFVSYFGGGG\HKPRWLCWGR\VLWGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HT3GLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSGCSPIYIAIFYTAAILGPAAGY LIGGALLMIYTEMGRITELITESPLWVGANWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLKNPTFILLCLAGATEATLITGMSTFSDKFLES QFSLSASRATLFGYIJVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVPSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG		i	1	
CLCITFVSYFGGGG\HKPRWLCWGR\VLWGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HT3GLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSGCSPIYIAIFYTAAILGPAAGY LIGGALLMIYTEMGRITELITESPLWVGANWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLKNPTFILLCLAGATEATLITGMSTFSDKFLES QFSLSASRATLFGYIJVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVPSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	6772	1	1400	AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLTASSYDIAA
P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIPYTAAILGPAAGY LIGGALLNIYTEMGRRTELITTSSPLWVGANWVGFLGSGAAAFFT AVPILGYPRQLPGSGRYAVMRAAEMHQLKUDSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSDKFLES QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLELRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGYTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG		_	[	
HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGANWVGPLGSGAAAFFT AVPILGYPRQLPGSGRYAVMRAAEMHQLKDSSRGEASNPDVGKT IRDLPLSIWLLLKNPTPILLCLAGATEATLITGMSTFSPKFLES QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLILGILVPSLHCPSVPMAGVTASYGGSLLPECHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG			1	
LIGGALLNIYTEMGRRTELTTESPLWVGANWVGFLGSGAAAFFT AVPILGYPROLPGSGRYAVMRAAEMHOLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG		}	}	
AVPILGYPROLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG		1	1	
IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES  QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK  FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL  TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG		i	l	
QFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG		1	<b>\$</b>	
FCLFCTVVSILIGILVPSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG		I	Í	
TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG		1	I	1 4
		1	]	
QKVYRDCSCIPQNLSSGFGHATAGKCTST		1	]	
		L	L	QKVYRDCSCIPQNLSSGFGHATAGKCTST

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
6773	1	630	PWEAPKEHKYKAEEHTVVLTVTGEPCHFPFQYHRQLYHKCTHKG
1			RPGPQPWCATTPNFDQDQRWGYCLEPKKVKDHCSKHSPCQKGGT
1	1		CVNMPSGPHCLCPQHLTGNHCQKEKCPEPQLLRFFHKNEIWYRT
1	1		EQAAVARCQCKGPDAHCQRLASQACRTNPCLHGGRCLEVEGHRL
6224	146	389	CHCPVGYTGPPCDVGE*GSGASRRPAPRWDGLAR
6774	146	389	LTBLSDQQYFLFFILSS/WVPTFLSMDVDGRVIKADSFSKIISS GLRIGFLTGPKPLIERVILHIQVSTLHPSTPNOLMISQ
6775	104	614	TCPSOLRVLTARGGRRAPSPOLNTLVLALIBEKWRSHRILRMNS
] 8,,,2	104	014	GRPETMENLPALYTIFQGEVAMVTDYGAFIKIPGCRKQGLVHRT
1			HMSSCRVDKPSEIVDVGDKVWVKLIGREMKNDRIKVSLSMKVVN
1	}	1	QGTGKDLDPNNV\SLSKKRGGGDPSRITLGRRSPLRLS
6776	3	1108	HERHERHEGALSQDALLRISIPLDSNMRPEKCRRFVHPQWQLLH
1	۱		LNGTFPNTSDADMBPCVDGWVYDRISPSSTIVTEWDLVCDSQSL
1		[	TSVAKFVFMAGMMVGGILGGHLSDRFGRRFVLRWCYLQVAIVGT
ł	ł		CAALAPTFLIYCSLRFLSGIAAMSLITHTIMLIAEWATHRFQAM
i			GITLCMCPSGIAFMTLAGLAFAIRDWHILQLVVSVPYFVIFLTS
i .	i		SWLLESARWLIINNKPBEGLKBLRKAAHRSGMKNARDTLTLBIL
			KSTMKKELEAAQKKKPFLGERLHMPNICKRISLLPFTKFANFMA
			YFGLNLHG/LKHLGNNVFLLQTLFGAV/TPPGQLVLHLGHNGSG
L			RVSSRGRVNCLGLFVLQVW
6777	779	63	CFFHGPAWRDCEVRATFAKKQGQSGIISCIAFSPAQPLYACGSY
1	<b>[</b>	<b>,</b>	GRSLGLYAWDDGSPLALLGGHQGGITHLCPHPDGNRFFSGARKD
1	1	}	AELLCWDLRQSGYPLWSLGREVTTNQRIYFDLDPTGQFLVSGST
ţ		١ .	SCAVSVWDTDGPGNDGKPEPVLSFLPQKDCTNGVSLHPSLPLIG
Ī			HCLPVSVCPLSPTESGGRRRGAGPSLGSPRRHVHLECRLQLWWC
6778	311	805	GGGARLQHP**SPRARKGR IQSITDESRGSIRRKNPANTRLRLNVP\BBTAGDSB/BRSPERB
"'"	311	803	VQADPRIRSASPKCPTSSPFPKGRSPEGEGET\DPEKVHFHPGP
ı	İ		KDKSVABKN\KGP\SPVSSEGIKDFFSMKPEWENLNQSNVRRMH
1	)	1	T\AVRLNEVIVKKSRDAKLVLLNMPGPPRNRNGDENY
6779	2	535	RALRROPRLLAANGIEPESMAISEPIKGSRKPCVNKEELALKKP
1	}		MAKCAWKGPREPPQDARAEAESPGGASESDQDGGHESPPKKKAV
			AWVSAKNPAPMRKKKKVSLGPVSYVLVDSEDGRKKPVMPKKGPG
1	(	{	SRREASDQKAPRGQQPAEATASTSRGPKAKPEGSPRRATNESRK
			v
6780	3	403	HEVNDNKPRININLMSPGKRRISY178GDPIDTFVALVRVQDKD
1		ļ	SGLNGEIVCKLHGHGHFKLQKTYENNYLILTNATLDREKRSEYS
J	l		LTVIAEDRGTPSLSTVKHFTVQINDINDNPPHFQRSRYEFVISE
			K
6781	1	1269	APTRPVFPTLQDLSSSKEPSNSLNLPHSNELCSSLVHPBLSEVS
1	1	ì	SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT
1	l	}	SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI
}	<b>{</b>	{	TPVFINSSSIIQVMKGSQPSTIPAAPLTTNSGLMPPSVAVVGPL
	ł	l	HIPONIKPSSAPVPPNALSSSPAPNIQTGRPLVLSSRATPVOLP
	l l	(	SPPCTSSPVVPSHPPVQQVKEINPDEASPQVNTSADQNTLPSSQ
1	l		STTMVSPLLTNSPGSSGNRRSPVSSSRGKGKVDKIGQILLTKAC
1		İ	KKVTGSLEKGEEQYGADGETEGQGLDTTAPGLMGTEQLSTELDS
] .	1	1	KTPTPPAPTLLKMTSSPVGPGTASAGPSLPGGALPTSVRSIVTT
6700		1200	LVPSELISAVPTTKSNHGGIASRSLAG
6782	3	1327	RKPTVIRIPAKPGKCLHEDPQSPPPLPAEKPIGNTFSTVSGKLS
1		<u> </u>	NVERTRNLESNHPGQTGGFVRVPPRLPPRPVNGKTIPTQQPPTK
}	į		VPPERPPPPKLSATRRSNKKLPFNRSSSDMDLQKKQSNLATGLS
	ł		KAKSQVFKNQDPVLPPRPKPGHPLYSKYMLSVPHGIANEDIVSQ
1	<b>!</b>	Į .	NPGELSCKRGDVLVMLKQTENNYLBCQKGEDTGRVHLSQMKLIT PIDEHLRSRPNPFSPPKAPSHAQKPVDSGAPHAVVLHDFPAEQV
1	l	L	THE THE PROPERTY OF THE SUMMER ADDRESS ADDRESS OF THE PROPERTY

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	}	\=possible nucleotide insertion)
· · · · · · ·			DDINLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI
			PEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
l	1	į	LKEYVNBEWARGEVRGRTGIPPLNFVEPVEDYPTSGANVLSTKV
			PLKTKKEDSGSNSQVNSLPAEWCEALHSFTAETSDDLSFKRGDR
			I
6783	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
			TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLQTSSKVT
	1	Ì	GPGAEAVQIVAKNTVILQVQATPPQPIKVPQFIPPPRLTPRPNF
	ł	ĺ	LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
		1	PTSQNS1HPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
	1	1	QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
	<b>f</b>	<b>!</b>	POKLAPMVSLGLVTHDHLEEIQSKRQERKRRTTANPVYSGAVPE
	1	1	PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGD1HEDFCSVC
	l	l	RKSGOLIMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCODOMLK
			KEEAIPWPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ
	1	l	LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH
	}	1	GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSOSCT
			ANCNOGEETK
6784	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
0.55	1		TMPASVVGORPTIAMVTAINSOKAVLSTDVONTPVNLOTSSKVT
			GPGARAVQIVAKNIVILQVQATPPQPIKVPQFIPPPRLTPRPNF
		]	LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
			PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
		ļ	QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
	1 .	}	PQKLAFMVSLGLVTHDHLBEIQSKRQERKRRTTANPVYSGAVFE
	) '		PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
			SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC
	i	İ	RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK
		Ì	KEEAIPWPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQERRQ
ļ		į.	LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH
	{	1	GIDLSKPVDSRATVGAISNGPDCTPPANAATSTPAPSPSSQSCT
CHOC	<del> </del>	F20	ANCNOGERTK
6785	1 *	528	LGNTVLHYCSMYSKPECLKLLLRSKPTVDIVNQAGETALDIAKR LKATQCEDLLSQAKSGKFNPHVHVEYBWNLRQEEIDRSDDDLDD
	1	1	KPSPVKKERSPRPQSPCHSSSISPQDKLALPGFSTPRDKQRLSY
	1		GAFTNQ1FVSTSTDSPTSPTTRAPPLPPRNAGKGPTGPP1TPHR
6786	1820	1397	RSPKVLVLAPTRELANHVSRDFKDI\TRKLTVARFYGGTSYQSQ
	1 \	1	INHIRNGIDILVGTPGRIKDHLQSGRLDLSKLRHVVLDEVDQML
		İ	DLGFAROVEDIIHESYKTDSEDNPOTLLFSATCPOWVYTVA\KK
1	1	1	YMKSRYEQVDLDGKMTQKAATTVEHLAIQCHWSQRPAVIGDVLQ
	1	1	VYSGSRGRAIIFCETKKNVTEMAMNPHIKONAQCLHGDIAQSQR
	1	ļ	EITLKGFREGSFKVLVATNVAARGLDIPEVDLVIQSSPPQDVES
	1	1	YIHRSGRTGRAGRTGICICFYQPRERGQLRYVEQKAGITFKRVG
1	l	İ	VPSTMDLVKSKSMDAIRSLASVSYAAVDFFRPSAQRLIEBKGAV
	1	1	DALAAALAHISGASSPEPRSLITSDKGFVTMTLESLERIQDVSC
	]	1	AWKELNRKLSSNAVSQITRMCLLKGNMGVCFDVPTTRSERLQAB
1	1	i	WHDSDWILSVPAKLPEIEEYYDGNTSSNSRQRSGWSSGRSGRSG
	1		RSGGRSGGRSGRQSRQGSRSGSRQDGRRRSGNRNRSRSGGHKRS
	{	}	FD*VFYHLVDFLSDFLVDSVYLTGRQIDHLTGLTGLIDHLTSHS
	1	1	SVWN
6787	2646	2270	PSSPPKNVPLEELEKPPK*KRSGLGSLTPKSQIQNGP*PQTFFF
			FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGIIGTCHHAWLI
	i		LVFLVRMGFHHVGQAGLKLLTL\VIHPPWPPKVLGLQT
6788	16	936	GGTVDLR\DMLAVSVLAAVRGGR/ATVRRVRESNVLHEKSKGKT
	t		REGARDKMTSGDVLSNRKMFYLLKTAFPSVQINTEEHVD\BLDQ

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł .	amino acid	residue of	S=Serine, TaThreonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
1	sequence	Bequence	\-possible nucleotide insertion)
<del></del>	Doquesto		EVILWGS*DS*GYPKGK*LLPKEVPSR/RVLLSGLTPLDATOE\
			FTEDLSK\YVTTMVCVAVNGKPMLGVIHKPFSBYTAWAMVDGGS
1			•
j			NVKARSSYNEKTPRIVVSRSHSCMVKQVALQTPGNQTTIIPAGG AGYKVLALLDVPDKSOEKADLYIHVTYIKKMDICAGNAILKALG
Į.			GHMTTLSGERISYTGSDGIEGGLLASIRMNHQALVRKLPDLEKT
ļ			GHK
6789	2	678	
0/83	-	676	GNGINVLKIAPESAIKFMAYEQIKRLVW**PGDS*GF/YERLVA
1	,		GSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMLDCARRILARE
i			GVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSAD
1			PGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVT
l			MSSLPKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLKI
6790	2	4068	TLGVQSR
6790	2	4068	APPAGRRRMQAAPRAGCGAALLLWIVSSCLCRAWTAPSTSQKCD
1			EPLVSGLPHVAFSSSSISGSYSPGYAKTNKRGGAGGWSPSDSD
			HYOWLQVDFGNRKQISAIATQGRYSSSDWVTQYRMLYSDTGRNW
1			KPYHQDGNIWAFPGNINSDGVVRHELQHPIIARYVRIVPLDWNG
į į			EGRIGLRIEVYGCSYWADVINFDGHVVLPYRFRNKKMKTLKDVI
1			ALNFKTSESEGVILHCEGQQGDYITLBLKKAKLVLSLNLGSNQL
1			GPIYGHTSVMTGSLLDDHHWHSVVIERQGRSINLTLDRSMQHPR
			TNGEPDYLDLDYEITFGGIPFSGKP8SSSRKNPKGCMESINYNG
1			VNITDLARRKKLEPSNVGNLSPSCVEPYTVPVFFNATSYLEVPG
l I			RLNQDLFSVSFQFRTWNPNGLLVFSHFADNLGNVEIDLTESKVG
ļ	•		VHINITOTKMSQIDISSGSGLNDGQWHEVRFLAKENFAILTIDG
			DEASAVRINSPLQVKIGEKYFFGGFLNQMNNSSHSVLQPSFQGC
1			MQLIQVDDQLVNLYEVAQRKPGSFANVSIDMCAIIDRCVPNHCE
			HGGKCSQTWDSFKCTCDETGYSGATCHNSIYEPSCEAYKHLGQT
{			SNYYWIDPDGSGPLGPLKVYCNMTEDKVWTIVSHDLQMQTPVVG
Į –			YNPEKYSVTQLVYSASMDQISAITDSAEYCEQYVSYFCKMSRLL
į .			NTPDGSPYTWWVGKANEKHYYWGGSGPGIQKCACGIERNCTDPK
}			YYCNCDADYKQWRKDAGFLSYKDHLPVSQVVVGDTDRQGSEAKL
]			SVGPLRCQGDRNYWNAASFPNPSSYLHFSTFQGETSADISFYFK
1			TLTPWGVFLENMGKEDFIKLELKSATEVSFSFDVGNGPVEIVVR
1			SPTPLNDDQWHRVTAERNVKQASLQVDRLPQQIRKAPTEGHTRL
			BLYSQLFVGGAGGQQGFLGCIRSLRMNGVTLDLBERAKVTSGFI
			SGCSCHCTSYGTNCKNGGKCLRRYHGYSCDCSNTAYDGTFCNKD
			VGAPFEEGMWLRYNFQAPATNARDSSSRVDNAPDQQNSHPDLAQ
			EBIRFSFSTTKAPCILLYISSFTTDFLAVLVKPTGSLQIRYNLG
			GTREPYNIDVDHRNMANGQPHSVNITRHEKTIFLKLDHYPSVSY
			HLPSSSDTLFNSPKSLFLGKVIETGKIDQBIHKYNTPGFTGCLS
]			RVQFNQIAPLKAALRQTNASAHVHIQGELVESNCGASPLTLSPM
			SSATDPWHLDHLDSASADFPYNPGQGQAIRNGVNRNSAIIGGVI
			A\VVIFTPSLCTP\VLP*SR*HVSPHKGTLPIPNEAKGAGSRQK
L			KPGRRPSMNNDPPTSQRPIDESKKEWPHLRGGYLAMG
6791	1801	1193	TGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPEL/PGW
	1		SAVV*SWLTAASTKVQAILLPQPLE*LGLQIAFMASLATHFSNQ
1			nsgiifssvetnignffdvmtgrfgapvsgvyfftfsmmkhedv
			BEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVW
	_		LRMGNGALHGDHQRFSTFAGFLLFBTK
6792	33	1073	VRHTNWGVDMYLPSLGSESPKGAIGHIVSTEKTILAVERNKVLL
J .			PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAV
			CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAV
			TCLAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISA
			ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPBGAITCC
			CLMEGPAWDTSOIIITGSODGMVRVWKT/VGCEDVCSWTASRRG
			APGSASKPKRPQVGEEPGLESRAGR+HCFDREAQQNQP\PVTAL
			AVSRNHTKLLVGDERGRIFCWSADG*BERGSRGSGTTVPG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, P=Phenylalanine, G=Glycine,
10.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
I .	sequence	Seducinee	\=possible nucleotide insertion)
6793	2340	805	GRKEANY\YGSLTQAGTVSLGLDAEGQEVFVPFSAVLPMVAPND
6/93	2340	805	LVFDGWDISSLNLAEAMRRAKVLDWGLOEQLWPHMEALRPRPSV
Į.	1	ļ.	<u> </u>
1	ł	ł	YIPEFIAANQSARADNLIPGSRAQQLEQIRRDIRDFRSSAGLDK VIVLWTANTERFCEVIPGLNDTAENLLRTIBLGLEVSPSTLFAV
ł	<u> </u>		
			ASILEGCAPLNGSPQNTLVPGALELAWQHRVFVGGDDFKSGQTK
Į.	<u> </u>		VKSVLVDFLIGSGLKTMSIVSYNHLGNNDGENLSAPLQPRSKEV
1		•	SKSNVVDDMVQSNPVLYTPGEEPDHCVVIKYVPYVGDSKRALDE
ţ	ł	į	YTSELMLGGTNTLVLHNTCEDSLLAAPIMLDLALLTELCQRVSF
}	!		CTDMDPEPQTFHPVLSLLSFLFKAPLVPPGSPVVNALFRQRSCI
Į.			ENILRACVGLPPQNHMLLEHKMERPGPSLKRVGPVAATYPMLNK
1			KGPVPAATNGCTGDANGHLQEBPPMPTT*GPGHTVSRLFLPAAP
<u></u>			HDPTLKAPTNKGRCHFSPPSTWGSWGL
6794	169	1349	DDVKRKPEASAH*RKPGPPSRPGVRGGRBRAGGRGSHGARSCR\
l		Ì	BPAPPAPAPPEDHPDERMGFTIDIKSFLKPGEKTYTQRCRLFVG
ŀ		]	NLPTDITEEDPKRLFERYGEPSEVFINRDRGFGFTRLESRTLAE
l	l	[	IAKAELDGTILKSRPLRIRFATHGAALTVKNLSPVVSNELLEQA
ľ			PSQFGPVRKAVVVVDDRGRATGKGFVEFAAKPPARKALERCGDG
			AFLLTTTPRPVIVEPMEQFDDEDGLPEKLMQKTQQYHKEREQPP
1		}	RFAQPGTPEFEYASRWKALDEMEKQQREQVDRNIREAKEKLEAE
I			MEAARHEHQLMLMRQDLMRRQEKLRRLEELRNQELQKRKQIQLR
			HEREHRREBEMIRHREQEBLRRQQEGFKUNYMENYVCHPLR
6795	1740	1010	GPRRQTQVRDIELDSF*DWAAQETDCAQNSGERL*KGV/LENFS
1		1	TMSKSAVKISLDLLSNPLCEQDQDLLNMVTALDTAMKRMDAFNQ
į.	ļ	į	EKVNQIQKTVIEPLKKFGSVFPSLNMAVKRREQALQDYRRLQAK
1		}	VEKYEEKEKTGPVLAKLHQAREELRPVREDFRAKNRQLLEEMPR
1		[	FYGSRLDYFQPSFESLIRAQVVYYSEMHKIFGDLSHQLDQPGHS
			DEQRERENEAKLSELRALSIVADD
6796	48	683	GKEIQIPTIKLANLLFGLE+PVGALGKGVVSF++SHVALGQLGW
}	Ì	} .	LTRAVRSSWRWELCVSAQEVVSQRSA*SSPSPVGACPSLNPPET SVORGRDCWOR*LPRLFSALVGOPGCWPOGAPPERCV*PGRCKW
i	,	İ	
ì		<b>]</b> .	HLOSQVLR*ERRRCCRCLPRFA*GWRRRHQRLGLG1HPAPLGST
			SPPHPEGNSQQCRR*GNAABLRLPSSVVL*GKLGC*
6797	1620	211	TERMTPSQPTRGSSCTRPSSMLWTSTWRCLTCHWAGMRMSVVGV
1			TIGPMAQGLLSASGTTTEATWTRPTTHLTLIRWWLLTASRVDPP
1	1	1	ERPPPPPSDDLTLLESSSSYKNL/DAQIPQ/DWSMSPSTSG*RP LTSRASSIMRSRTAIPSAS+SRLTTKHTVGGSPSAWRPRPTSRS
1	[		VSTPVSSSTRTTASGSCLTWWSSSPAPCPSSSAPAHSFEASCCK
1	}		TSLWGSCGGSGDGSSACGSGWNLSMAGTSCSSPAMCSPSRAPS*
1			RSASRPRTWRATTSAASSWAPRRCWCGNA*SAT*PSSTTTISSS
1	1	}	PHCGNPCPASCASAAAWLSSTWATASVAGSCWGPIM*SSAHSPW
			1 · · · -
}			CLSACSRSSMGTTCL*RSPP\SGASRAAAAWCGSSPSSTFTPSS ASSSTWCSASSSRSSPAPTTPSSIPAAQAQRASCRPTSHSART
1	Ì	İ	ASSSTWCSASSSRSSPAPITPSSIPAAQAQRRASCRPTSHSART APPPASSAAGAARPAAFSAAAEGTPRRSIRCW
	7004		STISWESLESWLNKATNPSNROEDWEYLIGFCDOINKELEG*VS
6798	3894	1696	
1	}		ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA
Ī			VRLLAHKIQSPQEWRALQALTYLGDRVSEKVKTKVIELLYSWTM
1			ALPEKAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
1			VFDDBEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
Į.	Į.		TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRBLMKELFDQC
İ	i		ENKRTLFKLASETEDNONSLGDILQASDNLSRVINSYKTIIEG
1	l		QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
1			PAPTPPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL
l			SNLDEKILCLGLADPAPNVPPKRSAGNSQWHLLQREQSDLDFFS
İ			PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFPAPVVPASVP
1	l		APSAGSSLFSTGVAPALAPKVRPAVPGHHGLALGNSALHHLOAL
L	L		DQLLERAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ
_			

SEO	Predicted	Predicted end	A. W. W. W. MAN WALL
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	mcleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	b=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ţ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Ì	residue of	amino acid	Waltryptophan, Yalyrosine, Xaline,
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	Doguesice	\=possible nucleotide insertion)
	1 -04-02-0		PLSFQSQGSPPKGPELSLASIHVPLBSIKPSSALPVTAYDKNGF
	1		RILPHPAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLOAAVPKS
}	]		MKVKLQPPSGTELSPFSPIQPPAALTQVMLLANPLKEKVRLRYK
1			LTFALGEQLSTEVGEVDQFPPVEQWGNL
6799	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
1 0,55	3034	1036	
			ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVILIVPQ\PQ\A
I			VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIKLLYSWIM
ľ			ALPERAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
			VFDDERKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
1			TKRLHTLEEVNNVRLLSEMLLHYSQEDSSDGDREIMKELFDQC
	<u> </u>	•	KNKRRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
			PAPTPPSSGIPILPPPPQASGPPRSRSSQAEATIGPSSTSNAL
1			SWLDEBLLCLGLADPAPNVPPKESAGNSOWHLLOREOSDLDFFS
			PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPPPPAPVVPASVP
1			APSAGSSLFSTGVAPALAPKVKPAVPGHEGLALGNSALHHLDAL
1 :			DQLLERAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFO
			PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
1			RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
1			MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKRKVRLRYK
1 1			LTFALGEQLSTEVGEVDQFPPVEQWGNL
6800	404	1646	RRSPSTGLSPVPQPSSPSLSDYSIPWSLLLSGTIAWATPGK*AG
1			*PQAN*LGLAPAIAFI/GLTRGRKQNKBKMAEGGSGDVDDAGDC
1		•	SGARYNDWSDDDDDSNESKSIVWYPPWARIGTEAGTRARARARA
1	, i		RATRARRAVQKRASPNSDDTVLSPQBLQKVLCLVEMSEKPYILE
[			AALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKAL
1			IVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLL
1			TNMTVTNEYQHMLAN9ISDFFRLFSAGNEETKLQVLKLLLNLAR
1			NPAMTRELLRAQVPSSLG\SLFNKKENKEVILKLLVIFENINDN
<b>!</b>			FKWEENEPTONOFGEGSLFFFLKEFQVCADKVLGIBSHHDFLVK
L. 1			VKVGKPMAKLARHMPPKSQE
6801	2	1755	SAEEVESQQASVTMHDVDAESFEVLVDYCYTGRVSLSEANVERL
1 1			YAASDMLQLEYVREACASFLARRLDLTNCTAILKFADAFGHRKL
} [			RSQAQSYIAQNFKQLSHMGSIREETLADLTLAQLLAVLRLDSLD
	1		VESEQTVCHVAVQWLRAAPKERGPSAAEVPKCVRWMHFTEEDQD
	1		YLEGLITKPIVKKYCLDVIBGALQMRYGDLLYKSLVPVPNSSSS
			/R*QQQLSCICSRKSTPETGYVCQGDGDLLWTPQRSLS\RYDPY
1 1			SGDIYTMPSPLTSFAHTKTVTSSAVCVSPDHDIYLAAQPRKDLW
1 1	ł		VYKPAQNSWQQLADRLLCREGNDVAYLNGYIYILGGRDPITGVK
	İ		LKEVBCYSVQRNQWALVAPVPHSFYSFBLIVVQNYLYAVMSKRM
	į	}	LCYDPSHNMWLNCASLKRSDFQBACVFNDBIYCICDIPVMKVYN
	1	l	PARGEWRRISNIPLDSETHNYQIVNHDQKLLLITSTTPQWKKNR
1 1	j		VTVYEYDTREDQWINIGTMLGLLQFDSGFICLCARVYPSCLEPG
	•	]	QSFITEEDDARSESSTEWDLDGFSELDSESGSSSSFSDDEVWVQ
			VAPQRNAQDQQGSL
6802	157	1341	ETFPLFFFLLSKTPGKTASMAHFVQGTSRMIAAESSTEHKECAE
		ļ	PSTRKNLMNSLEQKIRCLEKQRKELLEVNQQWDQQPRSMKELYE
	1		RKVAELKTKLDAAERFLSTREKDPHQRQRKDDRQREDDRQRDLT
	Ì		RDRLOREBKERENEBLHRLKBENKLLKGKNTLANKEKEHYEC
l l	į		EIKRLNKALQDALNIKCSFSEDCLRKSRVEFCHEEMRTEMEVLK
	1		QQVQIYEEDFKKERSDRERLNQEKEELQQINETSQSQLNRLNSQ
j	j		IKACOMEKEKLEKQLKOMYCPPCNCGLVFHLQDPWVPTGPGAVQ
		[	KQREHPPDYQWYALDQLPPDVQHKAN/DWCLAPPPVCCQAG/PR
		1	TPGLK+SSCLWLPKC+NPRPILSKBSPSVEVHTNRERQQATRER
		I	G
6803	1	2203	KLSGRPYRHMGVLGTSKLYDIRKTIFTFTPQFIDQQQFYLALDN
			THE PARKET AND

SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			KMIVEMLRTDLSYLCSRWRMTGQPTITFPISHSMLDEDGTSLNS
ŀ			SILAALRKMODGYPGGARVQTGKLSEFLTTSCCTHLSFMDPGPE
1		•	GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDEVARYLDHLL
			AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLVTKAKELHVQ
			NVHMYLPTKLPQASRPSFNLLDSPHPRQENQVPSVRVEIHLPRD
Į.			QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKGPDWNTELYN
		1	ERSATVRELLTKLYGKVGEIRHWGLIRYISGILRKKVEALDBAC
J	<b>)</b>	1	TDLLSHOKHLTVGLPPEPREKTISAPLPYEALTQLIDEASEGDM
		l	SISILTQEIMVYLAMYMRTQPGLFAEMFRLRIGLIIQVMATELA
	1	1	HSLRCSAKEATEGLMNLSPSAMKNLLHHILSGKEFGVERK/SVR
	ŀ	1	PTDSNVSPAISIHBIGAVGATKTERTGIMQLKSEIKQVEFRRLS
	ļ	1	ISAESQSPGTSMTPSSGSFPSAYDQQSSKDSRQGQWQRRRRLDG
1	l	ĺ	ALNRVPVGPYQKVWKVLQKCHGLSVBGFVLPSSTTREMTPGEIK
1			FSVHVES\VLNVLLRPEYRQLLVRAILVLTMLADIBIHSIGSII
1		l	AVEKIVHIANDLFLQEQKTLGP\DDTMLAKDPASG\ICTLR\YD
l	İ		SAPSGRFGTMTYLS\RAA\ATYVQEFLP\HSICAMQ
6804	1	951	GSPGKKEEKAKNKESLCMENSSNSSSDEDEBETKAKMTPTKKYN
	ĺ		GLEEKRKSLRTTGFYSGFSEVAEKRIKLLNNSDERLQNSRAKDR
İ			KDVWSSIQGQWPKKTLKELFSDSDTBAAASPPHPAPBEGVARES
			LQTVAEBESCSPSVBLEKPPPVNVDSKPIEEKTVEVNDRKAEFP
			SSGSNFSA*IPLPYLHLNRLHQSL*QKGSRQQSSVTVSBPLAPN
1 .		l	QEEVRSIKSETDSTIEVDSVAGELQDLQSERE*LASRF*CQCKL
j			KQ**SARTRTS*KSLYRSEKSERCSGRRKFIKKAEKKP*SNSGK
L			QQKEGKRHK
6805	1539	206	RQPDLKYFGKSFDVSVSESSSLLSNDLPKFADGIKARNRNQNYL
ł		ł	VPSPVLRILDHTAFSTEKSADIVICDEECDSPESVNQQTQEESP
			IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLQDQTDEEPPA
1		}	KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS
1			DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI
1	1	ł	CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY
l		ł	LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD
İ	1		KYNNGEHGQYSLLSKITFDKCKNPPVCQVCGFRSRLHTNVNRHV
		İ	AIEHTKIPPHVCDDCGKGFSSMLE\LAKHLNSHLSBGIYLCQYW
	1	1	EYSTGQIEDLKIHLDPKHSADLPHKCSDCLMRFGNERELISHLP
			VHETT
6806	272	3794	VALCFPNSDPVMFMDAFYGCLLARLGPVP1EVPLTRKDAGSQQV
ł	!	i	GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI
1	ł		DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA
1	1	1	SLLAQCRALTQACGYSRARTLTNVLDFKRDAGLWHGVLTSVMNR
1	1	1	MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ
1	1		RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV
1	1	1	ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD
1		1	TEEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV
-	[	1	SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPYTRTGLLG
1	1	1	FIGPDHLVPIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY
1 .		[	RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID
			SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN
1	1	]	VIMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR
i	1		KLAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT
	1		STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLLAA
1	ŀ	1	FYGCLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVSKSACVLTT
	1	1	QAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVFRPPSP
1	1		DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIKLQCKLYPSRQ
1	Į.	1	IAICLDPYCGLGFALWCLCSVYSGHQSVLVPPLELESNVSLWLS
i			AVSQYKARVTFCCYSVMBMCTKGLGAQTGVLRMKGVNLSCVRTC
1	I		MVVAEERP\RIALTOSFSKLFKDLGLPARAVSTTFGCRVNVAIC
I			

PCT/US00/34263

Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Predicted   Predicting   Pr		· · · · · · · · · · · · · · · · · · ·		
No:	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cortesponding   Cortesponding   Coffre				
corresponding to first amino acid anino acid residue of amino acid residue of amino acid anino acid anino acid anino acid anino acid anino acid anino acid acquence acid complete anino acid acquence acquence acid acquence acid acquence acid acquence acquence acquence acid acquence	NO:			
amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acquence  #Tryptophan, Y-Tyrosine, K-Uluknown, *-stop Codon, Apossible nucleotide deletion, Apossible nucleotide insertion Lographyrtyvydhealarndyvruvsessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyvyceral RDBFPARLispolygilendersessphearcytyricheral RDBFPARLispolygilendersessphearcyt	•			
### anino acid   residue of   amino acid   sequence   Seserine, T-Threonine, V-Valine,   setop   codon, /-possible nucleotide deletion,   v-possible nucleotide deletion,   v-possible nucleotide deletion,   v-possible nucleotide deletion,   v-possible nucleotide deletion,   v-possible nucleotide deletion,   v-possible nucleotide deletion,   v-possible nucleotide deletion,   v-possible nucleotide deletion,   v-possible nucleotide deletion,   v-possible nucleotide deletion,   v-possible nucleotide deletion,   v-possible nucleotide deletion,   v-possible nucleotide deletion,   v-possible nucleotide   v-				
### with a cid anino acid sequence (Codon, -possible mucleotide deletion, -possible mucleotide deletion, -possible mucleotide deletion, -possible mucleotide deletion, -possible mucleotide deletion, -possible mucleotide insertion			1	
amino acid sequence   Codon, /=possible mucleotide deletion,   Logisaphertyvydheniaendymusessyste.com   Logisaphertyvydheniaendymusessyste.com   Codon, /=possible mucleotide deletion,   Logisaphertyvydheniaendymusessyste.com   Codon, /=possible mucleotide mertion    Logisaphertyvydheniaendymusessyste.com   Codon, /=possible mucleotide with the codon     Codon, /=possible mucleotide with the codon     Codon, /=possible mucleotide with the codon     Codon, /=possible mucleotide with the codon     Codon, /=possible mucleotide with the codon     Codon, /=possible mucleotide with the codon     Codon, /=possible mucleotide with the codon     Codon, /=possible mucleotide with the codon     Codon, /=possible mucleotide with the codon     Codon, /=possible mucleotide with the codon     Codon, /=possible mucleotide with the codon     Codon, /=possible mucleotide with the codon     Codon, /=possible mucleotide with the codon     Codon, /=possible mucleotide with the codon     Codon, /=possible mucleotide with the codon     Codon		L		
Sequence   \ \possible nucleotide insertion		1	I .	
LOCTAGEDPTTYVDMRALREDRYRIVARSSPHASTPLMSSESS    PGWVV11AHTEKREPGLOSHLIGE WWSSPHANGYTYVGKRAL     RADHESARLSPGITYTINARTGYLGFLRRYTYTYGKRAL     RADHESARLSPGITYTINARTGYLGFLRRYTELTDASGGRRAD    VVUSLOGLEDODADLVALVTINVULSHEIKUVGVVVVIVDPGVIP     INSRESKQRWILRDGPLADOLDTIYVATMW     GOG		1	sequence	
### PGYNVI_INHTER(PLG)SHLGETWVSS_PINATGYTYVTGERGE ### RADHEPSARLS (#PGYTT)TUNATGY_IGH_RETELIDASGGRIDALY ### VVOSI_DIST_LELIGGRY_PID_TID_TIST_V_IRANE_TABGGRIDALY ### VVOVELOGLEQDALDUVALVTIVVLERET_LVVGVVVI_VDGVLP ### VVOVELOGLEQDALDUVALVTIVVLERET_LVVGVVVI_VDGVLP ### INSRGERGRMHIRTGFT-ADOLDET_TVATAM  ### SUBST_CONT_CONT_CONT_CONT_CONT_CONT_CONT_CON		sequence		
### HADNESARLS-PENTYTINANGYLAGELARYETETDASCGRIDAD.  VVOSLIDETLELIGGRYPIPTIGETS/PIGABLS-TAGEACCAPTYTTILL  VVVVELDGLEQDALDLVALYTNVVLSEHELYWGVVVIVDPGVIP  INSRESKQRMILRIDGPLADOLDPITYTAYNM  GOE VEIDTVERMITTEFEKGIGESPPYNVTVSFESEESHTTTVSGGNG  SVPONGFOLQALANLKARRASIGAALSEROVSGLEVYLAGGSGRA  RIADQAVAAP FORSAKLEHSSODDTMSLERS GEGESLESSGGAR  RIADQAVAAP FORSAKLEHSSODDTMSLERS GEGESLESSGGAR  RIADQAVAAP FORSAKLEHSSODDTMSLERS GEGESLESSGGAR  RIADGAVAAP CHARACHENGESPSTSULTEVAADGSS  FLERLIMGLSCLOVPHLINIQDSSTSULTEVAADGSS  FLERLIMGLSCLOVPHLINIQDSSTSULTEVAADGSS  FLERLIMGLSCLOVPHLINIQDSSTSULTEVAADGSS  FLERLIMGLSCLOVPHLINIQDSSTSULTEVAADGSS  FLERLIMGLSCLOVPHLINIQDSSTSULTEVAADGSS  FLERLIMGLSCLOVPHLINIQDSSTSULTEVAADGSS  FLERLIMGLSCLOVPHLINIQDSSTSULTEVAADGSS  FLERLIMGLSCLOVPHLINIQDSSTSULTEVAADGSS  FLERLIMGLSCLOVPH FORSAGLISTER ARRASIGGAR  REPCOMBURSPEGGUGLEL LILEPSVAAPTILSENEN  SRELISIALIKERGUVERPEGGUGLEL LILEPSVAAPTILSENEN  FLERLIMGLSCLOVPT FORSAGLISTER FRANKSTORDATETTTIL  LILDELGTSTERS TILIHIHLISELISTERCVPTHANGVAGSRILLI  FRITCCANTEDLETVILINIVELSPSAPLAAGGVIKGMILLIMPI  LASSVINIRIRHPVKQUVENDHMINGLAKS IREPOKRETSVARGKILLI  GEKTELSVALTARGVONTATAGVINDUVS SHAHLIBETICKAQN  PRVALVLITSTGGHIGFLEGI HPRQSTYMDRVFKQPVQAMVERICH  ELS   BIS  6809  939  65  DYSGGTPVYTBERGNTLYTTAQTHEBOPGSKASTOPLAGTOTVPQ  GOPGKILLIVE II FRERGSKGFGPVTFETSSDADRARRKLINGTIV  AVVIODGFYCASI LURATOPTTILSPLARRAPPPPPI PTYG  AVVYODGFYCASI LURATOPTTILSPLARRAPPPPPI PTYG  AVVYODGFYCASI LURATOPTTILSPLARRAPPPPPI PTYG  AVVYODGFYCASI LURATOPTTILSPLARRAPPPPPI PTYG  AVVYODGFYCASI LURATOPTTILSPLARRAPPPPPI PTYG  AVVYODGFYCASI LURATOPTTILSPLARRAPPPPI PTYG  AVVYODGFYCASI LURATOPTTILSPLARRAPPPPI PTYG  AVVYODGFYCASI LURATOPTTILSPLARRAPPPPI PTYG  AVVYODGFYCASI LURATOPTTILSPLARRAPPPPI PTYG  AVVYODGFYCASI LURATOPTTILSPLARRAPPPPI PTYG  AVVYODGFYCASI LURATOPTTILSPLARRAPPPPI PTYG  AVVYODGFYCASI LURATOPTTILSPLARRAPPPPI PTYG  AVVYODGFYCASI LURATOPTTILSPLARRAPPPPI PTYG  AVVYODGFYCASI LURATOPTTILSPLARRAPPPPI PTYG  SVGGTATALBLIDARRAPPPPI PTYTTATARTAPPROSPOLARRAPPPT TOTATATATATAPPPI PTYG  AVVTODGFYCASI LURATOPTTI				
VVOSIDETLELGGRYHPIDIETSVIRABESTAECAPFTWITE   VVVENIGGEGODALDVALVIVVURDEBTLYVVOVUTOPGVIP   INSRESKORMILROSPLADOLDPITVANM   O66			ł	
AUVIVELOCLEODALDIVALVITWIVELERSTIV/GVVVI/VDPGVIP   INSREKORMHLROPPIA/DOLIP/IVAYIN		]		<u>-</u>
1 INSRESKORMILROEFIJAOOLDET YVAYNM  606 VGRUTVIMMITTEPPKCIGSE PEWNYTVEPKESESHTTYTUSCION SVPOAGPQLQALANLEARRGSIGAALSSRDVSGLPVYAQSGEPR RITUAQVAAPFGENALEKISDQDYMOSLRSFGFCSELSSGGAB SIPPGGRAHARSLIGKUVOFPKGEQTEPKGLIFECLESISGGAB KILSUDSVANDCAVRITVYKKEQTOFFGSILIFECLESISGGIAN REPCOMEURISGGRELESVAVAGEANAA LKEPRSVLPTEVAAPPLE KILSUDSVANDCAVRITVYKKEQTOFFGSILIFECLESISGGIAN REPCOMEURISGGRELESVAVAGEANAA LKEPRSVLPTEVAAPPLE KILSUDSVANDCAVRITVYKKEQTOFFGSILIFECLESISGGIAN REPCOMEURISGGRELESVAVAGEANAA LKEPRSVLPTEVAAPPLE KILSUDSVANDCAVATVYKKEQTOFFGSILIFECLESISGGIAN REPCOMEURISGGRELESVAVAGEANAA LKEPRSVLPTEVAAPPLE KRISTILBEOURISGERISGERISGERISGERISGERISGERISGERISGE			į	
6807 1444 606 VGEDTVIRMITCEPKCIGESPEVWITVEPKSERSITTTVSGONG SVPOAGPOLQALANLEARINGSIGAALSSRDVSGLPVYAGSGEPR RITOAQVAAPFGENALEKSSTODTVINDSLASSFOPCSPLSSGGAP RITOAQVAAPFGENALEKSSTODTVINDSLASSFOPCSPLSSGGAP RITOAQVAAPFGENALEKSSTODTVINDSLASSFOPCSPLSSGGAP REPCOMEVHSGORELESVAVOGANA LIKEPMGAMSYCLORDSR PELPELIMALSCELOVQ  GVGSGANALARSPELASKISSERRTRAPESGAOGRIAMDILMIL SRELSILIEDGVOVEPFGSGUCULSLLIGFSVAAPAFYLSSLAKK PQLVTGGESPSRPLQDHCPVVTETYYPTVWCWGCGCQTLLRDP\ ITSKPPVQTMBLIKTADGGQISLDWIDNINSTCYMDASTRTI LLLDGLATSTKESYLLAMHLESELGGTGCVVVNNGGVAGEMILINTJ GKIGSKFPLMAAATFSVGNATFAGCSBLERHJAAVSMGGMLLINTJ GKIGSKFPLMAAATFSVGNATFAGCSBLERHJAAVSMGGMLLINTJ GKIGSKFPLMAAATFSVGNATFAGCSBLERHJAAVSMGGMLLINTJ GKIGSKFPLMAAATFSVGNATFAGCSBLERHJALBTYLITTC LOSSVINKRRIMFVKQVUMDEVVKAKS TREFDKRFTSVMFCYTT DDYYTDASPSPRLASVIFFUCLINSVDOVPSSHAIP ISTAXGN PRVALVILTSYGGHIGFLEGIWRQSTYMDRVFKQFVQAMVEHCH RLS  5809 939 65 DYSGQTFVPTEHSMTLYTDAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHFSDFTEKQQFKRLINVSNIFPFRFNDPLORMF GQPGKILIDVSI IFSNRGSKGFOFVTFTSTSBADAPAPPPPIPTY EGRILEVNANTARAVMTNKKTGRPYTNGKKINPVGAVYGPBYA VTGPFPTTTGTAAATGALIRGGRAVVNTFRAAPPPPPIPTY AVVYDOGFYGABI\LBATQPTTTLSPIGRRQFTATVTAESTQLP TETTPSGGAPPPTAEFCTFTRIPLLGP GGPKILIDVSI IFSNRGSKGFOFVTFFTSSDADARAKKINGTIVPQ TDEAAAQTUSQPLHFSDFTERQQFKRLINVSNIFPFRFNDPLAQMF GQPGKILIDVSI IFSNRGSKGFOFVTFFTSSDADARAKKINGTIVPQ AVVYDOGFYGABI\LBATQPTTTLSPIGRRQFTATVTAESTQLP TETTPSGGAPPPTAEFCTFTRIPLLGP GGRKILDVSI IFSNRGSKGFOFVTFFTSSDADARAKKINGTIVTT VTTPSGGAPPTALEFCTFTRIPLLGP SGGRESVTTTRANYFTAATGALIRGKGRAVVTTFRAAPPPPPIPTY AVVYDOGFYGABI\LBATQPTTTLSPIGRRQFTATVTAESTQLD TETTTPSGGAPPTALEFCTFTRIPLLGP SGGRESVTTTRANYFTAATGALIRGKGRAVVTTFRAAPPPPPIPTY AVVYDOGFYGABI\LBATGATKRIPLDCGT TTTTPSGGAPPTALEFCTFTRIPLLGP SGGRESVTTTRANYFTAAFCHLIRGKRIPHTVINATSSPAGSKS GRAVTTTRANYFTAAFCHLIRGKRIPHTVINATSSPAGSKS GRAVTTTRANYFTAATGALIRGKRIPHTVINATSSPAGSKS GRAVTTTRANYFTAAFCHLIRGKRIPHTRIPLLGP SGCRESPGALIGHTAAVKHQDGGALTGCFTGAVAAFTHEQ SCGRESPGALTGTBRCGGAPVCTFTAAPPPPPIPTY TDPAATTLTTFREVULTCELEKSRDFTAAFTHOOPPP HTUDFREHVVIHATTSKCWILLGREDAVAFFGVTVQDPPV HTUDFREHVVIHATTSKCWILLGREDAVAFFGVTV		l		<u></u>
SVPORGPOLGALANLEARRGSIGNALSSEDVSGLPVYAGSGEPE HLTONGOVARPERSNALERSSOLOTWOSLEAS PEPCSPLSSCOCAE SLPPGGPGHARAGHLGKVCDFHLNHQQPSPTSVLPTEVAAPPLE KILSVDSVAVDCANETYPKEGPQFEFRSBLITESCLESISSISIN RPPCCMBUHSGGRELESVVAVGAMA\LKETMGMSYCLRDESS FLEFILIPHOLSCPLQVQ  GVGSGASSALARSPELASKISSERRITRAPRSGAMQRLAMDLRIML SRELSIVLEHQVRUSPEGSGVGLISLLIGFSVAYAPPYLISJAKK PQUVYGGESSPSFLQDHCPVYTETYPTVVCGERGGTLLRPP\ LLLPGLTGTSKSPTLQDHCPVYTETYPTVCGERGGTLLRPP\ LLLPGLTGTSKSPTLQDHCPVYTETYPTVCGERGGTLLRPP\ LLLPGLTGTSKSPTLQDHCPVYTETYPTVCGERGGTLLRPP\ LLLPGLTGTSKSPTLQDHCPVYTETYPTVCGERGGTLLRPP\ LLLPGLTGTSKSPTLQDHCPVTTTYTYPTVCGERGGTLLRPP\ LLLPGLTGTSKSPTLQDHCPVTTTYTYPTVCGERGGTLLRPP\ LLLPGLTGTSKSPTLQDHCPVTTTYTYPTVCGERGGTLLRPP\ LLLPGLTGTSKSPTLQDHCPVTTTYTYPTVCHCGRGGTLLRPP\ LLPGLTGTSKSPTLQDHCPVTTTYTYPTVCHCGRGGTLLRPP\ LLPGLTGTSKSPTLANDAGGTSLANDAGVMGGMLLLNYL GKTGSKTPLMAAATTSVGNNTFAGSBSLKEPLMHLLFNTYLTTC LGSSVNKRHRMPVKQVMDMEVKAKSTREFERTSVMFGVGTI  DDYTTDSSPSPRLKSVG1PVLCLANSVDDVFSPSHALPITTTAGQ PNYALVLTSTGGGNTGFLGFLGF HERGGTGTTVDFQTAMVGUNEHLFNTYLTTC LGSSVNKRHRMPVKQVMDHVKAKSTREFTSVMFGVGTI DDYTTDSSPSPRLKSVG1PVLCLANSVDDVFSPSHALPITTATAGQ PNYALVLTSTGGGTGFPFFTSGGGGGATTGVMGTVAMPTFAGAPP FRODDAGATTSGPPHRAGGTGFTSTTAGAGTGTVFQ GQGGKLLUVRIT LPRRGGSKGFGPTFTSTSGAPTATATASTGLDFTY TOFFFTTTTAVATRGAHLRGGGRAVVTTFRAAPPPPPITTYG AVVYQDGFYGABTLLARTQFTTTLSFJCLRGFGFTATATASTGLP TRTTTPSGGRRFTALBFCSTFHRFLLGP TRTTTPSGGRRFTALBFCSTFHRFLLGP SGGRELITAVATAGAGHLGGGRAVVTTFRAAPPPPPITTSVERGDPME FSGSDEDFQDLLHFGGRRAVSTTFAAPPPPPTTTSVERGDPME FSGSDEDFQDLLHFGGRRADSTGGRAVTTFRAAPPPPTTTSVERGDPME FSGSDEDFQDLLHFGGRRADSTGGRRAVTTFRAAPPPPTTTSVERGDPME FSGSDEDFQDLLHFGGRRADSTGGRRAVTTRAPPPPTTTSVERGDPME FSGSDEDFQDLLHFGGRRAVTTTFAAPPPPTTTSVERGDPME FSGSDEDFQDLLHFGGRRAVSTRAPPPTTTSVERGPMF TDPAXTLGTFLCPMBOVPLLEPLICKLAHARRITVLJFLECCL KELQHRLLHAVKHQDGGGALVOFSCFGVQGSAALTGGSSPCALTGEC KLICHKLHAVKHQDGGALVOFSCFGVQGSAALTGGSSPCHL VVMMGRKHBLLLDARTGGRAVVTAPACHCRAFTKAGGGRVCAPFTVTT TDVSSMIVYPSGKVVYAAVLERCVLAFCGGRPVCTVAGGGFVCABCSHL VVMMGRKHBLLLDARTGGRAVAUTEGCGRPCCTVAGCGGAVCHYNY HTVPPRRTVYTHAPPVRLIDARTGGGRPVCTCBGGGFVCABCCAPFTVTT TDVSSMIVYPSGKVVYAAV				
RIJOQAVAPPGENALERISSIODITMOSLESPECSPELSECGARE SLDPGGPCHARACHLOKVOPHLINHQUDPSVLYTEVAAPPLE KILSVDSVAVDCAYRTVPKPGPQPGPGSLITEGCLESGIDIN RPPCCMEVHSGQRELSSVAVGEAMA\LKTPMGAMSYCLROESS FLFRLIMMISCPLQVQ FUFRLIMMISCPLQVQ GVGGASALARSRFLASRLSSRRTRAPRSGAMQRLAMDLRMI, SERSLSIVLERIQVEVAPFOSGGGLSLLIGEVAVAPFYLSSIJAKK POLVTGGSSPSRFLADHCPVVTTSTYPTVMCMCGRGCGTLLRPF\ ITSKPPUQYBRELIKTADGCJSLJAMENDMSTCYMDASTRPTI LLLPGLTGTSKESYILHMIHLSELGYRCVVPNNRGVAGENLLNT GKIGSKTPLHAMATESSVAMITFACSSELSEKLAMILLFRYYLTITC LQSSVNKHRIMPVKQVDMDHVMKAKSIREPDKRFTSVMFGQTI DDYTTDASPSPRLKSVGIFVLCLNSVDDUSPSHAP JETAKQN PNVALVLISYGGBIGFLEGIMPRQSTYMDRVFKQFVQAMVEHCH RLS  6809 939 65 DYSGGTPVPTSHGMTLYTPAQTHEBGPGSEASTOPLAGTOTVPQ TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFFRDPDDLRQMF GQGGILLIVSEI IFNRGSKGFGFVTFETSSDAPRAREKLMGTIV EGRKLEVANATARVMTNKKGNPYTHGKKLMPVVGAVCPEPYA AVVYQDGFYGABI\LBAGQPTDTLSPLQRRQPTATVTARSTCLP TRTTTPSGGRPTPALEPGCTFHPPLLGP GPGRILLVSEI IFNRGSKGFGFVTFETSSDAPRAREKLMGTIV EGRKLEVANATARVMTNKKGNPYTHGKKLMPVVGAVCPEPYA AVVYQDGFYGABI\LBAGQPTDTLSPLQRRQPTATVTARSTCLP TRTTTPSGGRPTPALEPGCTFHPPLLGP GPGRILLVSEI IFNRGSKGFGFVTFETSSDAPRAREKLMGTIV EGRKLEVANATARVMTNKKTGNPYTHGKKLMPVVGAVCPEPYA AVVYQDGFYGABI\LBAGQPTATVTARSTCLP TRTTTPSGGRPTPALBEGCTFHPPLLGP GPGRILLVSEI IFNRGSKGFGFVTFETSSDAPRAREKLMGTIV EGRKLEVANATARVMTNKKTGNPYTHGKKLMPVVGAVCPEPYA AVVYQDGFYGABI\LBAGQPTATVTARSTCLP TRTTTPSGGRPTPALBEGCTFHPPLLGP GPGRILLVSEI IFNRGSKGFGFVTFETSSDAPRAREKLMGTIV EGRKLEVANATARVMTNKKTGNPYTHGKKLMPVVGAVCPEPYA AVVYGDGFYGABI\LBAGTQCRLGRGRATAVTNTRAAPPPPPI IPTY AVVYGDGFYGABI\LBAGTQCRLGRGRATAVTNTRAAPPPPPI IPTY AVVYGDGFYGABI\LBAGTQCRLGRGRATAVTNTRAAPPPPPI IPTY AVVYGDGFYGABI\LBAGTQCRLGRGRATAVTRASTCLP TRTTTPSGGRPTPALBEGCTTHPPLLGP SVQGTQLCLMDLTSDLIPPGDCLGRRGTATVTARSTCLP FSGSDEDFDDLLHFGRDADSTQCRLGRRGNATGRPVTATTSSPGGE GRSVTTTGNSVPPPLERRANGTRURKRHFMURATSSPSAGE GRSVTTTGNSVPPPLERRANGTRURKRHFMURATSSPSAGE GRSVTTTGNSVPPPLERRANGTRURKRHFMURATSSPSAGE GRSVTTTGNSVPPPLERRANGTRURKRHFMURATSSPSAGE GRSVTTTGNSVPPPLERRANGTRURKRHFMURATSSPSAGE GRSVTTTGNSVPPPLERRANGTRURKRHFMURATSSPSAGE FSGDEVALENGTAGGRAVAVATARGGRAVAVATARGGRAVATATT TUPASS	6807	1444	606	i de la companya de la companya de la companya de la companya de la companya de la companya de la companya de
SLPPGGGHARAGHLGKYCDPHLINHQDPSPTSULPTWAAPPLE KILSVDSVAVDCAYRTVPKPGPQPGHGSLITEGTCKRASCHER RPFCCMEVHSGQRELESVVAVGRAMA_KKPRMGMSYCKRORSS PLYKLLPMGLSCPLQVQ  GVGGGASALFASRFLASSELSSRRRTRAPRSGAMQRLAMDLRML SRELSIVLEHQVRVUSPFGSGVGLSLLIGFSVAVAPFYLSSLAKK PQUATNGESPSRIJDHCVATTTYPYTVGSCRGCVGLLAUPPL 175KPPVQYRMELIKTADGCQISLDWFDNDMSTCYMDASTRPTI LLDFGLIGTSKRSYLILRHIHLSBEGYRCVVPNINKCYAGBSLLIT PRTYCCAMFUBLETVIHEUVHSLPSAPFLAAGVSMGGMLLIMYL GKIGSKTPLMAAATPSVGMYFFACSESLEKPLMNLLHMYL GKIGSKTPLMAAATPSVGMYFFACSESLEKPLMNLLHMYL GKIGSKTPLMAAATPSVGMYFFACSESLEKPLMNLLHMYL GKIGSKTPLMAAATPSVGMYFFACSESLEKPLMNLLHMYL GKIGSKTPLMAAATPSVGMYFFACSESLEKPLMNLHMYL GKIGSKTPLMAAATPSVGMYFFACSESLEKPLMNLHMYL GKIGSKTPLMAAATPSVGMYFFACSESLEKPLMNLHMYL GKIGSKTPLMAAATPSVGMYFFACSESLEKPLMNLHMYL GKIGSKTPLMAAATPSVGMYFFACSESLEKPLMNLHMYL RUNG PWALVLISYGGHIGFLEG UPRQSTTYMDRVKQVAMVECH RLS  6809  939  65  DYSGGTPVPTEIGMTLYTPAQTHPBQPGSEASTOPIAGTOVPQ TDBAAQTTDSQPLHFSDPTEKQQFKRLHWSN1PFRFRDPDLRQMF GQFGKLLUVBLIFNERPKKGNPTVAGNYGAVYGAPSPYA VTGPPPTTGTAVAYRGHLEGGGRAVYMTFRAAPPPPPPIPTYG AVVYODGFYGAEI\LBATOPIDTLSPLQRRQPTATVTAESTQLP TRTITPSGGREFPAGEFTFHEPLLGP GPGKLLDVBLIFNERPKGQPKRLHWNDTPFRFDPDLRQMF GQFGKLLDVBLIFNERPKGQPKRLHWNDTPFRFDPDLRQMF GQFGKLLDVBLIFNERPKGQPKRLHWNDTPFRFDPDLRQMF GQFGKLLDVBLIFNERPKGQPKRLHWNDTPFRFDPDLRQMF GQFGKLLDVBLIFNERPKGQPKRLHWNDTPFRFDPDLRQMF GQFGKLLDVBLIFNERPKGQPKRLHWNDTPFRFDPDLRQMF GQFGKLLDVBLIFNERPKGQPKRHWNDTPFRFDPDLRQMF GGFGKLEVBANTARAVHTNKTRNPYTTGKRMPVVGAVYGPBPYA VTGPPPTTTGTAVAYRGHLEGRRAVYMTFRAAPPPPPIPTYG AVVYDGFYGAEI\LBATOPIDTLSPLGRQPTATVTAESTQLD TRTITPSGGRRPTALBCFTFHRPLLGP TRTITPSGGRRPTALBCFTFHRPLLGP SVGDPTQLCLMDLTGDILFPRGDEATGTCRTSRNTTORFVSGTYTTRFG SVGQDTQLCLMDLTGDILFPRGDEATGTCRTSRNTTSRTSTSPRYSTTTRFG SVGQDTQLCLMDLTGDILFPRGDEATGTCRTSRNTSTSTSPRYSTTTRFG SVGQDTQLCLMDLTGDILFPRGDEATGTCRTSRNTSTSTSPRYSTTTRFG SVGQDTQLCCLMDLTGDILFPRGDEATGTCRTSRNTSTSTSPRYSTTTRFG SVGQDTQLCCLMDLTGDILFPRGDEATGTCRTSRNTSTSTSPRYSTTTRFG SVGQDTQLCCLMDLTGDILFPRGDPTGCCCLGARACTTVLTREDCL VTACQEGFICTGWCPCKVCFSNDT CRCCTCTGWCPCKVCFSNDTGCCCGAALTTQBSP UPHIL SPQDKVSLTPTTSBRVVLTCELSRVDFPATWKTGCGVE BSDFVVLE			Î	
KILSUDGVANDCAYRTVERCEOPOCERGSLLTEGCIRES CSIDIA RPPPCCMEVHSGQRELESVAVORBAMA\LKPPMCAMSYCLRDRS FERRLEMALSCPLQVQ GVSGGASALARSRFLASRLSSRRTRAPRSGAMQRLAMDLRMI. SRELSIVLERIQVEVERFOSGGLSLLIGESVAVAPTYLSSTAKK PQLVTGGSSPSRFLADHCPVVTETYYPTVWCHEGRGCTLLRPP\ LTSKPPVQYRNELIKTADGCGISLDWFDMDNTSTYDTSLTAKK PQLVTGGSSPSRFLADHCPVVTETYYPTVWCHEGRGCTLLRPP\ LTSKPPVQYRNELIKTADGCGISLDWFDMDNTCYMDASTRPTI LLLDELIGTSKESYTLERHHISEBLGYRGVVPNNRGVAGBRULLT PRTYCCANTEDLETVIHIVHSLYPSAPFLAAGGVMGGMLLINTI, GKIGSKFPLWAAATFSVGMYTFAGSSELGHAULLFRYTYITTC LQSSVNKHRHMFVKQUMDHVMKAKSIRBFDKRRTSVMGGQTI DDYYTDASPSPRLKSVGIPVLCLANSUDDVSFSHALFIFTAAGN PNVALVLTSYGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVEKH RLS  6809 939 65 DYSGGTPVPTEHGMTLTYPAQTHPBQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF GQPGKLILDVSIIFNRGSKGGFVYTETSIDADARARKLINGTIV BGRKLEVNNATARVMTNKKTGNPYTNGWKLMPVVGAVYGPSPYA AVVYQDGFYGABL\LBAGQPTDTLSSLGRRPATATVTARSTQLL TRTITPSGPRRPTALBPCETFHHFLLGP DSGGTPVPTHGCMTAYAGAHLRGRGRAVYNTFRAAPPPPIPTYG AVAYODGFYGABL\LBAGQPTDTLSSLGRRPATATVTARSTQLL TRTITPSGPRRPTALBPCETFHHFLLGP TDEAAQTDSQDLHPSDPTEKQQPKRLHVSNIPPPPPPIPTYG AVAYODGFYGABLYLBRGCRFAVYNTFRASPPSIPTY AVAYODGFYGABLYLBRGCRFAVYNTFRASPPSIPTY AVAYODGFYGABLYLBRGCRFAVYNTFRASPPSIPTY AVAYODGFYGABLYLBRGCRFAVYNTFRASPPSIPTY AVAYODGFYGABLYLBRGCRFAVYNTFRASPPSIPTY AVAYODGFYGABLYLBRGCRFAVYNTFRASPPSIPTY AVAYODGFYGABLYLBRGCRFAVYNTFRASPPSIPTY TYTYPSGPRRPTALBPCETTHHPLLGP SVGQDTOLCLMDLTEDILPPRQLESRAFTETNVMATSPPAGSN GRSYTTPGNSDPIPLAGP FSGSBEDFQLLHFGRDRANDFTAVYNCRGRYTTRFS SVGQDTOLCLMDLTEDILPPRQLESRAFTETNVMATSPPAGSN GRSYTTPGNSDPIPLISPANGSKSSVADGALASG SKPATLSHDRKRRHHBRDHKRNHSNGHISSKSSVADGALASG SKPATLSHDRKRRHHBRDHKRNHSNGHISSKSSVADGALASG SKPATLSHDRKRRHHBRDHKRNHSNGHISSKSSVADGALASG SKPATLSHDRKRRHHBRDHKRNHSNGHISSKSSVADGALASG SKPATLSHDRKRRHHBRDHKRNHSNGHISSKSSVADGALASG SKRATLSHDRKRRHBRDVFLLEPULTCKLARNDFORGAPTYTYT TOVSSNIVYPSGRVAVARDERSVLERVULTCELCRPBASVRTKDG BSDFVULBNGBPHRKULPATQBFDGGEFCULGDEAAUTTUGBSVFULD SQDRVLENGBGPHRAVLERVULTCELCRPBASVRTKDGB BSDFVULBNGBPHRKULPATQBFDGGEFCULGEDBARNTKDGB BVESSPALLLQKEDTVTCELCLULPHASVRTKDGG BVUESSPALLLQKEDTVTCEL			ŀ	1
RPPCCMEVHSQQRELESVVAVGRAMA\LKPPMGAMSYCLRORSR PLPRIPMGLESPLAYOU  6808  2063  737  GVGSGARSALARSRPLASRLSSRRITRAPRSGAMQRLAMDLRMI SRELSLYLERQVRVCPFCSGVGLSLLLGFSVAYAPFYLSTLAKK PQLVTVGGSSPSRFLDDHCVVTGTYSTYLVMCHCGRQTLLRPP\ 175KPPVQYRNELIKTADGSQ1SLDMFDNDMSTCYTJSSLAKK PQLVTVGGSSPSRFLDDHCVVTGTYSTYLVMCHGCRQTLLRPP\ 175KPPVQYRNELIKTADGSQ1SLDMFDNDMSTCYTJGSTRKT LLLDGLIGTSKESYLIAHHLISELGYRCVVPNNRGVAGGNLLTNYL GKIGKTPLMAAATPSVGNNTFACSPSLEKPLNMLLFNYLLTVL LQSSVNNRIRMPVKQVDDHVMGAKSIKEPDKRTSVMFGQTI DDYYTDASPSPRLKSVGIPVLCLNSVDDVFSPSHALFIYTLTTC LQSSVNNRIRMPVKQVDDHVMGAKSIKEPDKRTSVMFGQTI DDYYTDASPSPRLKSVGIPVLCLNSVDDVFSPSHALFIYTLTTC LQSSVNNRIRMFVKQVDDHVMGAKSIKEPDKRTSVMFGQTI DDYYTDASPSPRLKSVGIPVLCLNSVDDVFSPSHALFITTATAV PRVALVLISTGGHIGFLEGI MPRQSTYMDRVFKQFVQAMVEHGH RLS  6809  939  65  DYSGQTPVPTHGMTLYTPAQTHEEQGSEASTQPLAGTGTVFQ TDRAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFFDPDLRQMF GGFGKLLGVRATARAVHTNKKTGNPYTTGKHVVGAVVQFBYA AVVYDGFQCARIT\LRASGRAVYMTFRAAPPPPPIPTYG AVVYDGFGYGARIT\LRASGRAVYMTFRAAPPPPPIPTYG AVVYDGFGYGARIT\LRASGRAVYNTFRAAPPPPPIPTYG AVVYDGGFGRETYLTARAVTRARKINFPYTTGKHKINFVVGAVVGPBYA AVVYDGGFGRETYLTARAVTRARKINFVTGMAKINFVUGAVVGPBYA AVVYDGGFGRETYLTARAVTRAPHTAKINFYTTGKHKINFVVGAVVGPBYA AVVYDGGFGRETYLTARAVTRAPHTAKINFYTTGKHKINFVVGAVVGPBYA AVVYDGGFGRETYLTARAVTRAPHTAKINFYTTGKAKINFVUGAVVGAPBYA AVVYDGGFGRETYLTARAVTRAPHTAKINFYTTGKAKINFVUGAVVGAPBYA AVVYDGGFGRETYLTARAVTRAPHTAKINFYTTGKAKINFVUGAVVGAPBYAT AVVYDGGFGLETLJGREDKSTGCTLGSRRSTTSFBSTSGRPVSTTTFG SVGQTVQLCLMDLTGDLIFPFQELSRATHTNIVMATSPRAGSN GRSVTTPGNSATJEPLGSTTGLLEFRRSTTSGRPVSTTTFG SVGQTVQLCLMDLTGDLIFPFQELSRATHTNIVMATSPPAGSN GRSVTTPGNSATJEPLGSTTGLLEFRRSTTSGRPVSTTTFG SVGQTVQLCCLMDLTGDLIFPFQELSRATHTNIVMATSPPAGSN GRSVTTPGNSATJEPLSAVVNASKESSVDGGALASGV SKPATLSLHDRKERHHEKDHKRNISMGHISSKSSVDGGALASGV SKPATLSLHDRKERHHEKDHKRNISMGHISSKSSVDGGALAGG SKPATLSLHDRKERHHEKDHKRNISMGHISSKSSVDGGALAGG SKPATLSLHDRKERHHEKDHKRNISMGHISSKSSVDGGALAGG SPQUVSCLTFTTSERVVLTCELSRVDFPATWKGGGVEESELL VVKMGGRHRLILBVAHDGGSGFGCVLAGCUSALTTGSPPUHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWKGGGVEESELL VVKMGGRHRLILBVAHDGGSGFGCVLAGCUSALTTGSBPUHT TUVSSHIVVY		·		
6808 2063 737 GVGSGASALARSRPLASRLSSRRTTAPRSGAMQRLAMDLRML SRELSLYLERQVRVGPYGSGVGLSLILIGFSVAYAFYYISSITAK PQLVTGGSSPSRFLQDHCPVTETTYPTVVCWGERGQTILAPPY ITSKPPVQYDRBLIKTADGQISLUMPNDNDSTCYMDASTPPTI LLIPGLTGTSKESYILHMIHLSELGYRCVVPNNRGVAGENLLT PRTYCCANTEDLRTVIHLVHSLYPSAPFLAAVSHGGMLLINYL GKIGSKTPLMAAATPSVGWNTRACSSELRPLMWLLFNYLHTTC LQSSVNKHRHHFVKQVDMDHVMKAKSIRETUKRFTSVHFGYGTI DDYTTDASPSPRLKSVGIPVLCLMSVDUVSPSPHAIPITETAKQN PNVALVLTSYGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVERCH BLS 6809 939 65 DYSGQTFVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFDPDLAQMP GQFGKILLVDRIIFSNPTEKGQPKRLHVSNIPFRFDPDLAQMP GQFGKILLVDRIIFSNPTEKGQPKRLHVSNIPFRFDPDLAQMP GQFGKILLVNATARVMTNKKTGRPYTNGKKLNPVVGAVYGPEPYA AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTAESTQLP TRT1TPSGPRPPTALEPCSTPHRFILLGP  6810 939 65 DYSGGTPVPTEHGMTLYTPAQTHPPQGSEASTQPIAGTQTVPQ TDBAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFDPDLAQMP GQPGKILLVNATARVMTNKKTGRPYTNGKKLNPVVGAVYGPEPYA AVVYQDGFYGABI\LBATQPTDTLSPLQRPATAVTAESTQLP TRT1TPSGPRPPTALEPCSTPHRFILLGP  6810 939 65 DYSGGTPVPTHGMTLYTPAQTHPPQGSEASTQPIAGTQTVPQ TDBAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFDPDLAQMP GQPGKILLVNATARVMTNKKTGRPYTNGWKLNPVVGAVYGPEPYA AVVYQDGFYGABI\LBATQPTTLTSPLAGPTATVTAESTQLP TRT1TPSGPRPPTALBPCSTPHRFILLGP  6811 1522 658 DUTVTWSFYDCOVIASTGHINGNATSPARAG GRSVTTPGNSVPPPLORSSLPHGAVSVAAPDPYTTSVEEGDPME PSGSDEDFQDLLHPGDRADSTQCRLSRRNSTDSRPVSVTYTPG SVGQDTQLCLMDLTEDILPPHQPLGRARTHITMWATSPPARAG GRSVTTFORMSVPPPLGRSSLPHGAVSNAGSKSSVMOGALASGV SKRATLSLINDRKRRHHKOHKRNISMGHISSKSSDKLMLVTKYK TDPAXTLGTPLCPMBNOPVLLEPLICKKLARHERLFVLIPLEDCI VTAQQEGFICTWGRPGKVVSFNP  6812 4001 1682 EDAVFSLDLSTITGGTWFLNGERLKSREPEGQVPGAALTTGSPVHIL SCQDKVSLTPTTSERVVLTCELSRRVPPATWYRDGGVEBSBLL VVKMDGRKHRLIHAVKHQDGGLVSFSCTEBGAPFTVTT TUVSSKILVPSGKVVVAAPTLERVCHTCELGRPHAAVKRTRDGE EDAVFSDLLSTITTSECVMLACESVDPRATWKRDGGBVE SDSPVVLENBEPHRRULDATTJECCVHACESRDAPFWYTT TVSVSMIVYPSGKVVVAAPRLERVCHTCELGRPHAAVKRTRDGE EVESPALLLQKEDTVRRULDATTJEGGFFCVAGGCAYFTVTT TVSVSMIVYPSGKVVVAAPRLERVCHTCELGRPHAAVKRTRDGE EVESPALLLQKEDTVRRULDATTLECVTHAGLSRRDAPFRWY				
GUSGRASALARSPEASKLIGTSVAYAPYYLSSIAKK POLVTGGSFSRFLOHCPVVTETTYPUWCMGCROCTLLRPP ITSKPPVQYRNELIKTADGGJISLDWFDNDNSTCYMDASTRPTI LLLPGLISTSKEYILBHIHLSEBLGYVPNNCWAGRGGTLLRPP ITSKPPVQYRNELIKTADGGJISLDWFDNDNSTCYMDASTRPTI LLLPGLISTSKEYILBHIHLSEBLGYVPNNCWAGRGGNLLINYL GKTGSKTPLMAANFSVGWNTFAGSESLBLPLNWLLFRYILTT- LAGSUNKHRHPVKQVDMDHVMKAKS TEPTKEY TO DDYYTDASPSRLKSVGIPVLCLINSVDDVFSPSHAIPIETAKQN PNVALVLISYGGHIGFLEG IWPRQSTYMDVFKQFVQAWVEHCH ELS  6809 939 65 DYSGGTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVVQ GOFGKILDVBIIFNERGSKGFGFVTFFTSSDADARAEKLNGTIV EGRKIEVANATARVMTNKKTGRPYTNGKKINPVVGAVYGPBYA VTGFPYPTTGTAVAKRGAILBGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGAB'I LBATQPTDTLSPLQRRQPTATVTAESTQLB TTTITPSGPRPPTALBECTFWHFILLGT GOFGKILDVBIIFNBRGSKGFGFVTFTSSDADARAEKLNGTIV EGRKIEVANATARVMTNKKTGRPYTNGKKINPVVGAVYGPBYA VTGFPYPTTGTAVAKRGAILBGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGAB'I LBATQPTDTLSPLQRRQPTATVTAESTQLB TTTITPSGPRPPTALBECTFWHFILLGT GOFGKILDVBIIFNBRGSKGFGFVTFTSSDADARAEKLNGTIV EGRKIEVANATARVMTNKKTGRPYTNGKKINPVVGAVYGPBYA VTGFPYFTTGTAVAYKGAILBGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGAB'I LJKATQPTDTLSPLQRRQPTATVTAESTQLB TTTITPSGPRPTALBPCSTFWHFILLGP TTTTTPSGPRPTALBPCSTFWHFILLGP TTTTTPSGPRPTALBPCSTFWHFILLGP SSGSEDPQDLLHIGGBRADGTOCRLSRRNSTDSRPVSVTTRFG SVQQDTQLLADITEDLIPPHQPLGSRANTSTNSRPVSVTTRFG SVQQDTQLLADITEDLIPPHQPLGSRANTSTNSRPVSVTTRFG SVQQDTQLLADITEDLIPPHQPLGSRANTSTNSRPVSVTTRFG SVQQDTQLLADITEDLIPPHQPLGSRANTSTNSRPVSVTTRFG SVQQDTQLLADITEDLIPPHQPLGSRANTSTNSRPVSVTTRFG SVQQDTQLLADITEDLIPPHQPLGSRANTSTNSRPVSVTTRFG SVQQDTQLLADITEDLIPPHQPLGSRANTSTNSRPVSVTTRFG SVQQDTQLADITEDLIPPHQPLGSRANTSTNSMANTSTVA TDPAKTLTFPLCPRMSVPVLLEPLICLAHRELTVLIPLEDCT VTACQEGFICTWGRPCKVVSVMP EDAVFSLDLSTIIGGTWFLUGBEKKSNEPGSQVEPGALRYRIEQ KSLQHRLILHAVKHQDSGALLVGSEFEGUSAPFGVTVQDPPV HIVDPREHVFVHALTSSEVMLACEVVDR\EDAPFNWKDGGVEBSBLIL VWKMGGRRMRILIPELGSRAVDFSAFGGVTVOPPP HIVDPREHVFVHALTSSEVMLACEVVDR\EDAPFNWKDGGVEBSBLIL VWKMGGRRMRULIPPRGVLADAFREVULTCELCRPHABVKRTTDGE BVMSSPALLLQKBGDTWRIVLDAVQLEDSGGFLCAYFTVTI TUSWSWIVYPSGKVVVAAPRLEVVLICEUCRPHABVKRTTDGE BVMSSPALLLQKBGDTGRILDAGGRYCDAGDGA			}	,
SRELSLYLEHQVRVGPFGSGVGLSLILGFSVAYAPYYLSSIAKK PQLVTGESSPSRFLQHCCVVTETYTPTUNCHGEGGYTLLEPF, TITSKPPVQYRMELIKTADGGQISLUMPINNSTCYMDASTRPTI LLLPGLTGTSKESYTLEHMTHLSELGYRCVVPRNRGVAGBKLIT, PRTYCCANTEDLEFVILHHUSLYPSAPPLAAGVSNGGMALLINY, GKIGSKTELMAAATFSVGNTTEACSESLERPLANKLLFNYYLITC LQSSVNKIRHMPKKQVDMDHVMKAKSIREDGKRFTSVHFGVTIT DDYYTDASPSBRIKSVGIFVLCLMSVDDVSPSHAIP IETAKQN PRVALVLISYGGHIGFLEGINPRQSTYMDRVFKQPVQAMVEHGH BLS  6809 939 65 DYSGGTPVPTEHGMTLYTDAQTHPBQDGSEASTOPIAGTQTVPQ TDRAAQTDSQPLHPSDPTEKQQPKRLHVNNIPFRFRDPDLRQMF QGPGKILLVELIFNERGSKGFGPYTFETSSDADRAREKIMGTIV BGRKIEVNNATARWMINKKTGRPYTNGKKLNPVVGAVYGPBPYA AVVYODGFYGABI \LERTOPITUTGPLQRRQPTATVTAESTOLP TRTITPSGPRPTALEPCETFHIRPLLGP 6810 939 65 DYSGGTPVPTEHGMTLYTBAQTHPBQRGSEASTOPIAGTQTVPQ TDRAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRDPDLRQMF QGPGKILLVBII IPNERGSKGFGFYFTETSGDADRAREKIMGTIV BGRKIEVNNATARWMINKTGRPYTNGWKLNPVVGAVYGPBPYA AVVYODGFYGABI \LERTOPITUTGPLQRRQPTATVTAESTOLP TRTITPSGPRPTALEPCETFHIRPLLGP GQPGKILLVBII IPNERGSKGFGFYFTETSGDADRAREKIMGTIV BGRKIEVNNATARWMINKTGRPYTNGWKLNPVVGAVYGPBPYA AVVYODGFYGABI \LERTOPITUTGPLQRRQPTATVTAESTOLP TRTITPSGPRPTALBPCETFHRFILGP TRTITPSGPRPTALBPCETFHRFILGP  6811 1522 658 DVJVVSSYDCOVIASTHGHKSWVVAPDPYTTSVEEGDPME FSGSDEDFQDLLHFGRDRADGTCGLSRRNSTDSRPVSVTYRPG SVGQUTQLCLWDLITEDILFPHQPLGRARTHTWMATSPPAGEN GRSVYTFDRNSVPPLEPGRSNAGSKSSWDGALLSVTYKT TDPAATLGTPLCPMBROVPLLEPLLCKKLAHKELFVLLIPLEDCI VTACQEGFICTWGRPGKVVSPNP  6812 4001 1682 EDAVFSLDLSTITGGTWFINGBEKKSNEPEGQVEPGALRTRIEQ SCDRVSLTPTTSGRVVJTCELSRVDPPATWYRDGGVEBSELL VVKMDGRKHRLILHAVKHQDGGALVOFSCGPQOSAALTIQSSPYHIL SCDDKVSLTPTTSGRVVJTCELSRVDPPATWYRDGGVEBSELL VVKMDGRKHRLILHAVKHQDGGALVOFSCGPQOSAALTIQSSPYHIL SCDDKVSLTPTTSGRVVJTCELSRVDPPATWYRDGGVESSELL VVKMDGRKHRLILDPAKVDLAGPLGGFCCVSAPFGVTVQDPP HTVDFSWITVPSGKVVVAPRLEVVLITCELCRPHABVKRTRUGE BUVSESBALLQKEDTVRRJVLPAVQLEDGGEFCCVSAPFGVTVQDPP HTVDFSWITVPSGKVVVAPRLEVVLITCELCRPHABVKRTRUGE BUVSESBALLQKERGGPCCTLAUTLECCTHPHABVRTRTGE BVUSESBALLQKERGGPCCTLAUTLECCTRPHABVRTRTGE BVUSESBALLVLERGGPCCRLVLLPAVQLESGERDAPVRWY DOLKVESSBALVLERGGPCCRLVLTDAGGGSFVCDAGDGSA			L	I
POLVTGGSSPSRPILDEPVUTETYYPTWCEGRGQTLLRPP\ ITSKPPUQYRMELIKTADGGQ ISLDMYDDINSTCYMDASTRPTI LLLPGLITGTSKESYLLMIHILISELGYRCVUVRNNRGVAGRILLIYL PRITYCCANTEDLETVIHIVUSLYPSAPFIAAQVSMGGHLLIVYL GKIGSKTPIMAAATPSGVANTAGKSESLEKPLNNLHPYILTTC LQSSVNKHRHMFVKQVDMDHVMKAKSIREFDKRFTSVMFGYQTI DDYYTDASPSPRLKSVGIPVLINSUDDVFSSHAIPIETAKGN PRVALVLIYTGGHIGFLEG WPRQSTYMDRVFKQPVQAMVEHGH BLS  6809 939 65 DYSGQTPVPTEHGMTLYTPAQTHPBQPGSEASTQPIAGTQTVPQ TDSAAQTDSQPLHPSDPTEKQQFKRLHVSNIPFRFRDPDLRQMF GQPGKILLVER I FFRENGSKGFGFVTFETSSDADRAREKLNNTIV EGRKILEVSNATARVMYNKKTGNFYTNSKNINPVVGAVYGDFFYA VTGFPYPTTGTAVAYRGAHLAGGGRAVYMTFRAAPPPPP I PTYG AVVYQDGFYGABI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TTTITTPSGPRRPTALEPCETYHHFLLGP 6810 939 65 DYSGQTFVFERGMTLYTPAQTHPBQPGSEASTQPIAGTQTVPQ TTRAAQTDSQPLHPSDPTEKQQFKRLHVSNIPFRAPPPPP I PTYG AVVYQDGFYGABI\LEATQPTDTLSPLQRRQPTATVTAESTQLP GQFGKILDVBI I FNERGSKGFGFVTFETSSDADRAREKLNGTIV BGRKILEVSNATARAWMTKKTGNFYTNGWKINFVAAPPPPILTGY AVVYQDGFYGABI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRYTTPSGPRRPTALEPCETYHHFPLLGP 6811 1522 658 DLVTWSFVDCRVIASTHGH\KSWYSVVAFDPYTTTSVEEGDFME FSGSDEDFQDLLHFGRBRADSTQCRLSRRNSTGSRFVSVTTTRG SVGQDTQCLLMDLTGBLIPFHQLGBARPTTNVMNATSPPAGSN GNSVTTPGNSVPPPLESDLIPFHAQDFRCHSKSDKLNLVTKK TDFAXTLGTPLCFPMBDVPPLBSLICKKLAHSRIFTLYTHEQ SKGATLSLHDRKRRHHIKDHJLARVIGCKERSBILL VVXMCGGFICTWGRPGKVVSFNP 6812 4001 1682 EDAVFSLDLSTI IQGTWFLNGERLKGNEPEGQVPGAALTIGBSPVHIL SPQDKVSLTFTTSSRVVLTCELSRVDFPATYNCDGKVEESBILL VVXMCGGFICTWGRPGKVVSFNP HTVDPRENVFVHATTSSCVVLTCELSRVDFPATYNCGCKVEESBILL VVXMCGRKIRLILPBEAVQDGGFECCTEGVSAFFGVVQDPFV HTVDPRENVFVHATTSSCVMLACEV\DR\KDAPVRNYKDGQKVES BSDFVVLENBEGPHRULLAATQPSIGGEFCCTGGVARGECCATFTVTT TUSSSI VYYBGKVYVAAVELERUVLTCELCRPHARVRNTCDGC BVVSEPALLLQKBUTYPRGVVLTCELCRPHARVRNTCDGC BVVSEPALLLQKBUTYPRGVVLTCELCRPHARVRNTCDGC BVVSEPALLLQKBETALATURARDTURGCHELSREDAPVRWYY DGLKVVSEPSRAVLYDGFRCRLVLLPAAQDEGGBFVCDAGDGAAFT VTVTBPPVRITYPRDEVVILTCELGREDERDAPVRWYX DGLKVEBSBALVLERBCAPRCRLVLLAATQBCBGGGBFVCDAGDDAS	6808	2063	737	
TISKPPVQYRBLIKTADGGQISLDMEDBONSTCYMDASTRPTI LLLDGLTGTSKESYILBMIHLSELGYRCVVPNNRGVAGBRILLT PRIVCCANTEDLETVIHHUSELLYPSAPFIAAOVSMGGBLLNYI. GKIGSKTPIMBAATFSYGNNTFACSESLEKPLNMLLTBYYLITC LQSSVNKHRHMFVKQVDMDHVMKAKSIRBFDKRFTSVMPGYOTI DDYYTDASPSPRLKSVOIPVLCINSVDDVFSPSHHIPIETAKQN PRVALVLTSYGGHIGFLEGIWPRQSTYMDRVFKQPVQAMVEHCH BLS  6809 939 65 DYSGQTPVPTEHGMILYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHESDPTEKQQFKRLHVSNIFFRFROPDLRQMF QQPGKILLDVBIIFFRENGSKGFGFVTTSSDADARREKINGTIV EGRKIEVNNATARVMTNKKGNPYTNGWKINPVVGAVYGPBPYA AVVYQDGFYGABI\LBRATQPTDTLSFLQRRQPTATVTAESTQLD TTSTITPSGPRRPTALEPCETFHHFILGP 6810 939 65 DYSGQTPVPTEHGMILYPDAQTHPEQGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIFPRAPPPPPIPTYG AVVYQDGFYGABI\LBRATQPTDTLSFLQRRQPTATVTAESTQLD TTSTITPSGPRRPTALEPCETFHHFILGP GQPGKILLDVBIIFRAGSKGFGFVTFETSSDADARREKLMGTIV BGRKIEVNNATARVMTNKKTGNPYTTGSNAPVGGFPYAP VTOFPPYPTTGTAVAYRGAHLRGRGRAVVNTFRAAPPPPPIPTYG AVVYQDGFYGABI\LBRATQPTDTLSPLQRRQPTATVTAESTQLD TTSTITPSGPRRPTALEPCETFHHFILGP GQPGKILLDVBIIFPRAVSKAGRAVNTFRAAPPPPPIPTYG AVVYQDGFYGABI\LBRATQPTDTLSPLQRRQPTATVTAESTQLD TTTTTTPSGPRRPTALEPCETFHHFILGP TTTTTTSSGPRRPTALEPCETFHHFILGP  6811 1522 658 DEUTWSFYDGCVTASTHGH\KSWYSVVAPPPYTTSVEEGDPME FGSGDEDPQDLLHPGRDADSTQCRLSRRNSTDSRPVSVTYRFG SVGQDTQLCLMDLIEDILPPHQPLSRARTHTWNNATSPPAGSN GRSVTTFGNSVYPPLEPRSNSLPHSAVSNAGSKSSVMCAAIASGV SKRATISLHPRKREHHRKDHKRNHSKTSSKSSKNLNIVTKK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP  6812 4001 1682 ERDVFSLDISTIGGTMYLMGBLKSKSDKNLNIVTKK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVUSFNP HTYDPREHVPHATTSSCVMIACEV\DR KORQWEESBILL VVKMCGRKRHLIPFARAVQDSCEGFCCVAGDECAYFTVTI TVSSWIVYPSGKVVVAAVRLERVVLTCELGRPARAVGOGKVEESBILL VVKMCGRKRHLIPFARAVQDSCGEFCCVAGDECAYFTVTI TVVSSWIVYPSGKVVVAAVRLERVVLTCELGRPARAVRTCOGC BVVSSPALLLGKEDTVRRIVLPAVQLEDGGEFCCVAGDECAYFTVTI TVVSSWIVYPSGKVVVAAVRLERVVLTCELGRPARVTKDGCV BVVSSPALLLGKEDTVRRIVLPAVQLEDGGGEFCCVAGDECAYFTVTI TVVSSWIVYPSGKVVVAAVRLERVVLTCELGRPARVTKDGCV BVVSSPALLLGKEDTPRRIVLPAVQLEDGGGEFCCVAGDECAYFTVTI TVVSSWIVYBSGKVVAAAVRLERVULTCELGRPARVTKDGC			İ	<u> </u>
LLLPGLTGTSKESYILHMIHLSEELGYRCVVPNNFGVAGENILINT PRTYCCANTEDLETV HIHVHESLYPSAPFJAAGVSMGGENILINT GKTGSKTPLMAAATSSVGNKTFALSESLEKPLNNHLENTYTLTTC LQSSVNKIRHMPVKQVDMDIVMKAKSIREFDKRFTSVMPGVOTI DDYYTDASPSPERLESVGIPVLCLNSDUVSPSHALIPITETAKON PNVALVLTSYGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVEHCH RLS  6809 939 65 DYSGGTPVPTEHGMTLYTPAQTHPEQFGSEASTQFIAGTQTVPQ TDEAAQTDSQPLHFESDPTEKQQFKRLHVSNI PFRFRDPDLRCMP GQFGKILLVEI IFNERGSKGFGFVTFSTSDADRAREKLNGTIV EGRKIEVNNATARWMTMKKTGNSYTHGWKLNSVVGAVYGPSFYA VYTSFYPTTGTAVAYRGAHLRGEGRAVYMTFRAAPPPPPI PTYG AVVYQDGFYGABY LJRATQPTDTLSQDRQPATATVTAESTQLP TRT1TPSGPRPTALEPCETFHRFLLGP 6810 939 65 DYSGGTPVFTEHGMTLYTPAQTHPEQGGSEASTQPLAGTQTVPQ TDBAAQTDSQPLHESDPTEKQQFKRLHVSNI PFRFRDPDLRQMF GQPGKILLDVB I I PNERGSKGFGFVTFETSSDADRAREKLNGTIV EGRKIEVNNATARVMTMKKTGNSYTHGWAGNYGPSFYA VYTSFYPTTGTAVAYRGAHLRGEGRAVYNTYRAAPPPPPI PTYG AVVYQDGFYGABY LJRATQPTDTLSPLQRGPTATVTAESTQLP TRT1TPSGPRPTALEPCETFHFFLLGP 6811 1522 658 DLVTVWSFVDCRVTASTHGH\KSWVSVVAFDPYTTSVEEGDPME FSGSDEDFQDLLHFGCRRADSTQCRLSRRNSTGSRFVSVTYTRFG SVGQTQCLCLMDLTERLDFCFTHFFLLGSP WSGQTQCLCLMDLTERLDFCFTHFFLLGSP TSTTTSSGPRPTALIBCETFHRFTULMATSPPAGSN GRSVTTPGNSVPPPLEGBRHRKDHKRNHSMGILSKSSDKLMLVTKTK TDPAKTLGTELCFRMBOVPLBELLICKKLAHERLTVLIFYLEDCT VTACQEGFICTWGRPGKVUSFNP 6812 4001 1682 EDAVFSLDLSTTI GGTWFLMGEBLKSNEPEGQVBGALTYRISQ KSLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPWHIL SCQDKVSLTFTTSSRVVLTCELSRVDFPAFWYKDGQKVESSILL VVMMGRKHRILIPSRAVVONGEFECKTBGVSAFFGYTVQDPPY HIVDPREHVFVHAITSSCVMLACEV\DR\EDAPVRWYKDGQVE ESDFVVLENBEGHERULDATQPSGGEFQCCAGDECAYFTVTI TDVSSWIVPSGKVVYAAVELERUVULTCELCRPHAEVRWTTCDG BVVSSPALLLGKEDTVARAVLPAVOLEDSGEFTCLTGGTAPVRWTTUTOT TDVSSWIVPSGKVVYAAVELERUVULTCELCRPHAEVRWTTCDG BVVSSPALLLGKEDTVARAVLPAVOLEDSGEFTCLTGDFSASFT VTVTSBPVRI TYPRDEVTILAVTLECLGERDAAPVRWYK DOLEVESSBALVLEREGBRAVLNERGGROVCINGEGLEREDAPVRWYK DOLEVESSBALVLEREGBRAVLNERGGROVCINGEGLEREDAPVRWYK DOLEVESSBALVLEREGBRAVLNERGEREGBRAVCDREGBERVCDAGEDGSAFT		İ		
PRTYCCANTEDLETVIHIVHSLYPSAPFLAAGVSMGGMLLINYL GKTGKKTPLMAAATFSVGMTATACSEKPLMMLLFNYTLITC LQSSVAKHRHMPVKQVDMDHVMKAKS IREPDKRFTSVMFGQTI DDYYTDASPSPLKSVG IPVLCLMSVDDVFSPSHAIP IETAKQM PNVALVLTSYGGHIGFLEG IWPRQSTYMDRVFKQFVQAMVEHGH BIG  8809 939 65 DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIP PFRFNDPDLRQMF GQFGKILDVBI I FNERGSKGFGFVTFETSSDADRAREKLNGTIV EGRKIEVNNATARVMTNKKTGNPYTNGKKLMPVVGAVYGEPFYA AVVYQDGFYGASI \LEATQPTDTILSPLQRRPTATVTAESTQLP TRITIPSGPRRPTALEPCETFHEFLLGP GQFGKILDVBI I FNERGSKGFGFVTFETSSDADRAREKLNGTIV EGRKIEVNNATARVMTNKTGNPYTNGAKLMPVVGAVYGEPFYA AVVYQDGFYGASI \LEATQPTDTILSPLQRRQPTATVTAESTQLP TDRAAQTISQPLHPSDPYEKQQPKRLHVSNIP FFRNDPDLRQMF GQFGKILDVBI I FNERGSKGFGFVTFETSSDADRAREKLNGTIV EGRKIEVNNATARVMTNKTGNPYTNGAKLMPVVGAVYGEPFYA VTSFPYPTTGTAVARGAHLEGGRGAVYMTFRAAPPPPP I PTTG AVVYQDGFYGASI \LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP TRTITPSGPRRPTALEPCETFHRFLLGP FGSSDEFQDLLHHFGDRPABGTQCKLGSRNSTDSRPVSVTYTRFG SVGQDTQLCLWDLTEDILPPHQPLSRARTHTNVMNATSPPAGSN GRSVTTPGNSVP PLPRRSNSLPHGAVSNAGSKSSVMGGALASGV SKPATISLIDDRKERHHERDHKRNISMGHISSKSSDKINJUTKTK TDPAXTLGTPLCPRREDVPLLEPLICKKIAHERLTVLIPLEDCI VTAQCGEGTICTWGRPGKVVSTNP KGLQHRLILHAVKHQDGSALVGFSCPGVQDSAALTIQESPHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESHLL VVMMGCRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HTVDRREHPVHALTSECVMLACSV\DR\EDSPAFFGVTVQDPPV HTVDRREHPVHALTSECVMLACSV\DR\EDSPAFFGVTVQDPPV HTVDRSWIVPSSKVVVAAVRLERVVLTCELCRPBAKVRWTKDGE EDVFVLENEGPHRRLULPATQPSDGGFGCVAGDCCAYPTVTI TDVSSWIVPSSKVVVAAVRLERVULTCELCRPBAKVRWTKDGE EVUESPALLLQKEDTVRILIAVITLAVILECUTALDATIGECTAPBAKVRWTKDGE EVUESPALLQKEDTVRILIAVILAPAQQBUGGSFYLCEIDDBSASFT VTVTBPPVRI I YPRDEVTLIAVILAVCHGLEGERLACHEDADPRWYKYCDGG				
GKIGSKTPLMAAATFSVGNNTFACSESLEKPLNWLLFNYYLITTC LQSSVNKHRHFVKQVDMDHVMKAKS IREPDKRTISWFGYDTI DDYTTDASPSPRIKSVGIPVLCLINSVDDVFSPSHAIPIETAKGN PRVALVLTSYGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVEHCH RLS  6809 939 65 DYSGQTFVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKQQPKRLHVSN1PFPFRDPDLRQMF GQFGKILDVBIIFNERGSKGFGFVTFETSSDADRAREKLINGTIV VNGFPYPTTGTAVATRGAHLKGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTAESTQLP TTT1TPSGGRRPTALEPCETHRFLLGP 6810 939 65 DYSGQTPVPTEHGMTLYTPAQTHPPQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKQQPKRLHVSN1PFRPDPDLRQMF GQFGKILDVBIIFNERGSKGFGVTFETSSDADRAREKLINGTIV BGRKLEVNNATARVMTNKKTGNPYTNGKKLMPVVGAVYGPBFYA VTGFPYPTTGTAVAYRGAHLKGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTAESTQLP TTR1TPSGGRRPTALEPCETHRFLLGP TTR1TPSGGRRPTALEPCETHFRFLLGP TTR1TPSGPRPTALEPCETHFFLLGP TTR1TPSGPRPTALEPCETHFFLLGP TTR1TPSGPRPTALEPCETHFFLLGP TTR1TPSGPRPTALEPCETHFFLLGP SGGDTQLCLHBLTTDILIPPHQPLSRAFTHTNVMNATSPPAGSN GRSVTPCHNSVPPPLPRSNSLPPHSAVSNAGSKSSVMGATASGV SKPATLSLHDRKERHHEKDHKRNHSMGHISSKSDKLINLVTKK TDPAKTLGFBLCPRHEDVPLLEPLICKKIAHERLTVLIPLEDCT VTACCGETCTMGRPGKVVSTRP SGGDTQLCLHBLTTDILIPPHQPLSRAFTHTNVMNATSPPAGSN KSLQHRLILHAVKHQDGSALVGFSCPGVQDSAALTIQBSPVHIL SPQDKVSLTPTTSBVVLTCELSRVDPPATMYKDGQKVEESBIL VVKMGGRKHRLILEPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HTVDRREHFVHATTSBCVMTACSV\DR_KDBPPNTWKNGGE EDFVVLENEGPHRRULDPATQPSDGGEFCCADECAYPTVTI TTVSSWIVYPSGKVYVAAVALEERRVVLTCELGRWARKFRINGE BVVSSWIVYPSGKVYVAAVALERRUVLTCELGRWARKFRINGE BVVSSWIVYPSGKVYVAAVALERRUVLTCELGRWARKFRINGE BVVSSWIVYPSGKVYVAAVARLERRUVLTCELGRWARKFRINGE BVVSSWIVYPSGKVYVAAVALERRERVULTCELGRWARKFRINGE BVVSSWIVYPSGKVYVAAVALERRERVULTCELGRWARKFRINGE BVVSSWIVYPSGKVYVAAVALERERERDAPVRWKNGG BUVSSPALLLQKEDTVRTILIPATLEVTLEVTLECTERDARRAFTTOGE BVVSSWIVYPSGKVYVAAVAREERERDAPVRWKNGGE BVVSSBALLLQKEDTVRTILIPATLEVTLEVTLEVTLECTERDARRAFTTOGE BVVSSBALLLQKEDTVRTILIPATLEVTLEVTLECTERDARRAFTTOGE BVVSSBALLLQKEDTVRTILIPATLEVTLECTERDARRAFTTOGE BVVSSBALLQKEDTVRTILIPATLEVTLECTERDARRAFTTOGE BVVSSBALLQKEDGFCCLIALPTARGERDAPVRWYKODGLONG		ľ	İ	
LQSSVNKHRHMFVKQVDMDHVMKAKSIREFDKRFTSVMFGYQTI DDYYTDASESPRLKSVGIPVLCLMSVDUDVFSPRHAIPIETAKQM PNVALVLTSYGGHIGFLEGIWFRQSTYMDRVVFKQFVQAMVEHGH RLS  6809 939 65 DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVFQ TDRAAQTDSQPIHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF GQFGKILDVBIIFNBRGSKGFGFVTFETSSDADRAREKLNGTIV EGRKIEVNNATARVMTNKKTGNPYTNGKKHPVVGAVYGEPFYA AVVYQDGFYGAEI\LBATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGGRRPTALEPCETFHRFLLGF  6810 939 65 DYSGGTPVPTEGGWTLYTPAQTHPEQPGSEASTQPIAGTQTVFQ TDRAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF GQFGKILDVBIIFNBRGSKGFGFVTFETSSDADRAREKLNGTIV EGRKIEVNNATARVMTNKTGNPYTNGKKLMPVVGAVYGPEPYA AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTAESTQLF TRTITPSGGRRPTALEPCETHRFLLGF  6811 1522 658 DIVTWSFVDCLVIASTHGHKKSWVSVVAFDPYTTSVEEGDPME FSGSDEDFGDLLHFGRDFADSTQCRLGRRNSTDSRFVSVTTRFG SVGQDTQLCLWDLTEDILPPHQPLSRARTHTNVMNATSPPAGSN GRSVTTPGNSVPPLFRSNSLPHGAVSNAGSKSSVMGATASGV SKRATISLIDRKERHHBKDHKRNHSMGFISSKSSDKLINLVTKYK TDPAKTIGTPLCPRMBDVPLLBFLICKKLAHKRITVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP 6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGERLKSNEPSGQVEFGALRYRIBQ KGLQHRLILHAVKHQDGGALVGFSCPGVQDSAALTIGBSVHIL VVKMGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HTVDREHFYDHATTSBCVMLACSV\DR.KDAPWRWKNGGRVESBIL VVKMGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HTVDREHFYDHATTSBCVMLACSV\DR.KDAPWRWKNGGRVE BSDFVVLRNEGFHRELLVLDATQDFDGGGFFCCVAGDCAYTVTI TDVSSWIVYPSGKVVAAVRLERVULTCELCRPWAEVRWTKGG BVVGSFALLLQKEDTVARLUAPAQDSGGSFCCCAGDCAYTVTI TDVSSWIVYPSGKVVAAVRLERVULTCELCRPWAEVRWTKGG BVVGSFALLLQKEDTVARLUAPAQDSGGSFLCEIDDBSASFT VTVTBPPVRITYPROEVILIAVILAVCELSVEBCAPAVRWKKGG BVVGSFALLLQKEDTVRIULPAAQPBGGGFFCCTAGDASAFT VTVTBPPVRITYPROEVILIAVILAVCELSCEBADAPVRWXK DOLKWESSBALVLERDGGFCCLVLPAAQPBCGGFFCCDABDSA		Į.	}	
DDYYTDASPSPRIKSWGIPVLCILNSUDDVSPSHAI PIETAKQM PNVALVLTSYGGHIGPIEGI MPRQSTYMDRVFKQFVQAMVEHCH RIS  DYSGQTPVPTEHGMTLYTPAQTHPEQPESEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKQQFKRLHVSNIPFRFRDPDLRQMF GQPGKILDVEI I FINERGSKGFGPVTFETSSDADRARKKLMGTIV EGRKIEVINATARVMTINKKTGNPYTNGKKINPVGAVYGPEPVA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPI PTYG AVVYQDGFYGAEI LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRPPTALEPCSTFHRPLLGP  6810 939 65 DYSGQTPVPTEHGMTLYTPAQTHPPQEGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF GQPGKILDVBI I FINERGSKGFGPVTFETSSDADRARKKLMGTIV EGRKIEVINATARVMTINKTGNPYTINGMKLNPVVGAVYGPEPVA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPI PTYG AVVYQDGFYGAEI \ LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRPLLGP  6811 1522 658 DLVTWSFPUCRVIASTHGH*KSWVSVVAPDPYTTSVEEGDPME FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG SVGQDTQLCLMDLTEDILPPHQPLESRATHTHVMINATSPPAGSN GRSVTTPGRSVPPPLFRSNLPHSAVSNAGSKSSVMDGATASGV SKPATLSLHDRKERHHERDHKRNHSMGHISSKSSDKLINLVTKTK TDPAATLGFPLCPRMEDVPLLSPLICKKTAHRRLITVLIPLEDCI VTACQGEFICTMGPCKVVSFNP  6812 4001 1682 EDAVFSLDLSTI IQGTWFLNGBELKSNEPEGQVEPGALRYRIEQ KSLQHRLILHAVKHQDSGALVGFSCFSVQDSAALITJGSSVHTURI SPQDKVSLIPFTSGRVVATGESSKYDFPATWYNGGCKSESBILL VVKMDGRKHRLILPEAKVQDSGEFECTTEGVSAPFGVTVQDPPV HTVDFREHVPVHAITSBCVMTACEVQDRAGECSPYCTVQDPPV HTVDFREHVPVHAITSBCVMTACEVQDRAGECSPYCTVQDPPV HTVDFREHVPVHAITSBCVMTACEVQDRGECAPTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPMAEVRWTKGG BVVSSPALLLQKEDTVRRLVLPAAQDEGGSFCCVAGBECAPTVTI TVVSSWIVYPSGKVYVAAVRLERVVLTCELCRPMAEVRWTKGG BVVSSPALLLQKEDTVRRLVLPAAQDEGGSFCCVAGBECAPTVTI TVVSSWIVYPSGKVYVAAVRLERVVLTCELCRPBAEVRWTKGG BVVSSPALLLQKEDTVRRLVLPAAQDEGGSFCCVAGBECAPTWYK DOLEVUSSSBALVLKREGPGRUVLLPAAQDEGGSFCCVAGBECAPTWYK DOLEVUSSSBALVLKREGPGRUVLPAAQDEGGSFCCLAGEDEPVCNMK DOLEVUSSSBALVLKREGPGRUVLPAAQDEGGSFCCLAGEDDEPVCMYK DOLEVUSSSBALVLKREGPGRUVLPAAQDEGGGSFCCLAGEDDEPVCMYK DOLEVUSSSBALVLKREGPGRUVLPAAQDEGGSFCCLAGEDDEPVCM				
PRVALVLTSYGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVEHCH BLS  DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKQQFKRLHVSNIPFFFRDPDLRQMF GQFGKLLDVBIIFNERGSKGFGFVTFFTSSDADRAREKLMGTIV VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTAESTQLP TTPITPSGGRRPPTALEPCETFHEPLLGP  6810 939 65 DYSGQTPVPTEHGMTLYTPAQTHPEQFGSEASTQPIAGTQTVPQ TDBAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF GQFGKLLDVBIIFNERGSKGFGFVTFTSSDADRAREKLMGTIV BEGKLEVNNATARVMTNKTGMPYTHGWKLMPVVGAVYGPEFYA VTGFPYPTTGTAVAYKGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTAESTQLP TTRITTPSGPRRPTALEPCETFHEPLLGP  6811 1522 658 DLVTVWSFVDCRVIASTHGH\KSWVSVVAPDPYTTSVEEGDPME FSGSDEDFQDLLHFGRBRADSTQCRLSRRNSTSRSTSTRVSVTYRFG SVGQDYOLCLMDLTEDILPHQPLGSRRNSTTDNATTSPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKRRHHEKDHKRNHSMGHLSSKSSDKINIVTKTK TDPAXTLGTPLCFPMBOVPLBLBFLICKKIAHKRLTVLIFLEDCI VTAQQEGFICTWGRPGKVVSFNP 6812 4001 1682 EBAVFSLDLSTIIQGTWFLMGRELKSNEPGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQBSPVHIL SPQDKVSLTPTTSBRVVLTCELSRVDFPATWYKDGQRVE BSDFVVLRNEGPHRRIVLBATQPSDGGEFCCVAGDECAYFTVTI TDVSSWIVPPSKVVVAAVRLERVVLTCELCRPHAEVRHTKGE BVGSFALLLQKEDTVRRLVLERVOLGGGEFCCVAGDECAYFTVTI TDVSSWIVPPSKVVVAAVRLERVVLTCELCRPHAEVRWTKGE BVGSFALLLQKEDTVRRLVLERAQOEGGEFCCVAGDECAYFTVTI TDVSSWIVPPSGKVVAAVRLERVVLTCELGREDAPVRWXK DOLEVBSSBALLLQKEDTVRRLVLERAQOEGGFFCCVAGDECAYFTVTI TDVSSWIVPPSGKVVAAVRLERVVLTCELGREDAPVRWXK DOLEVBSSBALVLEREGGERFCULDABAGSFFCCNAGGDECAYFTWFX			Î	
BLS  DYSGCTPVPTEHGMTLYTPACTHPEQPSGEASTQPIAGTCTVPQ TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFKDPDLRQMF QQFGKILDVBIIFNBRGSKGFGFVTFETSSDADRAREKLNGTIV BGRKIEVNNATARVMTNKKTGNPYTNGMKLNPVVGAVYGPEPYA AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTAESTQLP TRTITTSGPRRPTALEPCETFHRFLLGP OQFGKILDVBIIFNBRGSKGFGFVTFETSSDADRAREKLNGTIV BGRKIEVNNATARVMTNKKTGNPYTNGMKLNPVGAVYGPEPYA AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTAESTQLP TRTITTSGPRRPTALEPCETFHRFLLGP OQFGKILDVBIIFNBRGSKGFGFVTFETSSDADRAREKLNGTIV BGRKIEVNNATARVMTNKKTGNPYTHGYNGPEPYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTAESTQLP TRTITTSGPRPTALEPCETFHRFLLGP  BGRKIEVNNATARVMTNKKTGNPYTNGMKLNPVVGAVYGFBYAA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTAESTQLP TRTITTSGPRPTALEPCETFHRFLLGP  6811 1522 658 DLVTVWSFDDCRVIASTHGH\KSWUSVVAPDPYTTSVEEGDPME PSGSDBDFQDLLHFGRDRADSTQCTLSRRNSTDSRPVSVTTYRG SVGQDTQLCLWDLTEDILPPHQPLSRARTHTNVMNATSPPAGSN GRSVTTPGRSVPP PLPERSNLPHSAVSNAGSEKSSWDGALASSU SKPATLSLHDRKRRHHEKDHKRNISMGHISSKSSDKIANLVTKK TDPAKTLGTPLCPRMBDVPLLBPLICKKLAHKRLTVLIPLEDCI VTACCEGFICTWGRPGKVVSFNP  6812 4001 1682 BDAVFSLDLSTIIQGTWFLNGBELKSNEPEGQVEPGALRYRIEQ KSLQHRLIHAVKHQDGAALVGFSCFGVQDSAALTIQBSPWHIL SPQDKVSLTPTTSBRVVLTCELSRVDFPATWYKDGQKVESBILL VVKMDGRKHRLILPARKVQDSGEFECRTEGVSAPFGVTVQDPPV HTVDREHVVRHAITSSCVMIACSVIDR\BDAPUNYKDGQEVE BSDFVVLKREGPHRRULDATQPSDGGFFCCVAGDESCAPFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPHAEVRWTKDGE BVVSSBALLLQKBDTVRRLULPAVQLEDSGSFYLCSIDDSASFT VTVTBPPVRITYPRDEVTLIAVTLECVVLMCELSREDAPVRWK DOLBVESSBALVLBRCOPCRULVPAAQFEDGGBFVCDAGDDSA		t ·		· · · · · · · · · · · · · · · · · · ·
65 DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKQQPKRLHVSN1 FFRENDPDLRQMF GQFGKLLDVBL IFNERGSKGFGFVTFETSDADRAREKLNGTIV BGRKLEVNNATARVMTNKKTGNPYTNGKKLNPVVGAVYGPEFYA VTGFPYPTTGTAVAYRGAHLAGRGRAVYMTFRAAPPPPPI PTYG AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TTTITTSGPRRPTALEPCETTHRFLLGP  6810 939 65 DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDRAAQTDSQPLHPSDPTEKQQPKRLHVSN1 PFRRDPDLRQMF GQFGKILDVBI I FNERGSKGFGFVTFETSSDADRAREKLNGTIV EGRKLEVNNATARVMTNKKTGNPYTNGMKLNPVVGAVYGPEFYA VTGFPYPTTGTAVAYRGAHLAGRGRAVYNTFRAAPPPPI PTYG AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLD TRTITPSGPRRPTALEPCETFHRFLLGP  6811 1522 658 DLVTVMSFVDCRVIASTHGH\KSWVSVVAPPPYTTSVEESDPME FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYFFG SVGQDTQLCLMDLTEDILPPRQPLSRARTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLFRSNSLPHSAVSNAGSKSSVMDGATASGV SKPATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKJNLVTKTK TDPAKTTGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP  6812 4001 1682 EDAVFSLDLSTITGGTWFLMGEELKSNEPEGQVEPGALRYREQ KGLQHRLILHAVKHQDGGALVGFSCPGVQDSAALTIQBSPVHIL SCRQKVSLTPTTSBRVVLTCELSRVDFPATWYKDGQKVEESKIL VVKMDGRKHRLILPEAKVQDSGEFECKTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\KDAPVRWYKDGQEVE SDDFVVLENEGPBRRLVLPATQPSDGGFFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWYKDGE BSDFVVLENEGPBRRLVLPATQPSDGGFFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWYKDGE BVMSSPALLLQKBDTVRRLVLPAYQLEDGGBFYCCAGDDSA VTVTBPPVRITYPRDEVTLIAVTLECVVLMCELSREDAPVRWXKDGE BVMSSPALLLQKBDTVRRLVLPAYQLEDGGBFYCDAGDDSA VTVTBPPVRITYPRDEVTLIAVTLECVVLMCELSREDAPVRWXKDGEVE BVMSSPALLLQKBDTVRRLVLPAYQLEDGGBFYCCDAGDDSA DALEWESSRALVURERCPPCCKLVLPAAQPEDGGBFYCDAGDDSA			i .	1
TDEAAQTDSQPLHPSDPTEKQQPKRIHVSNIPFRFRDPDLRQMP GQFGKILDVBI IFMERGSKGPGPVTFTSTSDADRAREKINGTIV EGRKIEVNNATARVMTNKKTGNPYTNGWKLMPVVGAVYGPEPYA VVGPPYPTTGTAVAYRGAHLRGEGRAVYNTPRAAPPPPPIPTYG AVVQDGFYGABI \LBATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP  6810 939 65 DYSGCTPVPTEHGWTLYTPAQTHPEQPSSEASTQPIAGTGTVPQ TDBAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMP GQFGKILDVBI IFMERGSKGFGFVTFTSTSDADRARBKINGTIV EGRKIEVNNATARVMTNKTGNPYTNGWKLMPVVGAVYGPEPYA AVVQDGFYGABI \LBATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP AVVQDGFYGABI \LBATQPTDTLSPLQRRQPTATVTAESTQLP TRTITTSGPRRPTALEPCETFHRFLLGP SGGDDFQDLLHFGRDRADSTQCRLGRRNSTDSRPVSVTYRFG SGGDDFQDLLHFGRDRADSTQCRLGRRNSTDSRPVSVTYRFG SGGDDFQDLLHFGRDRADSTQCRLGRRNSTDSRPVSVTYRFG SGGDPTQLCLWDLTEDLIPPHQPLSRARTHTNVMMATSPPAGSN GRSVTTPGNSVPPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKPATLSLHDRKRRHHBKDHKRNHSMGHISSKSSDKLMLVTTKK TDPAKTLGTPLCPRMBDVPLLEPLICKKIAHBRLTVLIFLEDCI VTACOEGFICTWGRPGKVVSYMP  6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGBELKSNEPEGQVEPGALRYRIEQ KSLQHBLILHAVKHQDGGALVGFSCPGVQDSAALTIQBSPVHIL SPQDKVSLTFTTSBRVVLTCELSRVDFPATWKDGQKVEESBLL VVKMDGRKHRLILPEAKVQDSGEFECKTBGVSAFFGVTVQDPPV HIVDPREHVPVHAITSBCVMLACEV\DR\EDSAPFRGVTVQDPPV HIVDPREHVPVHAITSBCVMLACEV\DR\EDSAPFRGVTVQDPV TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPHAEVRHTKDGE BSDFVVLENBGPHRRLVLPATQPSDGGEFCCVAGDECAYPTTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPHAEVRHTKDGE BSDFVVLENBGPHRRLVLPATQPSDGGEFCCVAGDECAYPTTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPHAEVRHTKDGE BSDFVVLENBGPHRRLVLPATQPSDGGEFCCVAGDECAYPTTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPHAEVRHTKDGE BVVBSFALLLQKBDTVRRLVLPAAQPEDGGBFVCDAGDDSA				l
GQFGKILDVBIIFNERGSKGFGFVTFETSSDADRAREKINGTIV BGRKIEVNNATARVMTNIKKIGHPYTNOWKLINPVUGAVYQPEFYA VTGFPYFTTGTAVARIGHRGKGRAVYNTPRAAPPPPPIPTG AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTAESTQLP TRTITESGPRRPTALEPCETFHRFLLGP  6810 939 65 DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDBAAQTDSQPLHESDPTEKQQPKRLHVSNIPFRPRDEDLRQMF GQFGKILDVBIIFNERGSKGFGFVTFETSSDADRARBKINGTIV BGRKLEVNNATARVMTNKKTGMPYTNGWKLINPVUGAVYGPEFYA AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTAESTQLP TRTITESGPRRPTALEPCETFHRFLLGP  6811 1522 658 DIVTVWSFVDCRVIASTHGH\KSWVSVVAPDPYTTSVEEGDPME FSGSDEDFQDLLHEGRDRADSTQCRLSRRNSTDSRFVSVTYRRG SVGQDTQLCLWDLTEDILPPHQPLSRARTHTNVMNATSPPAGSN GRSVTTPGNSVPPPLPRRSNSLPHSAVSNAGSKSSVMDGALASGV SKPATLSLAHDRKRRHHRBCHKRNHSMGHISSKSSDKJNLVTKK TDPAKTLGTPLCPRMBDVPLLEPLICKKLAHERLTVLIPLEDCI VTACOSGFICTWGRPGKVVSFPP  6812 4001 1682 BDAVFSLDISTIIQGTWPLNGEELKSNEPEGQVEPGALRYRIEQ KSLQHBLILHAVKHQDGSALVOFSCPGVQDSAALTIQRSPWHIL SPQDKVSLTFTTSBRVVLTCELSRVDFPATWKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGGFFCCTMGVSAFFGVTVQDPPV HIVDPREHVPVHAITSBCVMLACEV\DR\EDSAFTGVTVQDPPV HIVDPREHVPVHAITSBCVMLACEV\DR\EDSAFTGVTTQDPV TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPMARVRKDGGEV BSDFVVLKNEGPHRRLVLPAYQPSDGGEFCCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPMARVRKTKDGE BUVESBALLLQKEDTVRRLVLPAAQPEDGGBFVCDAGDDSA	6809	939	65	
EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEPYA VTGFPYPTTGTAVATRGAHLIRGGGRAVYMTFRAAPPPPPI PTYG AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTAESTQLP TTRTITPSGPRRPTALEPCETTHRRILLGP  6810 939 65 DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDRAAQTDSQPLHPSDPTEKQPKRLHVBNIPFRFRDPLRQMF GQPGKILDVBIIFNERGSKGJEFPVTFETSSDADRARBKLNGTIV BGRKLEVNNATARVMTNKKTGNPYTNGMKLNPVVGAVYGPEFYA VTGFPYPTTGTAVAXRGAHLIRGRGRAVYNTFRAAPPPPPI PTYG AVVYQDGFYGABI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETTHRFILLGP  6811 1522 658 DLVTVWSFVDCRVIASTHGH\KSWVSVVAPDPYTTSVEEGDPME FSGSDEDFQDLLHFGRDADSTQCRLSRRNSTDSRFVSVTYRFG SVGQTQLCLWDLTEDILPPHQPLSRARTHTNVMNATSPPAGSN GRSVTTPGNSVPPPLDFRSNSLPHGAVSNAGSKSSVMDGAIASGV SKPATLSLHDRKERHHEKDHKRNHSMGHISSKSSVMDGAIASGV SKPATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMBDVPLLBPLICKKIAHBRLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP  6812 4001 1682 BENAVSLDJSTIJQGTWFLNGBELKSNBPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSBRVVLTCELSRVDFPATWYKDGQKVEESBILL VVKMDGRKHRLILPEAKVDGSGEFECRTESVSAPFGVTVQDPPV HLVDPREHVFVHAITSBCVMLACEV\DR\EDSPRVTVQDPPV HLVDPREHVFVHAITSBCVMLACEV\DR\EDSPRVTVQDGSVE BSDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSNIVYPSGKVVVAAVRLERVULTCELCRPWAEVRWTKDGE BSDFVVLENEGPHRRLVLPAVQLEDSGEYLCEIDDBSASFT TDVSSNIVYPSGKVVVAAVRLERVULTCELCRPWAEVRWTKDGE BVVSSPALLLQKEDTVRRILVLPAVQLEDSGEYLCEIDDBSASFT TOVSSNIVYPSGKVVVAAVRLERVULTCELCRPWAEVRWTKDGE BVVSSPALLLQKEDTVRRILVLPAVQLEDSGEYLCEIDDBSASFT UTVTSBPVVILENGEVTLIAVTLECVVILMCELSREDAPVRWYK DGLEVEESBALVUKRDGPRCRLVLPAAQPEDGGEFVCDAGDDSA		İ '	1	
VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPP1PTYG AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP  6810 939 65 DYSGGTPVPTBERGMTLYTPAQTHPRQPGSEASTQPLAGTGTVPQ TDRAAQTDSQPLHPSDPTBKQQPKRLHVSNIPFRFDDDLRQMF GQPGKILDVBIIFNRGSKGFGFVTFETSSDADRARBKLNGTIV BGRKLEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFTVA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPP1PTYG AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTABSTQLP TRTITPSGPRRPTALBPCETFHRFLLGP  6811 1522 658 DLVTVWSFVDCRVLASTHGH\KSWVSVVAPDPYTTSVEBGDPME SYGQDTQLCLWDLTBDLLPPHQPLSRARTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGALASGV SKFATLSLHDRKERHHBKDHKRNISMGHLSSKSSDKLMLVTKTK TDPAKTLGTPLCPRMBDVPLLEPLICKKLAHBRLTVLIFLEDCI VTACQEGFICTWGRPCKVVSFNP  6812 4001 1682 EDAVFSLDISTIIQGTWFLNGBELKSNEPEGQVEPGALRYRIEQ KSLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQBSPVHIL SPQDKVSLTFTTSBRVVLTCELSRVDFPATWYKNGGKVEESEIL VVKMDGRKHRLLLPEAKVQDSGFFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHALTSBCVMLACEV\DR\KDAPVRNYKNGGSVE BSDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSNIVYPSGKVVVAAVRLERVVLTCELCRPWARVRWTKDGE BSDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSNIVYPSGKVVVAAVRLERVVLTCELCRPWARVRWTKDGE BVVSSPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDBSASFT TOVSSNIVYPSGKVVVAAVRLERVVLTCELCRPWARVRWTKDGE UTVTTBPPVRIITYPRDEVTLIAVTLECVVILMCELSREDAPVRWYK DGLEVBESBALVLKRDGPRCRLVLPAAQPEDGGEFVCDAGDDSA		l		1 17
AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALBPCETFHRFLLGP  6810  939  65  DYSGQTPVPTEHGMITLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDBAAQTDSQPLHPSDPTBKQQPKRLHVSNIPFRFRDPDLRQMF GQFGKILDVBIIPNBRGSKGFGPVTFETSSDADRARBKLNGTIV BGRKIEVNNATARVMINKKTGNPYTNGKKLNPVVGAVYGPBFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGABI\LBATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALBPCETFHRFLLGP  6811  1522  658  DLVTVMSFVDCRVIASTHGH\KSWVSVVAPDPYTTSVEBGDPMB FSGSDEDFQDLLHFGRDASTQCRLSRRNSTDSRFVSVTYRFG SVGQDTQLCLMDLTEDILPPHQPLSRARTHTNVMNATSPPAGSN GRSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKPATLSLHDRKERHHBKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMBDVPLEPLICKKLAHERLTVLIPLEDCI VTACQEGFICTWGRPCKVVSFMP  6812  4001  1682  EDAVFSLDLSTIIQGTWFLNGBELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQBSPVHIL SPQDKVSLTFTTSBRVVLTCELSRVDFPATWYKDGQKVESSBIL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVPHAITTSBCVULTACEV\DR\EDAPVRWYKDGQSVE BSDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERUVLTCELCRPWARVRWTKDGE BVWSSPALLLQKEDTVRLPAVQLBEDSGEFLCERDESSFT VTVTBPPVRIIYPRDEVTLIAVTLECVVIMCELSRBDAPVRWYK DGLEVBESEALVERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA				
TRTITPSGPRRPTALEPCETFHRPLLGP  6810  939  65  DYSGGTPVPTEHGMTLYTPAQTHPRQGGSEASTQPIAGTQTVPQ TDRAAQTDSQPLHPSDPTEKQQPKRLHVSNIP PRFFRDPDLRQMF GQPGKILDVBIIPNBRGSKGFGPVTFETSSDADRARKLNGTIV BERKLEVNNATARVMTNKKTGNPYTNGMKLNPVVGAVYGPBFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AAVYQDGFYGABI\LBATQPTDTLSPLQRQPTATVTABSTQLP TRTITPSGPRRPTALBPCETFHRPLLGP  6811  1522  658  DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEBGDPMB PSGSDBDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG SVGQDTQLCLWDLTEDILPPHQPLSRARTHTNVMNATSPPAGSN GNSVTTFGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGALASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSDKLNLVTKTK TDPAKTLGTPLCPRMBDVPLLBPLICKKLAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP  6812  4001  1682  EDAVFSLDLSTIIQGTWFLNGBELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSBRVVITCELSRVDFPATWYKDGQKVEBSELL VVKMDGRKHRLTLPEAKVQDSGEFECRTBGVSAFFGVTVODPPV HIVDPREHVFVHAITSBCVMLACEV\DR\EDAPVRWYKDGQEVE BSDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWLVYPSGKYVVAAVRLERVVLTCELCRPWAEVRWYKDGE BSDFVVLENEGPHRRLVLPAVQLEDSGEFLCEIDDESASFT TVTSBPLLQKEDTVRRLVLPAVQLEDSGEFLCEIDDESASFT VTYTBPPVRIIYPRDEVYLLAVTLECVVLMCELSREDAPVRWYK DGLEVBESBALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA		]	į	
6810  939  65  DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDRAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF GQFGKILDVBIIFNBRGSKGFGFVTFETSSDADRARBKLNGFIV BGRKIEVNNATARVMINKKTGNPYTNGMKLNPVVGAVYGPBFYA V7GFPYPTTGTAVAYRGAHLRGRGRAVYNTRAAPPPPPIPTYG AVVYQDGFYGAEI\LKATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP  6811  1522  658  DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME PSGSDEDFQDLLHFGRDADSTQCRLSRRNSTDSRPVSVTYRFG SVQQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN GNSVTTFGNSVPPPLPRSNSLPHSAVSNAGSKSSWMDGALASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP  6812  4001  1682  BDAVFSLDSTIIQGTWFLNGEELKSNEPESQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQRSPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGGKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAPFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWILVPSGKVYVAAVRLERVULTCELCRPAEVWRTKDGE BVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDRSASFT VTYTBPPVRIITYPRDEVYLLAVTLECVVLMCELSREDAPVRWYK DGLEVBESBALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA		1		, · · · · · · · · · · · · · · · · · · ·
TDRAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDIRQMF GQFGKILDVBIIPNERGSKGFGPVTFETSSDADRARBKLNGTIV EGRKIEVANATARVMTNKKTGNPYTNGKKLNPVUGAVYGGPEFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGABI\LBATAPPTDTLSPLQRRQPTATVTABSTQLP TRTITPSGPRRPTALBPCRTFHRFLLGP  658 DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTTRFG SVGQDTQLCLWDLTEDLLPPHQPLSRARTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKRRHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMBDVPLLBPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP  6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGBELKSNEPEGQVEFGALRYRIEQ KSLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQBSPVHIL SPQDKVSLIFTTSRRVLTCELSRVDFPATWYKDGQKVESBELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAPFGVTVQDPPV HIVDPREHVFVHAITSECVMIACEV\DR\EDAPVRWYKDGQBVE ESDFVVLENEGPHRRLVLPATQPSDGGGFQCVAGDECAYFTVTI TDVSSWIVYPSGKVVVAAVRLERVVLTCELCRPWARVRTKDGE BVVESPALLLQKEDTVRRLVLPAVQLEDSGEFLCELTRPWARVRTKDGE FVTSTBPVRIIYPRGBVTLTAVTLECVVIMCELSREDAPVRWYK DGLEVBESEALVLBRDGPRCRLVLPAAQPEDGGBFVCDAGDDSA	6010	020	ļ	
GQFGKILDVBIIFNERGSKGFGFVTFETSSDADRARBKLNGTIV  BGRKIEVNNATARVMTNKKTGNPYTNGMKLNPVVGAVYGPBFYA  VTGFPYPTTGTAVAYRGHLKGRGRAVYNTFRAAPPPPPIPTYG  AVVYQDGFYGABI\LBATQPTDTLSPLQRQPTATVTABSTQLP  TRTITPSCPRRPTALBPCBTFHRFLLGP  658  DLVTVWSFVDCRVIASTHGH\KSWVSVVAPDPYTTSVEEGDPMB  FSGSDBDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTTRFG SVGQDTQLCLWDLTEDLIFPHQPLSRARTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGALASGV SKFATLSLHDRKRRHHBKDHKRNHSMGHISSKSSDKINLVTKTK TDPAKTLGTPLCPRMBDVPLLBPLICKKIAHBRLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP  6812  4001  1682  EDAVFSLDLSTIIQGTWFLNGBELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQBSPVHIL SPQDKVSLTPTTSBRVVLTCELSRVDFPATWYKDGQKVEBSBLL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAPFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQBVE ESDFVVLENEGPHRRLVLPATQPSDGGGFQCVACDECAYFTVTI TDVSSWIVYPSGKVVVAAVRLERVVLTCELCRPWABVRWTKDGE BVVESPALLLQKBDTVRRLVLPAVQLEDSGEFLCRIDBSSSFT VTVTTBPPVRIIYPRDEVTLIAVTLECVVIMCELSREDAPVRWYK DGLEVBESEALVLBRDGPRCRLVLPAAQPEDGGFFVCDAGDDSA	9870	) 939	65	1
BGRKLEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPI PTYG AVVYQDGFYGAEI (LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP TRTITPSGPRRPTALEPCETFHRFLLGP  6811 1522 658 DLVTVVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG SVGQDTQLCLWDLTEDILPPHQPLSRARTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKPATLSLHDRKRRHHEKDHKRNHSMGHISSKSSDKIALVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP  6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGSELKSNEPEGQVEFGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSBRVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHATTSBCVMIACEV\DR\EDAPVRWYKDGQBVE BSDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVVVAAVRLERVVLTCELCRPWAEVRWTKDGE BVVESPALLIQKEDTVRRLVLPATQLEDGGEFYCCTGDBSASFT VTVTBPPVRIIYPRDEVTLLAVTLECVVIMCELSREDAPVRWYK DGLEVBESEALVLBRDGPRCRLVLPAQPEDGGEFVCDAGDDSA		ľ		
VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPP1PTTG AVVYQDGFYGARI\LEATQPTDTLSPLQRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP  6811 1522 658 DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG SVGQDTQLCLWDLTEDILPPHQPLSRARTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKPATLSLHDRKRRHHEKDHKRNHSMGHISSKSSDKINLVTKTK TDPAKTLGTPLCPRMRDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP  6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGEBLKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDGGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHATTSBCVMIACEV\DR\EDAPVRWYKDGQBVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE BVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT VTVTTBPPVRIIYPRDEVTLLAVTLECVVIMCELSREDAPVRWYK DGLEVBESEALVLBRDGPRCRLVLPAAQPEDGGBFVCDAGDDSA		Į.	1	1 15
AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP  6811 1522 658 DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME PSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG SVGQDTQLCLWDLTEDILPPHQPLSRAETHTNVMNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP  6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGBELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAPFGVTVQDPPV HIVDPREHVPVHAITSBCVMLACEV\DR\EDAPVRWYKDGQBVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVULTCELCRPWAEVRWTKDGE BVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT VTVTTBPPVRIIYPRDEVTLIAVTLECVVIMCELSREDAPVRWYK DGLEVBESEALVLBRDGPRCRLVLPAAQPEDGGBFVCDAGDDSA		1		
TRTITPSGPRRPTALBPCETFHRFLLGP  6811  1522  658  DLVTVWSFVDCRVIASTHGH\KSWVSVVAPDPYTTSVEEGDPME FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRFVSVTYRFG SVGQDTQLCLWDLTEDILPPHQPLSRRRTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMBDVPLLBPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP  6812  4001  1682  BDAVFSLDISTIIQGTWFLNGBELKSNEPEGQVEFGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLIFTTSBRVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAPFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQBVE ESDFVVLENEGPHERLVLPAATQPSDGGGFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE BVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT VTVTTBPPVRIIYPRDEVTLIAVTLECVVIMCELSREDAPVRWYK DGLEVBESEALVLERDGPRCRLVLPAAQPEDGGBFVCDAGDDSA		[		
6811 1522 658 DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME FSGSDEDFQDLLHFGRDADSTQCRLSRRNSTDSRPVSVTYRFG SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPRAGSN GNSVTTPGNSVP PPLPRSNSLPHSAVSNAGSKSSVMDGALASGV SKFATLSLHDRKRRHHEKDHKRNHSMGHISSKSSDKIALUTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP  6812 4001 1682 EDAVFSLDLSTI IQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVVQDSAALTIQESPVHIL SPQDKVSLTPTTSBRVVLTCELSRVDFPATWYKDGQKVEESBLL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGFFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRTKDGE  BVVESPALLLQKEDTVRRLVLPAVQLEDSGEFLCEIDDESASFT VTVTTBPPVRI IYPRDEVTLIAVTLECVVIMCELSREDAPVRWYK DGLEVBESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA		1		1 · · · · · · · · · · · · · · · · · · ·
FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG SVGQDTQLCLWDLTEDILPPHQPLSRARTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHRKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMBDVPLLBPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP  6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSBRVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFBCRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSBCVMIACEV\DR\EDAPVRWYKDGQBVE BSDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDCAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPHAEVRWTKDGE BVVESPALLLQKEDTVRRLVLPAVQLEDSGEFYLCEIDDBSASFT VTVTBPPVRIIYPRDEVTLLAVTLECVVLMCELSREDAPVRWYK DGLEVBESEALVLBRDGPRCRLVLPAQPEDGGEFVCDAGDDSA	6011	1533	650	I
SVGQDTQLCLWDLTEDILPPHQPLSRARTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKPATLSLHDRKRRHHEKDHKRNHSMGHISSKSDKINLVTKTK TDPAKTLGTPLCPRMBOVPLLBPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP  6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRVRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEPSELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAPFGVTVQDPPV HIVDPREHVFVHATTSBCVMLACEV\DR\EDAPVRWYKDGQBVE ESDFVVLENEGGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPMAEVRWTKDGE BVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDBSASFT VTVTBPPVRIIYPRDEVTLTAVTLECVVLMCELSREDAPVRWYK DGLEVBESEALVLBRDGPRCRLVLPAQQEDGGEFVCDAGDDSA	9011	1 +344	050	
GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKPATLSLHDRKRRHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMBOVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFPD  6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGBELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDGGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSBCVMLACEV\DR\EDAPVRWYKDGQBVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE BVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT VTVTBPPVRIIYPRDEVTLIAVTLECVVIMCELSREDAPVRWYK DGLEVBESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA			ì	_ =
SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMBDVPLLBPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP  6812 4001 1682 EDAVFSLDISTIIQGTWFLNGBELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGPSCPGVQDSAALTIQESPVHIL SPQDKVSLIFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAPFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\KDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE EVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASPT VTVTBPPVRIIYPRDEVTLTAVTLECVVIMCELSREDAPVRWYK DGLEVBESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA		1	ļ	
TDPAKTLGTPLCPRMRDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP  6812 4001 1682 EDAVFSLDISTIIQGTWFLNGBELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLIFFTTSBRVVLTCELSRVDFPATWYKDGQKVEBSELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHATSBCVMLACEV\DR\EDAPVRWYKDGQBVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE BVVESPALLLQKEDTVRRLVLPAVQLEDSGBYLCBIDDSSASFT VTVTBPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK DGLEVBESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA		I	<b>}</b>	
VTACQEGFICTWGRPGKVVSFNP  6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGBELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLIFFTSBRVVLTCELSRVDFPATWYKDGQKVEESBLL VVKMDGRKHRLILPEAKVQDSGEFECRTBGVSAFFGVTVQDPPV HIVDPREHVFVHAITSBCVMLACEV\DR\KDAPVRWYKDGQBVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE BVVESPALLLQKEDTVRRLVLPAVQLKDSGBYLCBIDDSSASFT VTVTBPPVRIIYPRDEVTLIAVTLBCVVLMCELSREDAPVRWYK DGLEVBESEALVLKRDGPRCRLVLPAAQPEDGGBFVCDAGDDSA		1	1	
6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGRELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQBSPVHIL SPQDKVSLTFTTSBRVVLTCELSRVDFPATWYKDGQKVEESBLL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSBCVMIACEV\DR\EDAPVRWYKDGQBVE BSDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWABVRWTKDGE BVVESPALLLQKBDTVRRLVLPAVQLEDSGBYLCEIDDBSASFT VTVTBPPVRIIYPRDEVTLLAVTLECVVLMCELSREDAPVRWYK DGLEVBESEALVLBRDGPRCRLVLPAAQPEDGGBFVCDAGDDSA		1		t i
KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSBRVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFBCRTEGVSAFFGVTVQDPPV HIVDPREHVFVHALTSBCVMIACEV\DR\EDAPVRWYKDGQBVE BSDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE BVVESPALLLQKEDTVRRLVLPAVQLEDSGEFYLCEIDDBSASFT VTVTBPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK DGLEVBESEALVLERDGPRCRLVLPAAQPEDGGBFVCDAGDDSA	60.0		1600	
SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAPFGVTVQDPPV HIVDPREHVFVHATTSECVMIACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE EVVESPALLIQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT VTVTBPPVRITYPRDEVTLTAVTLECVVIMCELSREDAFVRWYK DGLEVBESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA	6812	4001	1083	•
VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAPFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQBVE ESDFVVLENEGPHERLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE BVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT VTVTBPPVRIIYPRDEVTLIAVTLECVVIMCELSREDAPVRWYK DGLEVBESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA		1		1 = = = = = = = = = = = = = = = = = = =
HIVDPREHVFVHAITSECVMIACEV\DR\EDAPVRWYKDGQBVE BSDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE BVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT VTVTBPPVRIIYPRDEVTLIAVTLECVVIMCELSREDAPVRWYK DGLEVBESEALVLERDGPRCRLVLPAAQPEDGGBFVCDAGDDSA		1		
ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE BVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT VTVTBPPVRIIYPRDEVTLIAVTLECVVIMCELSREDAPVRWYK DGLEVBESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA		1		
TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE  BVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT  VTVTBPPVRIIYPRDEVTLIAVTLECVVIMCELSREDAPVRWYK  DGLEVBESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA		1	ļ	
, BVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT VTVTBPPVRIIYPRDEVTLIAVTLECVVIMCELSREDAPVRWYK DGLEVBESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA		]		\frac{1}{2}
VTVTBPPVRIIYPRDEVTLIAVTLECVVIMCELSREDAPVRWYK DGLEVBESEALVLERDGPRCRLVLPAAQPEDGGBFVCDAGDDSA				
DGLEVBESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA				
1				
PFTVTVTEPPVQFLALETTPSPLCVAPGEPVVLSCELSRAGAPV		<b>{</b>		
		L		FFTVTVTEPPVQFLALETTPSPLCVAPGEPVVLSCELSRAGAPV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1 .	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
L	sequence		\=possible nucleotide insertion)
1		ļ	VWSHNGRPVQEGEGLELHAEGPRRVLCIQAAGPAHAGLYTCQSG
		ŀ	AAPGAPSLSFTVQVAEPPVRVVAPEAAQTRVRSTPGGDLELVVH
i	ľ	l	LSGPGGPVRWYKDGERLASQGRVQLEQAGARQVLRVQGARSGDA
1	ļ		GEYLCDAPQDSRIFLVSVEEPLLVKLVSDLTPLTVHEGDDATFR
1		[	CEVSPPDADVTWLRNGAVVTPGPQRQSCCSYGGCRMCGQRKART
		i	CVSKWRQAEWVQRGPCAGCEVGSPCPTTLACPWPRMGTSTASSS MVSYWPTRAPTAARATTIAPWPGSA
6813	9	836	
""	1	0.50	SSTQQRPGVPAGPRPLDGYLGVADHKPLKMHCRDCALVTSSCHL LHSRQGSQ1DQTECV1RMNDAPTRGYGRDVGNRTSLRV1AHSS1
1	]		QRILRNRHDLLNVSQGTVFIFWGPSSYMRRDGKGQVYNNLHLLS
i i		}	QVLPRLKAFMITRHKMLQFDELFKQETGQ\NRKISNTWLSTGWF
ł		·	TMTIALELCDRINVYGMGPPDFCRDPNHPSVPYHYYEPFGPDEC
1			TMYLSHERGRKGSHHRFITEKRVFKNWARTFNIHFFQPDWKPES
İ	l		LAINHPENKPVF
6814	3	737	KFRRQEAN/ARKRNRMHGLNDALDNLRKVVPCYSKTQKLSKIET
1			LRLAKNYIWALSEILRIGKRPDLLTFVQNLCKGLSQPTTNLVAG
İ			CLQLNARSFLMGQGGKAAHHTRSPYSTFYPPYHSPKLTTPPGHG
1			TLDNSKSMKPYNYCSAYESFYRSTSPECASPQFEGPLSPPPINY
ľ			NGIFSLKQEETLDYGKNYNYGMHYCAVPPRGPLGQGAMFRLPTD
6815	906	553	SHFPYDLHLRSQSLTMQDBLNAVPHN
0013	306	333	QGLDPASQTKVVELLKDGSGRRGDRRSSRDMAGGAGPRSESDLE DVGPTAEWNGDGSGSLRRSGSPGKLRDALRRSSEMLVKKLQGGT
	ļ		PQEPPNPRMKRASSLNFLNKSVEEPTOPGG
6816	1	803	NLLKTHKF\LLGQDEDSLHSVPVAQMGNYQBYLKTLASPLREID
1			PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN
ì	1		
			SPMSSKRRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN
			SPMS5KRRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFL9KSAPSELINM
			LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS
			LIKPTLVHTDATIIHDGHEEKMENGQITPDGFL9KSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF
6018			LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LCMMDSPKIGNGLPVIGPGTDIGISSLHNVGYLGKNFDSAKVPS
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LCMMDSPKIGNGLPVIGPGTDIGISSLEMVGYLGKNFDSAKVPS DBYCPACKERGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LCMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DBYCPACKEKGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTIGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LCMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DBYCPACKERGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLILANSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLPDSSGQQNPIRTADSLERNEI
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTIGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DBYCPACKERGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTIGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DBYCPACKEKGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NKLISPDLEBCHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSKLPDSSGQQNPIRTADSLERNBI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEKLKNTVTGLCSKB
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTIGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLEMVGYLGKNFDSAKVPS DBYCPACKERGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEBCHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCKLDCILSALVHSERLKNTVTGLCSKR ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSBIFABIET
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LCMMDSPKIGNGLPVIGPGTDIGISSLHWGYLGKNFDSAKVPS DBYCPACKERGKLKALKTYRISFQBSIFLCEDLQCTYPLGSKSL NNLISPDLEBCHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHINGEVYDBTSSNLPDSSGQQNPIRTADSLERNBI LEADTVDMATTKDPATVDVSGTGFPSPQNBGCTSKLEMPLBSKC TSFPQALCVQWKNAYALCWLDCILSALVHSERLKNTVTGLCSKR ESIFMRLLTKYNQANTILYTSGLSGVKDGDCKKLTSBIFABIET CLNEVRDEIFISLQPOLRCTLGDMESPVPAFPLLLKLETHIEKL
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTIGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLEMVGYLGKNFDSAKVPS DBYCPACKERGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEBCHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNBGCTSKLEMPLESKC TSFPQALCVQWKNAYALCKLDCILSALVHSERLKNTVTGLCSKR ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSBIFABIET
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFL9KSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKTGNGLPVIGPGTDIGISSLEMVGYLGKNFDSAKVPS DBYCPACKERGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEBCHTPHKPQKRKSLESSYKDSLLLANNSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLPDSSCQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNBGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSERLKNTVTGLCSKR ESIFWRLLTKYNQAWTLLYTSQLSGVKDGDCKKLTSBIFABIET CLNEVRDEIFISLQPOLRCTLGDMGSPVPAFPLLLKLETHIEKL PLYSFSWDFECSQCGHQYQNRHWKSLVTPTNVIPEWHPLNAAHP GPCNNCMSKSQIRKWVLEKVSPIFMLHFVBGLPQNDLQHYAFHP EGCLYQITSVIQYRANNHFITWILDADGSWLBCDDLKGPCSERH
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTIGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKTGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DBYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEBCHTPHKPQKRKSLESSYKDGLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLPDDSSGQDNPIRTADSLERNEI LERDTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKR ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFABIET CLNEVRDEIFISLQPQLCTLGDMESPVFAFPLLLKLETHIEKL PLYSFSWDFECSQCGHQYQNRHMKSLVTPTNVIPEWHPLNAAHP GPCNNCMSKSQIRKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQTTSVIQYRANNHFITWILDADGSWLBCDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKUGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LCMMDSPKIGNGLPVIGPGTDIGISSLHWGYLGKNFDSAKVPS DBYCPACKERGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGKVLNSKHINGEVYDBTSSNLPDSSGQQNPIRTADSLERNBI LEADTVDMATTKDPATVDVSGTGFPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSERLKNTVTGLCSKR ESIFMRLITKYNQANTILYTSGLSGVKDGDCKKLTSBIFABIET CLNEVRDEIFISLQPOLRCTLGDMESPVPAFPLLLKLETHIEKL PLYSFSWDFECSQCGHQYQNRHMKSLVTPTNVIPEWHPLNAAHP GPCNNCNSKSQIRKNVLEKVSPIFMLHFVBGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKPEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNB KPVSLTSCSVGDAASABTASVTHPKDISVAPRTLSQDTAVTHGD
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKUGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LCMMDSPKIGNGLPVIGPGTDIGISSLHWGYLGKNFDSAKVPS DBYCPACKERGKLKALKTYRISFQBSIFLCEDLQCTYPLGSKSL NNLISPDLEBCHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHINGEVYDBTSSNLPDSSGQQNPIRTADSLERNBI LEADTVDMATTKDPATVDVSGTGFPSPQNBGCTSKLEMPLBSKC TSFPQALCVQWKNAYALCWLDCILSALVHSERLKNTVTGLCSKR ESIFMRLLTKYNQANTILYTSGLSGVKDGDCKKLTSBIFABIET CLNEVRDEIFISLQPOLRCTLGDMESPVPAFPLLLKLETHIEKL PLYSFSWDFECSQCGHQYQNRHMKSLVTPTNVIPEWHPLNAAHP GPCNNCNSKSQIRKNVLBKVSPIFMLHFVBGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWLDADGSWLBCDDLKGPCSERH KKPBVPASBIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNB KPVSLTSCSVGDAASABTASVTHPKDISVAPRTLSQDTAVTHED HLLSGPKGLVDNILPLTLEBTIQKTASVSQLNSEAPL\LENKPV
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LCMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DBYCPACKEKGKLKALKTYRISFQBSIFLCEDLQCTYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQMEGCTSKLEMPLBSKC TSFPQALCVQKNAYALCWLDCLILSALVHSELKNTVTGLCSKR ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSBIFABIET CLNEVRDEIFISLQPQLRCTLGDMSSPVFAFPLLIKLETHIEKL PLYSFSWDFECSQCGHQYQNRHMKSLVTPTNVIPEWHPLNAAHP GPCNNCNSKSQIRKMVLEKVSPIFMLHFVBGLPQNDLQHYAFHF EGCLYQTTSVIQYRANNHFITWILDADGSWLBCDDLKGPCSBRH KKFBVPASEIHIVIWERKISQVTDKBAACLPLKKTNDQHALSNB KPVSLTSCSVGDAASABTASVTHPKDISVAPRTLSQDTAVTHGD HILSGPRGLVDNILPLITLBETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQBSLMASSVSAPCNEKLIQDQFVDISFPSQ
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKUGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LCMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DBYCPACKEKGKLKALKTYRISFQBSIFLCEDLQCTYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQMEGCTSKLEMPLBSKC TSFPQALCVQKNAYALCWLDCLILSALVHSELKNTVTGLCSKR ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSBIFABIET CLNEVRDEIFISLQPQLRCTLGDMSSPVFAFPLLIKLETHIEKL PLYSFSWDFECSQCGHQYQNRHMKSLVTPTNVIPEWHPLNAAHP GPCNNCNSKSQIRKMVLEKVSPIFMLHFVBGLPQNDLQHYAFHP BGCLYQTTSVIQYRANNHFITWILDADGSWLBCDDLKGPCSBRH KKFBVPASEIHIVIWERKISQVTDKBAACLPLKKTNDQHALSNB KPVSLTSCSVGDAASABTASVTHPKDISVAPRTLSQDTAVTHGD HILSGPRGLVDNILPLTLEBTIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQBSLMASSVSAPCNEKLIQDQFVCDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIBKDAQ
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFL9KSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTIGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHWGYLGKNFDSAKVPS DBYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEBCHTPHKPQKRKSLESSYKDGLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLDPDSSGQONPIRTADSLERNEI LERDTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKR ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFABIET CLNEVRDEIFISLQPQLRCTLGDMESPVFAFPLLLKLETHIEKL PLYSFSWDFECSQCGHQYQNRHMKSLVTPTNVIPEWHPLNAAHP GFCNNCMSKSQIRKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQTTSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFBVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASABTASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LKNKPV ARNTGILKTNTLLSQBSLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGYKSVEIBKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTIGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK  LGMMDSPKIGNGLPVIGPGTDIGISSLEMVGYLGKNFDSAKVPS DBYCPACKERGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEBCHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNBGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSERLKNTVTGLCSKR ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSBIFABLET CLNEVRDEIFISLQPOLRCTLGDMESPVFAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEMHPLNAAHP GPCNNCNSKSQIRKMVLEKVSPIFMLHFVBGLPQNDLQHYAFHF EGGLYQTTSVIQYRANNHFITWILDADGSWLBCDDLKGPCSERH KKFBVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASABTASVTHPKDISVAPRTLSQDTAVTHGD HILISGPKGLVDNILPLILEBTIQKTASVSQLNSEAFL\LEMKPV AENTGILKTNTLLSQBSLMASSVSAPCNEKLIQDGFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIBKDAQ LKQFLTPKTBQLRPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAINRNTITIDLQPS
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTIGAMPNTLQITPAMAQGIMADIKHQLMKEVRKF GRSK  LGMMDSPKIGNGLPVIGPGTDIGISSLEMVGYLGKNFDSAKVPS DBYCPACKERGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGBVYDBTSSNLPDSSGQQNPIRTADSLBRNBI LEADTVDMATTKDPATVDVSGTGRPSPQNBGCTSKLEMPLESKC TSFPQALCVQWKNAVALCWLDCILSALVHSERLKNTVTGLCSKR ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSBIFABIET CLNEVRDBIFISLQPOLRCTLGDMESPVFAFPLLLKLETHIEKL FLYSFSNDFECSQCCHQYQNRHMKSLVTFTNVIPEWHPLNAAHP GPCNNCNSKQIRKNVLBKVSPIFMLHFVBGLPQNDLQHYAFHP EGGLYQITSVIQYRANNHFITWILDADGSWLBCDDLKGPCSERH KKFBVPASBIHIVIWERKISQVTDKBAACLPLKKTNDQHALSNB KPVSLTSCSVGDAASABTASVTHPKDISVAPRTLSQDTAVTHGD HILSGPRGLVONILPLILEBTIQKTASVSQLNSBAFL\LENKFV ABNTGILKTNTLLSQBSLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTBDTVNTKSVNNTDATGLIQGVKSVBIBKDAQ LKGFLTPKTBQLKPBRVTSQVSNLKKKBTTADSQTTTSKSIQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKUGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LCMMDSPKIGNGLPVIGPGTDIGISSLHWGYLGKNFDSAKVPS DBYCPACKERGKLKALKTYRISFQESIFLCEDLQCTYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA LUGKVLNSKHNGEVYDBTSSNLPDSSGQQNPIRTADSLERNBI LEADTVDMATTKDPATVDVSGTGFPSPQNBGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSERLKNTVTGLCSKR ESIFMRLLTKYNQANTILYTSGLSGVKDGDCKKLTSBIFABIET CLNEVRDEIFISLQPOLRCTLGDMESPVPAFPLLLKLETHIEKL PLYSFSWDFECSQCGHQYQNRHMKSLVTPTNVIPEWHPLNAAHP GPCNNCNSKSQIRKNVLEKVSPIFMLHFVBGLPQNDLQHYAFHF EGGLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKPBVPASBIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNB KPVSLTSCSVGDAASABTASVTHPKDISVAPRTLSQDTAVTHED HLLSGPKGLVDNILPLTLEBTIQKTASVSQLNSEAPL\LENKPV AENTGILKTNTLLSQBSLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGYKSVBIBKDAQ LKQFLTPKTBQLKPERVTSQVSNLKKKETTAGQTTTYSKLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKUGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LCMMDSPKIGNGLPVIGPGTDIGISSLHWGYLGKNFDSAKVPS DBYCPACKERGKLKALKTYRISFQBSIFLCEDLQCTYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHINGBVYDBTSSNLPDSSGQQNPIRTADSLERNBI LEADTVDMATTKDPATVDVSGTGRPSPQNBGCTSKLEMPLBSKC TSFPQALCVQWKNAYALCWLDCILSALVHSERLKNTVTGLCSKR ESIFMRLLTKYNQANTILYTSQLSGVKDGDCKKLTSBIFABIET CLNEVRDEIFISLQPOLRCTLGDMESPVPAFPLLLKLETHIEKL PLYSFSWDFECSQCGHQYQNRHMKSLVTPTNVIPEWHPLNAAHP GPCNNCNSKSQIRKNVLBKVSPIFMLHFVBGLPQNDLQHYAFHP EGCLYQITSVIQYRANNHFITWLDADGSWECDDLKGPCSERH KKPEVPASBIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASABTASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEBTIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQBSLMASSVSAPCNEKLIQDGFVDISFPSQ VVNTNMGSVQLNTEDTVNTKSVNNTDATGLIQGVKSVBIBKDAQ LKQPLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKFFVGSWVKGLISRGSFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGQIHKLRLKLKKKKKKABEKKKLAALMSSPQSKTVRSENLE
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFL9KSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK  LGMMDSPKIGNGLPVIGPGTDIGISSLEMVGYLGKNFDSAKVPS DBYCPACKEKGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEBCHTPHKPQKRKSLESSYKUSLLLANNSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLPDSSGQQNPIRTADSLERNBI LERADTVDMATTKDPATVDVSGTGRPSPQNBGCTSKLEMPLBSKC TSFPQALCVQWKNAYALCWLDCILSALVHSERLKNTVTGLCSKR ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSBIFABIET CLNEVRDEIFISLQPQLRCTLGDMESPVPAFPLLLKLETHIEKL PLYSFSWDFECSQCGHQYQNRHMKSLVTPTNVIPEWHPLNAAHP GFCNNCMSKSQIRKMVLBKVSPIFMLHFVBGLPQNDLQHYAFHP BGCLYQITSVIQYRANNHFITWILDADGSWLBCDDLKGPCSERH KKPBVPASBIHIVIWERKISQVTDKBAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASABTASVTHPKDISVAPRTLSQDTAVTHED HLLSGPKGLVDNILPLTLEBTIQKTASVSQLNSRAFL\LENKPV VANTMQSVQLNTEDTVNTKSVNNTDATGLIQGYKSVEIBRDAQ LKQFLTPKTBQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENOKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGGIHKLRKNKRKKKARKKKAKKNSKYPPISKPSENLE
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFL9KSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTIGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK  LGMMDSPKIGNGLPVIGPGTDIGISSLEMVGYLGKNFDSAKVPS DBYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEBCHTPHKPQKRKSLESSYKDGLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLDPDSSGQONPIRTADSLBRNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTTVTGLCSKR ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFABIET CLNEVRDEIFISLQPQLRCTLGDMSSPVPAFPLLLKLETHIEKL PLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHP ESCLYQTTSVIQYRANNHFITWILDADGSWLBCDDLKGPCSBRH KKFBVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASABTASVTHPKDISVAPRTLSQDTAVTHGD HILISGPKGLVDNILPLITLEETIQKTASVSQLNSEAFL\LKRNEV VNNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGYKSVEIBKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHESSYGNISSANH EDLVEGQIHKLRLKLKKKKKARKKKAALMSSPQSRTVRSENLE QVPQDCSSPNDCRS IEDLLMELPPPIDIANESACTTVPGVSLYSS QTHERILAELLSPTPVSTRLSENGEGDFRYLGMGDSHIPPPVPS
6817	172	3457	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKNGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTIGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK  LGMMDSPKIGNGLPVIGPGTDIGISSLEMVGYLGKNFDSAKVPS DBYCPACKERGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEBCHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNBGCTSKLEMPLESKC TSFPQALCVQWKNAVALCHLDCILSALVHSERLKNTVTGLCSKR ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSBIFABLET CLNEVRDEIFISLQPOLRCTLGDMESPVFAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEMHPLNAAHP GPCNNCNSKSQIRKMVLEKVSPIFMLHFVBGLPQNDLQHYAFHF KKFBVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASABTASVTHPKDISVAPRTLSQDTAVTHGD HILISGPKGLVDNILPLITLEBTIQKTASVSQLNSEAFL\LEMKPV AENTGILKTNTLLSQBSLMASSVSAPCNEKLIQDGFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIBKDAQ LKQFLTPKTBQLKPERVTSQVSNLKKKETTADSGTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGQIHKLRLKLKKKLKAEKKLAALMSSPQSRTVSESNLE CVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS QTHERILARLLSPTPVSTELSENGEGPFYLGMGDSHIPPPVPS
6817	172	240	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFL9KSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTIGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK  LGMMDSPKIGNGLPVIGPGTDIGISSLEMVGYLGKNFDSAKVPS DBYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEBCHTPHKPQKRKSLESSYKDGLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLDPDSSGQONPIRTADSLBRNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTTVTGLCSKR ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFABIET CLNEVRDEIFISLQPQLRCTLGDMSSPVPAFPLLLKLETHIEKL PLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHP ESCLYQTTSVIQYRANNHFITWILDADGSWLBCDDLKGPCSBRH KKFBVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASABTASVTHPKDISVAPRTLSQDTAVTHGD HILISGPKGLVDNILPLITLEETIQKTASVSQLNSEAFL\LKRNEV VNNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGYKSVEIBKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHESSYGNISSANH EDLVEGQIHKLRLKLKKKKKARKKKAALMSSPQSRTVRSENLE QVPQDCSSPNDCRS IEDLLMELPPPIDIANESACTTVPGVSLYSS QTHERILAELLSPTPVSTRLSENGEGDFRYLGMGDSHIPPPVPS

SEQ	Predicted	Predicted end	Limina and aggreet
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.03	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	ocqueme	\=possible nucleotide insertion)
-			DGGE/LHS/ATTEHKP/VQATPVNLT\TILTSTWQARLPQI
6819	1	961	GIPCTEMGNFDNANVTGEIEFAIHYCFKTHSLEICIKACKNLAY
1	-	702	GEEKKKKCNPYVKTYLLPDRSSQGKRKTGVQRWTVDPTFQETLK
			YQVAPAQLVTRQLQVSVWHLGTLARRVFLGEVIIPLATWDFEDS
			TTQSFRWHPLRAKADKYEDSVPQSNGELTVRAKLVLPSRPRKLQ
			BAQEGTDQPSLHGQLCLVVLGAKNLPVRPDGTLNSFVKGCLTLP
			DQQKLRLKSPVLRKQACPQWKHSFVFSGVTPAQLRQSSLKLTVW
1			DQALFGMNDRLLGGT\RLGSKGDTAVGGDACSQSKLQWQKVLSS
			PNLWTDMTLVLH
6820	1014	340	GDMVYIVGHVPPGFFBKTQNKAWPREGFNBKYLKVVRKHHRVIA
1			GQFFGHHHTDSFRMLYDDAGVPISAMFITPGVTPWKTTLPGVVN
1	]		GANNPAIRVFEYDRATLSLKDMVTYPMNLSQANAQGTPRWELBY
1			QLTRAYGVPDASAHSMHTVLDRIAGDQSTLQRYYVYNSVSYSAG
1	ŀ		VCDBACSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLPLLLMAL
1			LGLCT
6821	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN
1			RPCVLTLDPBTLPAIATTLIDVLFYSHSTPKRAASSSPEPSSIT
1			FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSEGELWRMVRIG
			GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
			GSVIEVLQRRQEGLAS
6822	1088	518	BFDIYR/BVGGBFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN
			RFCVLTLDPETLPALATTLIDVLFYSHSTPKRAASSSPEPSSIT
1			FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG
			GOPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
6823	654	221	GSVIEVLORROEGLAS
0523	554	221	PPKLLSRWARMCHGDBIV\LSDLNFPGLLHLPVVGPWRSVQTAC
			GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL
			ILRKGVLAINPLL
6824	858	104	LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLTQFGFRG
			ALPKLGICAGLQVVLGLPFILENPSGYLSRSFDLGRQFLFHWTV
1			NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS
1 :			LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQPYV
1	1		WYFHTLPYLLWAMPARWLTHLLRLLVLGLIBLSWNTYPSTSCSS
1 1	•		AALHICHAVILLQLWLGPQPFPKSTOHSKKAH
6825	3	1173	SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL
			PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ
			NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM
}			KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI
	ļ		GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDBDGYFQFMGRADD
	•		IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAP
			VILALQFLSHDPEQLTKBLQQHVKSVTAPYKYPRKIBFVLNLPK
]	j		TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF
L-6055	336.		PFGPLALPMDGYGDSLWBEHEYKFCLALVISTKLYHVRC
6826	2304	954	LKTESFKPW/VN1ALAFHLLGERASPNSFWQPYIQTLPREYDTP
j	1		LYFEEDEVRYLQSTQAIHDVFSQYKNTARQYAYFYKVIQTHPHA
	ļ		NKLPLKDSPTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPLW
1 1	İ		DMCNHTNGLITTGYNLEDDRCECVALQDFRAGEQIYIFYGTRSN
	į		ABFVIHSGFFFDNNSHDRVKIKLGVSKSDRLYAMKABVLARAGI
[	Ì		PTSSVFALHFTBPPISAQLLAFLRVPCMTKEELKEHLLGDSAID
į (	į	1	RIFTLGNSEFPVSWDNEVKLWTFLEDRASLLLKTYKTTIERDKS
) }	ļ		VLKNHDLSVRAKMAI KLRIGEKEILEKAVKSAAVNREYYRQQME
1		ļ	BKAPLPKYEESNLGLLESSVGDSRLPLVLRNLEERAGVQDALNI
	į	}	REALSKAKATENGLVNGENSIPNGTRSENESLNOESKRAVEDAK
L			GSSSDSTAGVKE

Predicted   Predicted   Predicted end   Depiming   Depiming   Depiming   Decation   De				
Degiming   location		[ D-m2[ at - 2	I manada and	
Docation   Corresponding		1		
location   corresponding   to first   amino acid   residue of anino acid   residue of anino acid   sequence			1	
corresponding to first anino acid reduce of anino acid reduce of anino acid calba of anino acid sequence  8627 1 779 Section, T-Throntine, V-Valine, anino acid sequence (Coden, /-possible mucleotide deletion, /-possible mucleotide deletion, /-possible mucleotide deletion, /-possible mucleotide deletion, /-possible mucleotide deletion, /-possible mucleotide insertion)  8628 3 1654 Severed anino acid sequence (Coden, /-possible mucleotide deletion, /-possible mucleotide insertion)  8628 3 1654 Severed anino acid converted anino acid sequence (Coden, /-possible mucleotide insertion)  8629 1654 Severed anino acid converted anino acid converted anino acid sequence (Coden, /-possible mucleotide deletion, /-possible mucleotide anino acid converted anino acid converted anino acid converted anino acid converted anino acid converted anino acid converted anino acid code anino acid converted anino acid converted anino acid converted anino acid converted anino acid code anino acid converted anino acid code anino acid converted anino acid code acid converted anino acid code acid converted anino acid code acid code acid converted anino acid converted anino acid code acid c	NO:			
to first amino acid residue of amino acid residue of amino acid sequence  8-esteine, T-Thronnine, V-Valine, amino acid sequence  779  8-TYPYTOPHAN, Y-TYXOSHINE, X-UNKNOWN, *-Stop Codon, /-possible nucleotide deletion (N-possible nucleotide insertion)  8-esteine, T-Thronnine, V-Valine, A-possible nucleotide insertion (N-possible nucleotide insertion)  8-ENTRILDPENGSGMALQPIQAAPEPGACQREKNSQHIPPALAPE (NGHSHGNGCOTDITWINIAGDDIRNITGGAIAGAAPSDGFSSG (NGHSHGNGCOTDITWINIAGDDIRNITGGAIAGAAPSDGFSSG (NGHSHGNGCOTDITWINIAGDDIRNITGGAIAGAAPSDGFSSG (NGHSHGNGCOTDITWINIAGDDIRNITGGAIAGAAPSDGFSSG (NGHSHGNGCOTDITWINIAGDGFRELIAGS)  8-ENTRILDPENGSGMALQPIQAAPEPGACQREKNSQHPALAPEGSG (NGHSHGNGCOTDITWINIAGDGFRELIAGSCHAPTITGGA (NGHSHGNGCOTDITWINIAGDGFRELIAGSCHAPTITGGAIAGAAPSDGFSSG (NGHSHGNGCOTDITWINIAGDGFRELIAGGAAPSGGAIAGAARAAPSTARAAPSAAPAAPSAGGAAPSGAAPSTARAAPSAGGAAPSGAAPSTARAAPSAGGAAPSGAAPSGAAPSGAAPSGAAPSGAAPSGA		[ =====		
amino acidd sequence alone of amino acid sequence and acidd sequence and acidd sequence and acidd sequence (codon, /=possible nucleotide deletion, /=possible deletion, /=possible nucleotide		1		
amino acid sequence  ### Stylengham, Y=Tyxrosine, X=Dknown, *=Stop Coden, /=possible nuclectide deletion (			1	
amino acid sequence    Codom, /=possible nucleotide deletion,    -possible deletion,    -possible nucleotide deletion,    -possible nucleotide deletion,    -possible nucleotide deletion,    -possible nucleotide deletion,    -possible nucleotide deletion,    -possible nucleotide deletion,    -possible nucleotide deletion,    -possible nucleotide deletion,    -possible nucleotide deletion,    -possible nucleotide deletion,    -possible deletion,    -possible nucleotide deletion,    -possible nucleotide deletion,    -possible nucleotide deletion,    -possible nucleotide deletion,    -possible nucleotide deletion,    -possible nucleotide deletion,    -possible nucleotide deletion,				
Sequence   \ \possible nucleotide insertion		1		
1		<b>1</b>	sequence	
### ETRINLDPENGSGHALQPICAAPERGACGOREKINSCHIPPALAPS HOGSHERGGGGTITWWILLIGGISHINLTICHALTGAAPSICEPSSG LSTTLAWSCHELPHALGSGLSTREILLSLTVERGHE GGAVLAYGUSLGPVPLTPWVPGVPAUPLYVALVORLPALPPSS GAPAZA\NVILLGGLGILLIGGCHMAITLLEERILLEVTTEG  ### REGET/MILGGEGILLIGGCHMAITLLEERILLEVTTEG GAPAZA\NVILLGGLGILLIGGCHMAITLLEERILLEVTTEG  ### REGET/MILGGEGILLIGGCHMAITLLEERILLEVTTEG GAPAZA\NVILLGGLGILLIGGCHMAITLLEERILLEVTTEG  ### REGET/MILGGEGILLIGGCHMAITLLEERILLEVTTEG GAPAZA\NVILLGGLGILLIGGCHMAITLLEERILLEVTTEG  ### REGET/MILGGEGILLIGGCHMAITLLEERILLEVTTEG GAPAZA\NVILLGGLGSTASILMSSS:POSGRODTRAKTFRENAPVERLUTKLIVLS GLENWHSLIVALITGGLABACTGCHSAKTYGGRAPGCHAITLLIGGT HARDITARITURS:TALEITENDLLQTIQDLIDLGRUKCHAITLUS GLENWHSLIVALITURGLESTITEPSCHLIVLUSCHSTEVENDH TAREITENDLEGTTALEITENDLLQTIQDLIDLGRUKCHAITLUS CKPGERSYPGQPKTQEEVCQLSINIMOVPITCLEGLSTEVENDH TAREITENDLEGTSITEPSCHLIVLUSCHGSCHSCHGHAIT TAREITENDLEGTSITEPSCHLIVLUSCHGSCHGHAITLUSCHGENTITENDLICTERINGTENDLICHTENDLICHTENGTETTYTT ### PIMIABHEBRINPGGIERITTORSTERGRUNTLUSCHGENTYLTERQTICER CKPGERSYPGDPKTQBERCHGPTRANTLANGLAPOLNSCHANTLANGLAG ### PIMIABHEBRINPGGIERITTORSTERGRUNTLUSCHGORUNGLAGUNG ### PIMIABHEBRINPGGIERITTORSTERGRUNTLUSCHGORUNGCHTVPLTTEQTICER ### REGET/MICHCHGAASSTROMET ### REGET/MICHGAASSTROMET ### REGET/MICHGAASSTROMET ### REGET/MICHCHGAASSTROMET ### REGET/MICHGAASSTROMET ### REGET/MICHCHGAASSTROMET ### REG				
HQGHSHEGIQGTITTWWILGDGLHNILTGIALGAPSIGNES	6827	1	779	
6830 1 1087 SLEPPENLIAGOPAMILOSGI-SPRELILIS-INVERGINE 6831 1 1087 KSQR-VHILOGHERMINGS-CHERM-LIGHT-VITTEG 6832 1 1654 KSQR-VHILOGHER-KEGVYRDLKGSPG-LERAHLDLDBIGTFS-E GRAVA-NVILOGLELICGCUMLATTILEERILI-PVTTEG 6828 1 1654 KSQR-VHILOGHER-KEGVYRDLKGSPG-LERAHLDLDBIGTFS-E GRAVA-NVILOGLELICGCUMLATTILEERILI-PVTTEG 6828 LGHES-STABLKGS-POSERDTRINKTFHRW-PVFRUKTKUVLS GLENWELSVALIRGALI-PLS-I REGRAVINGER-KEGGVILA- HALGOVER-INTERLIA-BES-POSERDTRINKTFHRW-PVFRUKTKUVLS GLENWELSVALIRGALI-PLS-I REGRAVINGER-KEGGVILA- HALGOVER-INTERLIA-BES-POSERDTRINKTFHRW-PVFRUK-GSGVILA- HALGOVER-INTERLIA-BES-POSERDTRING-CHERT-STRUCK-SGR-SE-POSERD-TH- TARE TREIL-BRESDRIV-POSE-POSE-POSE-POSE-POSE-POSE-POSE-POSE				
GGAVIGVELSLEPVELTEWYEOVTAGUTLYTALUMINEALPEPS GAPAN/ANNIALGELLLIGGCUMIATTLIERELLEPTES GAPAN/ANNIALGELLILIGGCUMIATTLIERELLEPTES GAPAN/ANNIALGELLILIGGCUMIATTLIERELLEPTES GAPAN/ANNIALGELLILIGGCUMIATTLIERELLEPTES GEGEN GEGEN GEGENVERTE GEGNVERTE GEGNVERT				
6828 3 1654 KSQHJWILQLMISCKENYVKDLKCHPOLINGKULDSGYNESS  LGHLGYTASILKRGSSFQSGKDITWRYKTFRETAVURKUTKLVLS QLDNIWKIM IS YWNGSLESKTIAKKGGJCHRSKMVKQKIDDKKM IQSVMHSLVKLINGGALDLS IR ROBGRANYGGKGNEVKKLISGQHLA HARGYVRITHRISLTALE TPROLLQYTQDLILDLRWCCWMATLQH TAREKKHLAKKEMI VDNIGSLTBLOQPRGCUCGLQSLIGSUM REGENYPQQPKTQBEWCQLSINIMQPIYCLEQLSTKYRDADI DTYHLSUWSSPDLPGSI HEDPSLISGGRLLNCCYLBERTH FINIABHPBKHNPQGI ERKTQVSMASILKRLQQRLERNY IELKAD PIVGSLBEG I YARYPDMKOLDPPTUNWRYLKRLOCYLBERTH FINIABHPBKHNPQGI ERKTQVSMASILKRLQQRLERNY IELKAD PIVGSLBEG I YARYPDMKOLDPPTUNWRYLKRLOCYLBERTH FINIABHPBKHNPQGI ERKTQVSMASILKRLQQRLERNY IELKAD PIVGSLBEG I YARYPDMKOLDPPTUNWRYLKRLOCYLBERTH KKESSMHILLITCQASSITEMAT KKESSMHILLITCQASSITEMAT KKESSMHILLITCQASSITEMAT KLULIKMABREQUIERARFYNIOPLIKI I ROBMBERDYTTYTQVP PHRYTVIVQCQEBELQMSUBETGANILINGSYNYGSSG QABPICVUSKRIHSTPHOLSSESSEKTKSTERQLBEQOQBEEV BEVENVOQVUSKBLADGEK/CVKRRAPCCEAPHLGGGVBI ARPTICKUSKRIHSTPHOLSSESSEKTKSTERQLBEQOQBEEV BEVENVOQVUSKBLADGEK/CVKRRAPCCEAPHLGGGGVBI ARPTICKUSKRIHSTPHOLSSESSEKTKSTERQLBEQOGBEEV BEVENVOQVUSKBLADGEK/CVKRRAPCCEAPHLGGGGVBI ARPTICKUSKRIHSTPHOLSSESSEKTKSTERQLBEQOGBEEV BEVENVOQVUSKBLADGEK/CVKRRAPCCEAPHLGGGVBE BEGGGCENPRPSILTDLVVLBHIGLYAGDPVSKVLLKPLTGRTHQL RVHGCSALGHBYWOOLDTYGBERVTISHALGRINSTEGRAHTMCI BEGGGCENPRPSILTDLVVLBHIGLYAGDPVSKVLLKPLTGRTHQL RVHGCSALGHBYWOOLDTYGBERVTISHALGRINSTEGRAHTMCI BEGGGCENPRPSILTDLVVLBHIGLYAGDPVSKVLLKPLTGRTHQL RVHGCSALGHBYWOOLDTYGBERVTISHALGRINSTEGRAHTMCI BEGGGCENPRPSILTDLVVLBHIGLYAGDPVSKVLLKPLTGRTHQL RVHGCSALGHBYWOOLDTYGBERVTISHAGDRSTEGRAHTMCI BEGGGCENPRPSILTDLVVLBHIGLYAGDPVSKVLLKPLTGRTHQL RVHGCSALGHBYWOOLDTYGBERVTISHAGDRSTEGRAHTMCI BEGGGCENPRPSILTDLVVLBHIGLYAGDPVSKVLLKRUTTROCHQENALATA BEGGGCENPRPSILTDLVVLBHIGLYAGDPVSKVLLKRUTTROCHQUBERNITAVUNTRO BEGGGCENPRPSILTDLVVLBHIGLYAGDPVSKVLLKRUTTROCHQUBERNITAVUNTROCHQUBERNITAVUNTROCHQUBERNITAVUNTROCHQUBERNITAVUNTROCHQUBERNITAVUNTROCHQUBERNITAVUNTROCHQUBERNITAVUNTROCHQUBERNITAVUNTROCHQUBERNITAVUNTROCHQUBERNITAVUNTROCHQUBERNITAVUNTROCHQUBERNITAVUNTROCHQUBERNITAVUNTROCHQUBERNITARATATAPAGRTUTLARSTTPFFTUNTROGRAGGHPPPSYL				_
1654   KSORJ WILGUMSICKEGYVEDLKENFÜLRRAMLDLÜDGTPES		1		1
G833  LIGILSGYTASILMEGS POGGEDDTWRYTPERVAFVERLITALIALS QLPNFWALM IS YVNGSLEPSTARKSGQI BERSINVERQUIDFKMM IQXVMHSLVKLITEGALGPLES IRDGERGYGGUSWCKELSGQHEA HALGYVRITHESUTALE PROBLIGYTIQDELLOLARRCCAMATIQE TABEZIKHLARKEM VUDNEGUTSLPCOPEGC LVGSLGSLKGVLA CKPGEASVPQQPETGBEWCQLSINIMQVFIYCLEGLSTKPDADI DTYHLSUWVSS PDLPGS IRBDEPSLTSCOPELINCCYLERSHT FINIABHPEKHNPQG ERKITQVSMASLKERLQQRLPENY IELKAD PIVGSLERGIYAGYVPROMCLEPYTGVRNYLKBALVNI LAVIBEV FITISKELVPRIVENCLEPYTGVRNYLKBALVNI LAVIBEV FITISKELVPRIVENCH VIDENGSTENKAPQUSSGADKKLLEBLIN KFRSSMHGLITCQBASSTFMAT  RESS				1
GENOMESTIAL SYNOSUS STATAKS GOLDEN SINVERGENDE KONTAGEN STATE I QUE WHIS LY KLITRGALLEL SI ERIGRANY GORDEN WORK LISCHEM.  HAI QI'VALTIRISITALE I PROLLOTI QUILILLE REVORDENCE SERVEL SER	6828	3	1654	KSQHG/WILQLMHSCKEGYVKDLKGNPGLHRAMLDLDNGTRPSB
TORWHISLUKLTRGALLPLS TROGRARQYGGREVICCIS.GQNLA HALQTVELTHERUTALE IPROLLQTIQUELLDLEVICVMATULA TABELKELARKEDMI VIDNEGUTSLPCOPFAQCITVCSLQSLAGVILE CKSGEASVPQOPKTQSEVCQUSINIMQVETYCLEQUSTKEDADI DTHILSUVDSSPDLPGS ILEBPSITTSEQUILUSINGCVLEBRHT FINIASHPERINNCGIEKTTQVSMASLKELOQUSIFKEDADI PIVGSLERGIYLAGYPDNIKOLPPTYGWNTULUSINGCVLEBRHT FINIASHPERINNCGIEKTTQVSMASLKELOQUSIFKEDADI PIVGSLERGIYLAGYPDNIKOLPPTYGWNTULUSINGCVLEBRHT FINIASHPERINNCGIEKTTQVSMASLKELOQUSIFKEDANI ILAVIARV PTISKELVPRVLSKVIEAVSERLERLMQUSSFSKNGALQARLE ICALBUTVAVYLIPPSKSSFFQALBRALPQUSSGADKKLEELLN ICALBUTVAVYLIPPSKSSFFQALBRALPQUSSGADKKLEELLN RKESSHHJULTCHQAASSTMMKT  MRMEAGERAPPBGAGGERAAGGGREWVELNVGSTVFTTQTLCR KKRSSHHJULTCHQAASSTMMKT  MRMEAGERAPPBGAGGGRAAGGGREWVELNVGSTVFTTQTLCR KKRSSHHJULTCHQABSTMMKT  MRMEAGERAPPBGAGGGRAAGGGREWVELNVGSTVFTTQTLCR KKLJCABRAGGRAAGGGREWVELNVGSTVFTTQTLCR KKLJCABRAGGARCHVELNVGSTVFTTQTLCR KKLJCABRAGGARCHVELNVGSTVFTTQTLCR KKLJCABRAGGARCHVELNVGSTVTTQTVGSFTYTTQTLCR RYSPELADDTTCTGFRFCHGLDSTSGALCVALNKAAGSAYR CFRERRVTKAVLALLEGHIJOVRKHUWTURGSTSGALCVALNKAAGSAYR CFRERRVTKAVLALLEGHIJOVRKHUWTURGSTSGALCVALNKAAAGSAYR CFRERRVTKAVLALLEGHIJOVRKHUWTURGSTSGALCVALNKAAGSAYR CFRERRVTKAVLALLEGHIJOVRKHUWTURGSTSGALCVALNKAAGSAYR CFRERRVSTAVLALLAGENJOVRKHUMTURATTQAC RYNGSALGHPVVGBUTYGGEVGSGREDPFRTWILLAFTLTGAC RYNGSALGHPVVGBUTYGGEVGSGREDPFRTWILLAFTLTGAC RYNGSALGHPVVGBUTYGGEVGSGREDPFRTWILLAFTLTGAC BGGGCERPRSSUTDLVVLBIGUTVAGDPSTSGALCVALNKAAGSAYR CFRERRVSTBAVLAGEBLETQPSPSVEKAVTVUDPGSTTPTNG BCGRACGCERPRSSUTDLVVLBIGUTVAGDPSTVLARFKTLTGACH RYNGSSTSPANNITAGE BCGLAGGGRAPPPEPTTRYPRTTSPARGGGFCQMISEKRI LEPDS  10879 SLEFEGSSTDDNKVAEQEBLETQPSPSVEKAVTVUDPGSTTPTNG RYNGSSTDLKSKRTTDPSBARTITAG RYNGSALGARCHVARNITAGA RYNGSGALGARCHVARNITAGAC RYNGSALGARCHVARNITAGAC RYNGSSTDLKSCRTTTPTTTCATTGACAC RYNGSALGARCHVARNITAGAC RYNGSALGARCHVARNITAGACAC RYNGSALGARCHVARNITAGACAC RYNGSALGARCHVARNITAGACAC RYNGSCALGARCHVARNITAGACAC RYNGSALGARCHVARNITAGACAC RYNGSALGARCHVARNITAGACAC RYNGSALGARCHVARNITAGACAC RYNGSALGARCHVARNITAGACACAC RYNGSALGARCHVARNITAGACACAC RYNGSALGARCHVARNITAGACACACACACACACACACACACA				LGHLSQTASLKRGSSFQSGRDDTWRYKTPHRVAFVEKLTKLVLS
HATGTVRITHESITALRITENDILGTTQDLIDLEURCVMATIGE TABETERLABERDMIVDINGGITSLPQFRQCIUSLQSLKGVUE CREGESVPQQPKTQBEVQDLSINIMQVFIYCLEQDSTKPDADI DTTHLSVDVSSPDLPGSIHEDPSITEGQHLITUSRCYLERHT FINIASHPERBINGQGIEKITQOSMASIKBLQQRIFRRYIELKAD PIVGSLERGIYAGYPDINGCLPPTGVRIVLKRALVNILAVHAEV FTISKELVPRVLSKVIEAVSRELSRLMQCVSSPSKNGALQARIA ICALBUTVAVYLIPESKSSPKQALEALPQSSSGADKKLLEBLIN KYKSSHHIQHICCQAASSTMAKT  80KSPLSELCGEBLGSDRDETGAYLIDEDPTYPGTLAFLERIG KLVIJOKDAMBERGVLEENSPYNIGPLIRILERIGEDPTYPTTTRQTLCR BQKSPLSELCGEBLGSDRDETGAYLIDEDPTYPGTLAFLERIG KLVIJOKDAMBERGVLEENSPYNIGPLIRILERIGEGOQDEBEV QASPLSVVSKELISTPNGLSSESSRKTKSTERGLEBEQQQBEV PKHVYRVLQCQSEBLTQMVSTMSDGWRFGQLVNIGSSYNYGSED QASPLCVVSKELISTPNGLSSESSRKTKSTERGLEBEQQQBEV PKHVYRVLQCQSEBLTQMVSTMSDGWRFGQLVNIGSSYNYGSED QASPLCVVSKELISTPNGLSSESSRKTKSTERGLEBEQQQBEV PKHVYRVLQCQSEBLTQMVSTMSDGWRFGQLVNIGGSYNYGSED QASPLCVVSKELISTPNGLSSESSRKTKSTERGLEBEQQQBEV PKHVYRVLQCQSEBLTQMVSTMSDGWRFGQLVNIGGSYNYGSED QASPLCVVSKELISTPNGLSSESSRKTKSTERGLEBEQQQBEV PKHVYRVLQCQSEBLTQMVSTMSDGWRFGQLVNIGGSYNYGSED QASPLSVVSTARABOVALTHAGASSAYR CPKERVYKLAGLGGBDLTQWSDKSCLAGFDQHEGGGVVEN REVEYDQVSLADAGRKCCVKKERAGCAEDPHLQGLGVBI  BERVEVQQVQVSLADAGRKCCVKKERAGCAEDPHLQGLGVBI RVHGSALGIRBVVGDLTVSBEDFLVVNIKHMDVRIDSSLAWRETDTTQF BERVEVQCVQVSLADAGRKCTSGDSERMINISTVTSADGSRL RVHGSALGIRBVVGDLTVSBEDFLAVKNTVIDDPSE DRGPRGSSFSALLFGPGRPPPPTKPPFTERAGGGCLQMLSRKMILFA LEPDS  BORGPRGSSFSALLFGPGRPPPPTKPPFTERAGGGCLQMLSKKMILFA VEDLQQPKPISEVSREDVGKKEISDSERMINISTVTSADGSRL LEPDS  NAMBKRABERAGTERVALTTVPPPHTUSKYCHALAFYLLITTGTTTGL LEPDS  BORGPRGSSFSALLFGPGRPPPPTKPPFTERAGGGCTTPTTLTNF NAMBKRABERAGTARGTTTPPPHTTSANTTRAGGGBFGFTTTLV SEKREDBRKKK  BERKDEKKK  BORGPRGSSFSALLFGPGRPPPPTKPTPFTERAGGGCTTPTTLTNF NAMBKRAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT				QLPNFWKLWISYVNGSLFSETABKSGQIERSKNVRQRQNDPKKM
TARETRILARREDMITUDINGGITSLPCOPROCITOGISLIGNUE.  CKPGEASUPQQPKTQBEVCQLSINIMQVFIYCLEQLISTEPDADI DTTHLSUPUSSPDLPGS HEBPSLTSEQRILIVLISNCCYLERHT PINILASHPERHINGGIEKTTQVSMASLKRIDQRIFRNYIELKAD PIVGSLEPGITAGYPMIKOLPPTYGWRISALVIILLAVGARV FTISKELVPRVLSKVIERAVSRELSRLMQCUSSFSKNGALQARLIK ICALROTUAVILTPBSKSSFSKNALKALPGSADVKILLEGLIN KPKSSMHIQHTCPQAASSTMMKT  ARREGERAPPAGAGGRAAGGWKWVRLNVGGTVPLTTRQTLCE ERGEFLSILCQGBELQSDRDETGAYLIDRDPTYPGPTLARFLENG KULLKDMARBGULBERRYNIGPLIRITRORMERGVYTVTCVP PRHYNVRULQCSBELLQWSTMSDGWRFDVINGGSTWYTGSPD PRHYNRVLQCSBELLQWSTMSDGWRFDVINGGSTWYGSED QARPLCUVSRELIGSTBNGISSESSRKTKSTERGLBEDQQQBEEV EBVEVEQUVSRADQREV,CCYKERAPGAGAGAAGAAY CVERREVERGVAKALLAGHIGHGSRWTISHANGGSTGATLTLQKQL RYRFPELADPDTCTGFRFCHGLDFSTGGALCVALNKAAGSAYR CVERREVIKSVALLALLGHIGSRWTISHALGGRUFT BGGGCERPRFSLITDLVVLBHGLYAGDFVSKVLLKFLTGRTHGL RVHGGALGHBVVGDLTYGGSVGVGSRGENFSGGGRVKEKSMITEN GGGGCERPRFSLITDLVVLBHGLYAGDFVSKVLLKFLTGRTHGL RVHGGALGHBVVGDLTYGGSVGTSGRGGGRVKEKSMITEN FEGSSTDDNKVAEQRDLETGPSPSVEKAVTVUDPBGTTPINF ECVEVCTPDPFLPSLDACNSPHTLLQSLDQLVQALRATDPPDPB DRGPRGSFSALLPGFGRRPPPFFTRPBTRQGGPCLQMLSBWT LEPDS SLEPGSSTDNKVAEQRDLETGPSPSVEKAVTVUDPBGTTPINF VEDLQQPFLSEVISRDVGKRGISGDSERMINSVVTSADGERNI SLEPGS SLEPGSSTDNKVAEQRDLETGPSPSVEKAVTVUTDPBSKNI ELQSYSILGBKLVMEERASTTUPPHVTDSKRVQKPALAPPSKNITK SKENSPSTEKKONLENGNSTTALARSKURGNDVFSLKISERSTK LRSVSPTEKKONLENGNSTTALARSKURGNDVFSLKISERSTK LRSVSPTEKKONLENGNSTTALARSKURGNDVFSLKISERSTK LRSVSPTEKKONLENGNSTTALARSKURGNDVFSLKISERSTK LRSVSPTEKKONLENGNSTTALDFSLGRRUGVAPPHQNDEDYNERPRITUG SEKKIDEKKKK  6832 1809 412 MGSGLISGPPQDNSGEALKEPERAGEHSLFMFAGGGHFPEYLLV VSLKKKRSEDDYRST LITTGPFRRENLLAGGQEREBELLGAI PLF CPPDGMEMBASLITEYRETFSFVLINTNOSKRIKGNVAPPHAGLALA PPSMAHTYLDVUSSLATVRCSTFFVLINTNOSKRIKGNVAPPHAGGGHFPEYLLV SKKKRSEDTATVLCSTFFVLINTNOSKRIKGURPHENGERGFCK ALTSKTNERFYKKYNKTOLFSLATVCCTPFPWGVDMFRQGVENDSYMG EVLLVNLGEGTFFMSVGGBEKDLIPFRIGDRESHEJERGFRESSDIN ARGHREFFRANGFFFFFFFAGRFGFFFFFFFFFFFFFFFFFFFFFF				IQEVMHSLVKLTRGALLPLSIRDGBAKQYGGWBVKCBLSGQWLA
CKSGERSVPQOPKTQBEVCQLSINIMOVETYCLEQLSTKPDADI DTTHLSVDVSSPDLFGS HEBPSLTSEQRILIVISNCCYLERHT FINIAHFEKHNRQGI EKTQVSMASLKELDQRLFRNYI ELKAD PIVGSLEPGI YAGYPDWKDCLPPTGVRNYLKRALVNI LAVHARV FTISKELVPRUSKVIERAVSREISLRM.QCVSSFSKNGALQARLE ICALRUTVAVYLTPESKSSFKQALKALPQLSSFSKNGALQARLE ICALRUTVAVYLTPESKSSFKQALKALPQLSSGADKKLLERILN KFKSSMHLQLTCPQAARSTMKT  6829  1 782 MRNEAGERAPPAGAGGRAAGGWGWVRLNVGGTVFLTTRQTLCR BQKSFLSRLCQGEELQSDRDETGAYLDDDPTYGPITLAFLERIG KLVLJKDHABEGULEEBRYSVIGFLIRI KROPMERKDYTVTQVP PHHVYRVLQCQBEELTQMVSTMSDGWRFQLVNIGSSYNGGSD QAEFLCVUSKELHSTPNGLSSESSRKTKSTEEQLBEDQCQBEEV KLVLJKDHABEGULEEBRYSVIGFLIRI KROPMERKDYTVTQVP PHHVYRVLQCQBEELTQMVSTMSDGWRFQLVNIGSSYNGGSD QAEFLCVUSKELHSTPNGLSSESSRKTKSTEEQLBEDQCQBEEV FRYPPELADDPTTCTGFRFCHQLDSTSTGALCVALNKAAAGSAYR CPKERRVTKAYLALLEGHLQBERVTISHALGGRIGGARATMCI BGSQGCENFKPSILTDLVVLEHIGLYAGDPVSKVLJKPLTGRTHQL RV\HCSALGHPVVGDLTYGBVSGREDFFRMMLHAFYLRI PHIDT ECVEVCTDPPLPSLDACNSPHTLLGSLDQLVQALKRIPTGRTHQL RV\HCSALGHPVVGDLTYGBVSGREDFFRRMLHAFYLRI PHIDT ECVEVCTDPPLPSLDACNSPHTLLGSLDQLVQALKRIPTGRTHQL RV\HCSALGHPVGDLTYGBVSGREDFFRRMLHAFYLRI PHIDT ECVEVCTDPPLPSLDACNSPHTLGSLGLOVQALKRIPTDPDFB DRGPRRGSFSALLPGGGREPPPPFTKPPFTERQGFCLQWLSENT LEPDS  1087 1087 1087 1087 1087 1087 1087 108				
DITHLSUNDYSPOLFGS HIRDPSLITSCRILLTULSNCCTLERHT PINIAEHPEKHNPGGIEKITQUSMASLKELQRILFRNYIELKAD PIVGSLEBGIYAGYFDWKDCLPPTUVRNYLKRALUNI LAVIAEV FTISKELVPRULSKVIEAVSREISKLMQCUSSPSKAGALQARLE ICALRITVAVVITPESSESPKQALKULGSGADKKLLEELIN KPKSSMHLQLTCPQAASSTMAKT  6829 1 782 MRREAGEAPPAGAGGRAAGGWGKWVRLINVGGTVFLTTRQTLCE GKSPLSELCQGEBLGSDRDETGAT-LIDRPTYFGFILMFLEHG KLVLJKDMABERGVLEEABFYNIGPLIRIIGDRMERKDYTVTUVP PHRVYRVLQCDSELLTJOMASTMSOMERGVVVILDRPTYFGFILMFLEHG KLVLJKDMABERGVLEEABFYNIGPLIRIIGDRMERKDYTVTTQVP PHRVYRVLQCOSELLTJOMASTMSOMERGVAVIGSED QAEFLCVVSKELHSTPNGLSSESSRKTKSTEEQLEEQQQQEEBV ERWEVSQVQVSADAQEK/CCYKRBAPGCEAPPHLGGLGVPI RWFGSVENISIIVYRSEBFIJVUNKHENDVRIDSKAMRETLTIQKQL RYRPPELADPDTCGFFFFCHGLDFSTSGALCVALINKAAAGSAYR CYKERRVTKAYLALLRGHIQESKVTISHALGRNSTEGRAFTMCII BGSQCCEMPRPSILTDLVVLEHGLYAGDPVSKVLLKRLTGRTHQL RV\HCSALGHPVVODLTYGBVSGREDRFFRMMLHAFYLRIPTDT ECCEVCTTEPPFLPSLADACNSPHTLLGQLVQALKATPDPDPE DRGPRPGSFSALLPGPGRPPPPPTKPPBTRAQRGPCLQWLSEWT LEPDS  6831 3 1087 SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNP NVABKRADHSLSSVKLKTADBPGTLVKSGGGONVEKSMILSR VEDLQQPKSISEVSREVYGKKSISGGBENINSVVTSADGENL ELQSYSLIGHKLVMERAKTIVPPHTDSKRVQKDALAPPSKNITK SIFKEEPPSDQKQKSILLSFDVVDKVPQQDKSASSNFASKNITKE SKEMPSSI LIPVESSGGSLDFSEDRIKKFMMNFTSIKISEEBTK LRSVSFTRKKDNLENR\SYTILABRKGPMNFTSIKISEEBTK LRSVSFTRKKDNLENR\SYTILABRKGPMNFTSIKISEEBTK LRSVSFTRKKDNLENR\SYTILABRKGPMNFTSIKISEEBTK LRSVSFTRKKDNLENR\SYTILABRKGPMNFTSIKISEEBTK LRSVSFTRKKDNLENR\SYTILABRKGPMNFTSIKISEEBTK LRSVSFTRKKDNLENR\SYTILABRCHSTLARQGEEBEBLLKAIPLF CPPGCMEMASLTRYPRRTSFVLINVOGSKRIGYCRELLPAGPG PRILFKVTCIIGCFGLPSKILDEVEKRIGISMAVIYPPMQGI RRAAPPAGKTVTLKSFIPDSGTFRFISITRPLDSHLEHUDFSSL LHCLSFEQILGITASAVLRRKIIFLAGGGEBEBELLATIFLF PSWARITYTIVPVPRSLLATATVCCPTFFMQGGHPGEFFCYLLV PSWARITYTIVPVPRSLLATATVCCPTFFMQGGHPGEFGFCK ALTSKTINRFYVKKVTGLATATVCTPTFMQGGRPGGPGFPEYILLV PSWARITYTIVPVPRSLLATATVCCPTFMQGGRPGGPGGFGEFFCX ALTSKTINRFYVKKVTGLATATVCTAFTRAGGRFGGHPGFFCYLLV PSWARITYTIVPVPRSLLATATVCCPTFAGGRGFGGFGFFCFSFCC ALTSKTINRFYVKKVTGLOFLPFSFTGGERSKKNPAGYFGGYFCCHALP PERMATTATUPPSTSLATATVCCPTFFGGSBDIN		1		TAEEIKRLAEKEDWIVDNEGLTSLPCQFRQCIVCSLQSLKGVLE
FINIAEHPEKHNPQGIEKTTQVBMASLKELDQRLFRNYIELKAD PIVGSLEBGIYAGYTØNKDCLPPTGVRNYIKRALDVRILAVILAVIELKUN FITSKELVPRVLSKVIEKUVSERISKUMQCVSSFSKMGALQARLE ICALRDTVAVYITPESKSSFKOALKALPQLSSGADKKLLEELIN KFKSSHLUQTGPDAASSTMMKT  MRNEAGERAPPAGAGGRAAGGWGKWVRLNVGGTVFLTTRQTLCR BQKSFLSRLCQGBELQDRDETGAYLIDRDFTYTGPTLMFLEHG KLVLIXDMABEBULLEBREYNTOPLIRIIKINGENSKYYTTYDVP PKHYYRVLQCQBEBLTQMVSTMSDGWRFEQLVNIGSSYNYGSED QARFICVUSKBLHSTPRIGISSSSSKTKSTERGLBEQQQBEBV GREVEVEQUQVEADAQEK/CCYKFRAPGCAPDHLQGIGVFI FRYPPELADPDTCYGFFFCQLDFSTSGALVALNKAAAGSAYR CFKERRYKKATLALLKGHLQBSRVTISHAIGRNSTSGRAHTMCI BGSQGCBPRFSLTDLVVLEHGLYAGDFVSKULHKLTGTRTQL RVHCGALGHPVWGDITYGBVSGREDAPFFRMHLAFYLRIPTDT ECVEVCTPDPFLPSLDACNSPHTLLQSLQQLVQALRATPDPDPB DRGPRRGSFSALLBGPGRPFPPFTAFFFERRAGREPLIPTINF ECVEVCTPDPFLPSLDACNSPHTLLQSLQQLVQALRATPDPDPB DRGPRGSFSSALLBGPGRPFPPFTAFFFERRAGREPLIPTINF ECVEVCTPDPFLPSLDACNSPHTLLQSLQQLVQALRATPDPDPB DRGPRGSFSSALLBGPGRPFPPFTAFFFERRAGREPLIPTINF ECVEVCTPDPFLPSLDACNSPHTLLQSLDQLVQALRATPDPDPB DRGPRGSFSSALLBGPGRPFPPTAFFFERRAGREPLGWLSSH SERBDS SLFFGSSTDMKVAEGEBLETGDSSVKAVTVIDDEGTIPTINF ECVEVCTPDPFLPSLDACNSPHTLLQSLDQLVQALRATPDPDPB DRGPRRGSFSSALLBGPGRPFPTAFFFTRAGRAGRAFT SLFBDS SLFFGSSTDMKVAEGEBLETGDSSVKAVTVIDDEGTIPTINF ECVEVCTPDPFLPSLDACNSPHTLLGSLDGERNINSVVTSADGENL EQSYSLIGBRLVWERKATIVPPHTDSKRVQKRADAPPSKNITKE SEKPBSILLPVESKGSLDFSSDALKKEMQNPTSLKISGESERK LESVSFTEKKDNILERN STYLLARKKVLAEKGNVALPELBRDS SLFKEBPRSDQKKKSLLSFDVVAKVVQQPKSASSNFASKNITKE SEKPBSILLPVESKGSLLDFSSDALKKEMQNPTSLKISGESERK LESVSFTEKKDNILENR STYLLARKKVLAEKGNVALPELBRDS SEKREDBKKKK SEKPSSILLPVESKGSLLDFSSDALKKEMQNSTDAKSHTIKE SEKREDBKKKK SEKPSSILLPVESKGSLLDFSSDALKREMQNSTALKLLAELDSHLEH PREMATTIVLVESSLAFTAVTCPTPFTWGVQMRDYMENDENTERKILVG SEKRKDBKKKK BARPPAGKTVTLKSPIPDSGTRFISLTRPLDSHLEHUDFSL LHCLSFEGLLGITASAVLARKILIFLABEGLETLAGCHAAAALLY PESWANTIVIVVPSSLLAATVCCTPTFWGVQMRPQQCHAPMSMD EVLLVNLCBCTFLMSVGDEKDILLPRUGUMBFMQECHDERFK EVLLVNLCBCTFLMSVGDEKDILLPRUGUMBFMQEWBFMG EVLLVNLCBCTFLMSVGDEKDILLPRUGUMBFMQEWSPMG EVLLVNLCBCTFLMSVGDEKGLISRAVVNRND ALTISKTMRFFVKKFVKTOLDFSFFTGAREKKNPAGYFQQKTLL YBEQKKQ/TETKGRNCEIRAVVNRN		1	•	CKPGEASVPQQPKTQREVCQLSINIMQVPIYCLEQLSTKPDADI
PIYGSLEPGIYAGYEDRKOCLPPTGVRNYLREALVNI LAVERBY PTISKELVPRVLSKVIEAVSERLSRLMQUSSPSKRGALQARLM ICALRUTVAVYLTPESKSSFKQALKALPQUSSGADKKLLEBILM KFKSSMHLQLTCPQAASSTMMIT  6829 1 782 MRHEAGEARAPGAGGGEANAGGWKVRLNVGGTVFLTTRQTLCR BQKSPLSRLCQGBELQSDRDETGAYLIDRDPTYFGPILNFLRHG KLVLDXDRABBGVLECABFYNIGPLIRIIDRDPTYFGPILNFLRHG KLVLDXDRABBGVLECABFYNIGPLIRIIDRDRTSFGSTNYGSED QABFYLCVVSKELHSTPNGLSSSSSKTKSTEGLBCQCQBEBY EBVEVEXQVQVSADAQUSK/CCXVRRAPGCBAPDHLQGLGVPI  6830 1 939 MEPGSVENLSIVYRSRDFLVVNKHWDVRIDSKAWRETLTLQKQL RYRFPELADPDTCYGFFFCHQLDFSTSGALCVALINGAAGSAYR CPKERRVKAXLALLBGHLQBSRVTISHAIGRNSTEGRAHTMCI BGSQCCEMPKPSLTDLVVLEHGLYAGOPVSKVLLKELTGRTHQL RV\HCSALGHPVVGDLTYGEVSGREDRPFRMILHAFYLRI PTDT ECCEVCTEDPFLPSLDACNSPHTLLQSLQULVQALRATDPDPB DRCPPRGSSSALLPGDGRPPPPPTKPPETRAQRSPCLQWLSEWT LEPDS  6831 3 1087 SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPBGTI PTNF NVABKRAHARLSLSSVKLKTADBSRGTLVKSGCGQNXEKKMILGS VEDLQQPKJ ISEVSERDYGKKISGSBRNINSVVTSADGENL ELQSYSLGGRKUKWERAKTIVPPHYTDSKRVQKPALAPPSKWIL ELGSYSLIGBKLWMERAKTIVPPHYTDSKRVQKPALAPPSKWIL ELGSYSLIGBKLWMERAKTIVPPHYTDSKRVQKPALAPPSKWIL ELGSYSLIGBKLWMERAKTIVPPHYTDSKRVQKPALAPPSKWIL ELGSYSLIGBKLWMERAKTIVPPHYTDSKRVQKPALAPPSKWIL ELGSYSLIGBKLWMERAKTIVPPHYTDSKRVQKPALAPPSKWIL ELGSYSLIGBKLWMERAKTIVPPHYTDSKRVQKPALAPPSKWIL ELGSYSLIGBKLWMERAKTIVPPHYTDSKRVQKPALAPPSKWIL ELGSYSLIGBKLWMERAKTIVPPHYTDSKRVQKPALAPPSKWIL ELGSYSLIGBKLWMERAKTIVPPHYTDSKRVQKPALAPPSKWIL ELGSYSLIGBKLWMERAKTIVPHYTDSKLKGQOEBEBLLKATIFLF CEPGCHEWASLTRYPRETTSFVLINVOGSKRLGGCREALLFATIFLF CEPGCHEWASLTRYPRETTSFVLINVOGSKRLGGCRELLKATIFLF CEPGCHEWASLTRYPRETTSFVLINVOGSKRLGGCRELLLKATIFLF CEPGCHEWASLTRYPRETTSFVLINVOGSKRLGGCRELLLFATIFLF PSWARTTIVPVPRSLLATATVCCPTFFWGVQMRPQGEVMDSPMZ EVLLVNLCBGTFFLMSVGDEKDILPPKLQDDILDSLGGCINELKT ARQUEHHGGFFQFVGFVKIVGGVGAFASYLRRBANGGGHFGERSFCK ARTJSKTNRRFFVKKFVKTOLFJFSFFLGBARKSKNPAGYFQCYCQKLLE YBBQKKQ/TETKGKNCEIRAVVNRND VARGEGGDQETNTLVANTSNSNGLKLDPADFEMPRSGDTVEV		1		DTTHLSVDVSSPDLFGS IHEDPSLTSEQRLLIVLSNCCYLERHT
6829  1 782 MRKEASENHAULTCPQARSSTMAKE  KPKSSMHAULTCPQARSSTMAKE  RYKSSHHAULTCPQARSSTMAKE  RYKSSHHAULTCPQARSSTMAKE  RYKSSHHAULTCPQARSSTMAKE  RYKSSHHAULTCPQARSSTMAKE  RYKSPLSRLCQEBLQSDRDETGAYLIDRDPTYPGPTLINFLERI  RYKPGRAUPAYLACQGEBLAGWOSTMSDGWRPGLUNIGSSYNYGSED  QARPICVUSKEHLISTPNICLSGESKTKSTEGLBEGEOQQBBEV  EBVEVEQVQVEADAQEK/CCYKPEAPGCEAPDHLQGLGVPI  RYKPPELADPDTCYGFPFCHQLDFSTGGALCVALIKEGOQGBEV  RYKPPELADPDTCYGFPFCHQLDFSTGGALCVALIKARAGSAYR  CPKERRVTKAYLALLRGHIQRSRVTISHAIGRNSTEGRAHTMCI  BGSQCCENPKPSLIDLVVLEHIGLYAGDVSKAKETLITLQKQL  RYLFGSLADPDTCYGFPFCHQLDFSTGGALCVALIKARAGSAYR  CPKERRVTKAYLALLRGHIQRSRVTISHAIGRNSTEGRAHTMCI  BGSQCCENPKPSLIDLVVLEHIGLYAGDVSKVLLKPLITGRTHQL  RVHCSALGHEVVGOLTYGBVSGREDRPFRMMLHAFYLRIPTDT  ECCEVCTTPPFIPSIDACMSPHTLLQSLOQLVQALRATTPDPDFE  DRCPRPGSPSALLPGPGRPPPPPTKPPETBAQRGPCLGWLSEWT  LEPDS  1087 SLFFGSSTPDMKVAEQEDLETQPSPSVEKAVTVIDPESTIPTNP  NVBKRKARHSLSEVKLKTADEPBRGTLVKSCDGGNVKEKSMILSH  VEDLQQPKFISEVSREDYGKKEISGDSERMINSVVTSADGENL  EQSYSLIGHKLVMEERKTIVPPHVTIDKVRDAPADPSKWNI  SIEKEBPRBDQRQKSLLSFDVVDKVPQOPRSASSNFASKNITKE  SEKPPSILLPVERSKGSLIDPSBORLKKRMONVTSALGENL  LRSVSPTEKKDMLENR\SYTL\ABKKULBEKONVVAPLELEDS  NEIGKTQITILGSRSTELKKESKADANPQHFYQREDVNREPKIIVV  SEKEKDBKKKK   MGGGLISGPPQDNSGBALKEPBRAQEHSLPNPAGGGHFFEYILD  VSLKKKRSEDDYBFIITYQPPKRENLLRGQGEBERLLKAIPLP  CPPDGMEMASLTEVPRSTFSFVLINVDGSRKIGYCRRLLPAGOG  PRILKVYCLISGIGGFGLASTLTDAUGSRRNITYPPMGGUNTPFSSL  LHCLSFEQILQIPASAVLRKXIIFLAEGLSTILGCHAAAALLY  PFSMAITYIPVPBEJLATVCCPTPPWGGNFQQGWNDSFMS  EVLLVMLCSGTFRIMSVGDEKOLLPPRWGGNFQQGWNDSFMS  EVLLVMLCSGTFRIMSVGDEKOLLPPRWGGNFQQGWNDSFMS  EVLLVMLCSGTFRIMSVGDEKOLLPPRWGGNFQQGWNDSFMS  EVLLVMLCSGTFRIMSVGDEKOLLPPRRAGGGHFFRSSDIN  VARGEGGDDQFTTTLVANTSNNGLKLDPADPERPRAGTYQCKLLE  YBRQKKQ/TETRIGNCSIRAVVKNND  PLWTLSQCGGTFGHGHSHGGHCHGRLPKGFPGSSDIN  VARGEGGBDGCETNTLVANTSNNGLKLDPADPERPRAGGDTVEV		Ť .		PLNIAEHFEKHNEGIEKITOVSMASLKELDORLFENYIELKAD
ICALRDTVAVYITPESKSSFRQALEALPQLSSGADKKLLRELLN KFKSSMHLQLITCPQAASSTMMKT  MRHEAGEAAPPAGAGGRAAGGWGWWLINVGGTVFLTTRQTLCR BQKSFLSHLCQGBELASDRDETGAYLLDRDPTYPGPLINFLHG KLVULNDMABBGVLEEABFYNIGPLINI IKDRMEEKDYTVTQVP PHHVYRVLQCGBELASDRDETGAYLLDRDPTYFGPLINFLHG KLVULNDMABBGVLEEABFYNIGPLINI IKDRMEEKDYTVTQVP PHHVYRVLQCGBELASDRDETGAYLLDRDPTYFGPLINFLHG KLVULNDMABBGVLEEABFYNIGDLINI IKDRMEEKDYTVTQVP PHHVYRVLQCQBEBLTQMVSTMSDGWRFEQLWNIGSSTNYGSED QABFLCVUVSKELHSTPNGLSSESSKITKSTERGLEBOQQOBEBV EBVSVEQVQVBADAQEK/CCYKPEAPGCEAPDHLQGLGVPI  6830  1 939 MERGSVENISIVYRSRBFLVVNIKHWDVRIDSKAWRETLITLQKQL RYNFPBLADPDTCYGFFFCHQLDFSTSGALCVALNKAAAGSAYR CYKERRVTKAYLALKGKIQESEVTI SHALGGRISFGRAHTMCI BGSQCENPKPSLTDLVVLEHIGLYAGDFVSKVLLKPLTGRTHQL RV\HCSALGHFVVGDLTYGBVSGREDRFFWHHAFYLRI PTDT ECVEVCTPDPFLPSLDAACNSPHTLAGATPDPDFB DRGPRPGSPSALLPGPGRPPPPTKPPBTEAQRGPCLQWLSEWT LEPDS SLFPGSSTDDMKVAEQRDLETQPSPSVEKAVTVIDPEGTIPTNP NVAEKPADHSLSEVKLKTADEPRGTLVKSCDGONVERKSMILSN VEDLQQPKFISEVSREDYGKKGISGDSEEMINSVYTSADGENL ELQSYSLIGHKLWWEBARTIVPPHVTDSKRVQEPALAPPSKNNI SIFKEEPRSDQKQKSLLSFDVVDKVPQQPRSASSMFASKNITKE SEKKPESILLPVESKGSLIDFSEDRLKKRPQNPTSLKISEEETK LESVSSTTEKKDNLERR\SYTL\ARKKVLAEKQNDYTSLKISEEETK LESVSSTTEKKDNLERR\SYTL\ARKKVLAEKQNDYTSLKISEETK LESVSSTTEKKDNLERR\SYTL\ARKKVLAEKQNDYTSLKISEETK LESVSSTTEKKDNLERR\SYTL\ARKKVLAEKQNDYNAERPKIIVG SEKKEKDEKKK MSGLISGPPQDNGGBALKEPPERAGEHSLPNFAGGGHFFEYLLV VSLKKKRSEDDYEPITTYQPPKRENLLAGQGSEERRLLKATPLF CPPDGNEWASLTEYPRETFSFVLTNVGSRKIGYCRILLPAGFG RRAAPPAGKTVTLKSFIPDSGTKFISLTEDLSHLEHUDFSSL LHCLSFEQILQIFASAULRKIIFLAGGGTSEERLLKATPLF PENARTYIPVVPBSLLATVCCPTPWUGUNGFRQGEMDFSKL LHCLSFEQILQIFASAULRKIIFLAGGISTLSQCIHAAAALLY PSWARTYIPVVPBSLLATVCCPTPWUGUNGFRQGENGKH EVLLVNLCEGTFMSVGDEKDILPPKLQDLILDSIGGGINEKT ARQINEHVSGPFPVQFFVKIVGTNSKSKMPPAGYFTQKLLE YBBQKKQ/TETRIGNCSIRAVVNNDD PLWTLSQCGGTPGHGHSHGGHCHGLPKGPFGSSDTNEV VARGEGGDDGETTTLVAMTSDNGLKKLDPADPERPRSGDTVEV				PIVGSLEPGIYAGYFDWKDCLPPTGVRNYLKBALVNIIAVHAKV
KFKSSMHIQLITCRQAASSTMMTT    MRMEAGEARPPAGAGGRAAGGWGKWRINVGGTVFLTTRQTLCR   BQKSFLSRLCQGGELQSDRDETGAYLIDRDFTYPGPTLNFLRHG   KLVLJADMABEGVLEEARFYNIGPLIRITKDRMEKGDTVTVJVP    FKHVYRVLQCGEELTQMVSTMSDGWRPEGLVNIGGSYNYGSED    QARFLCVUSKELHSTPNGLSSESSKKTKSTERGLEEQGQEGEEV    GARFLCVUSKELHSTPNGLSSESSKKTKSTERGLEEQGQGEEKV    GARFLCVUSKELHSTPNGLSSESSKKTKSTERGLEEGOQQGEEV    GARFLCVUSKELHSTPNGLSSESSKKTKSTERGLEEGOQQGEEV    GARFLCVUSKELHSTPNGLSSESSKKTKSTERGLEEGOQQGEEV    ERVEVEQVQVEADAGEK/CCYKPRAAGGCAPPHLQGLGVPI    GARGCENPRFSLTDLVVLEHGLGVAGDEVISKAWRETLTLQKQL    RYRFPELADPDTCYGFRFCHQLDFSTSGALCVALNKAAAGSAYR    CFKERRVTKAYLALLEGHLQSEGVTISHALGRNSTEGRAHTMCI    RV\HCSALGHPVVGDLTYGBVSGREDRPFRMMLHAFYLRIPTDT    ECCYEVCTPDFFLPSLDACKSPHTLLQSLQDVQALARTPDTDPB    CCYEVCTPDFFLPSLDACKSPHTLLQSLQDVQALARTPDTDPB    CCYEVCTPDFFLPSLDACKSPHTLLQSLQDVQALARTPDTDPB    CCYEVCTPDFFLPSLDACKSPHTLLQSLQDVQALARTPDTDPB    CCYEVCTPDFFLPSLDACKSPHTLLQSLQDVQALARTPDTDPB    CECYEVCTPDFFLPSLDACKSPHTLLQSLQGGVUNGESMILSSNILSPD   CECYEVCTPDFFLPSLDACKSPHTLAGGGCCGNVKRESMILSNILSPD   CECYEVCTPDFFLPSLDACKSPHTLAGGGCGNVKRESMILSNILSPD   CECYEVCTPDFFLPSLDACKSPHTLAGGGCGNVKRESMILSNILSPD   CECYEVCTPDFFLPSLGACKSPHTLAGGGCGNVKRESMILSSNILTSCHALLSNIL				FTISKELVPRVLSKVIBAVSEBLSRLMQCVSSFSKNGALQARLE
6832 1809 412 MRMEAGEAAPPAGAGGRAAGSWKWRINVGGTVFLTTRQTLCR EQREFISELCQGEELQSDRDETGAYLIDPETYRGP LINFIGHER KLVILDKMABEGU HEEREFYNIGPLIRI I KDRMEEKDTYTVTVP PKHYYRVLQCQEEBLTQMVSTMSDGWRPEQLVNIGGSYNYGSED QARFILCVVSKELHSTPNGLSESSERTKISTEQLBEDQQGEBUY PKHYYRVLQCQEEBLTQMVSTMSDGWRPEQLVNIGGSYNYGSED QARFILCVVSKELHSTPNGLSESSERTKISTEQLBEDQQGEBUY GEWEVSQVQVEADADGEK/CCYKPRAPGCEAPPHLQGLGVPI 6830 1 9339 MEPGSVENISIVYEREDPIJVWKHRDVR TDSKAWRETLTLQKQL RYRFPELADPDTCYGFRFCHQLDFSTSGALCVALNKAAAGSAYR CCYEERRVTKAYLALLRGHIQDESCYTISHAIGRNSTEGRAHTMCI EGSQGCENPRPSLITDLVVLBHGLYAAGDEVSKVLLKPLTGRTHQL RV\\CSALGHPVVGDLTYGBVSGREDTPFRMIHAAFYLR I PTDT ECVEVCTPDFFLPSLDACKSPHTLLQSLDQDVQALRATPDPDPB DRGPRCSSPSALLPGFGRPPPPPTKPPRTEAQRGPCLQWLSEWT LEPDS  8087ESSTALLPGFGRPPPPPTKPPRTEAQRGPCLQWLSEWT LEPDS VEDLQQPKPISEVSREDYGKKEISGDSEBMNINSVYTSADGENL VEDLQQPKPISEVSREDYGKKEISGDSEBMNINSVYTSADGENL SIEKEBPRSDQKQKSILSFDVVDKVPQQPKSASSNFASKNITKE SERVESILIPVEESKGSLLDFSGRIKKEMQNPTSLKISERETK SERVESILIPVEESKGSLLDFSGRIKKEMQNPTSLKISERETK LERSYSTTEKKDIKERN\SYTLABEKKVALDEKKNSV\APLEIDGS NBIGKTQITIGSRSTELKESKADAMPQHFYQNEDYNRRPKIIVG SEKKEDBKKKK SEKPESDDYRPIITTQFFRRENLLARQQEBEBRLLKAIPLF CPPPDGMWASLTEYPRETFSFVILNVDGSRKIGYCRELLPAGPG PRLPKYYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFWQGL REAAPPADGKTYTLKSFI PDSGTRFISITPLDSHLEHUDESSL LHCLSFEQILQIFASAVLRKKILFLABEGLSTLSQCIHAAAALLY PESWARTYIPVYPRESLLATVCCPTPFWGVQMRPQQEVMDSPMS EVLLVNLCGGTFIMSVGDBKDILPFKLQDDILDSLGQGINELKT APQINEHVSGPPVQFFVKIVGHYASYI KREANGQGHPQERSFCK ALTSKTNRRFVKKFVKTQLFSLPTIGEARKSKNPPAGYFQQKILLE YEBQKKQ/TETIGNCETRAVVNKXD PEMTLSQCGGTPGGESHGGHDEKGPRFKSDTVVB				ICALROTVAVYLTPESKSSFKQALKALPQLSSGADKKLLEBLLN
BQKSFLSRLCQGEELQSDRDETGAYLIDRDPTYPGPILNFLRHG KLVLJNKNABEGVLEEABFYNIGPLIRI IKDRMEKKDYTVTQVP PHRVYRVQCQDEBLTJOWNSTNSDGWRFGQLVNIGSSYNYGSED QAEFLCVVSKELHSTPNGLSSESSRKTKSTEEQLEEQQQQBEEV ERVEVSQVQVEADAGEK/CYKPRAFGCEAPDHLQGLGVPI  6830 1 939 MENGSVENISIVYESEDFLVWKHEVDVRIDSKAMETUTLQKQL RYRFPELADPDTCYGFRFCHQLDFSTSGALCVALNKAAAGSAYR CFRERRVTKAYLALLEGHLQRSGRVTISHAIGRNSTEGRAHTMCI RSQGCCHNRFPSLTDLVVLBEHGLYAGDPVSKVLLAFLTGRTHQL RV\HCSALGHPVVGDLTYGBVSGREDRPFRMMLHAFYLRIPTDT ECVEVCTPPPFLPSLDACKSPHTLLQSLQDLQVQALRATPDPDPB DROPRFCSFPSALLPGPGRPPPPPTKPPBTEAQRGPCLQWLSEWT LEPDS  6831 3 1067 SLFFGSSTFDNKVAEQRDLETQPSFSVEKAVTVIDPEGTIPTNF VVNBKADHSLSEVKLKTADBPRGTLVKSGGGQNVKRKSMILSN VKDLQQPKFISEVSREDYGKKBISGDSEBRNINSVVTSADGENL ELQSYSLIGBKLVMERAKTIVPPHYTDSKRQKPALAPSKNNITKE SKEPESILPVBESKGSLLDFSGRUKKEMQNPYSLKLSEBETK LRSVSFTRKKDMLERN\SYTL\ARKKVLAEKQNSV\APLEILEDS NBIGKTQITLGSRSTRLKESKADANPQHFYQNEDYNERPKIIVG SEKRKDBKKKK VSLKKKRSEDDYRPIITYQPPKRENLLRGQCGEBERLLKAIPLF VSLKKKRSEDDYRPIITYQPPKRENLLRGQCGEBERLLKAIPLF PRIPKVYCIISCIGCFGLFSKLLDRVBKRHQISMAVIYPPMGGL RBAAFPAGKTYTLKSFIPDGTHEFTVLITVDGSRKIGTCRRLLPAGFG PRIPKVYCIISCIGCFGLFSKLLDRVBKRHQISMAVIYPPMGGL RBAAFPAGKTYTLKSFIPDGTHEFTSQCIHAAAALLY PFSWAHTYIPVVPBSLLATVCCPTPFMVGVQMRPQQEVMDSPME EVLLVNLCGSTFLMSVGDEKDLLPFKCJQLIDLBSLGQGLINELKT ARQIMENVGGPPVQFVKIVGHYASYIKRENGGHHFGERSFCK ALTSKTNRRFVKKFVKTQLFSFIJQEAEKSKNPPAGYFQQKLLE YBBQKKQ/TETKGRNCEIRAVVNKND PRIMTLSQCGGIFGRHSHGGHGHCKJPKGPRVKSTRPGSSDIN VARGEQGPDQEETNTLVANTSNSNGLKLDPADPENPRSGDITVEV				KFKSSMHLQLTCFQAASSTMMKT
KEVLDKDMABBGVLEEABFYNIGPLIRIIKDRMERKDYTVTQVP PRHVYRVLQCQEELIGTMOSTMSDGWRFQLVNIGSSTNYGSED QABFLCVVSRELHSTPRGLSSESSRKTKTSTEGLEEQQQGEBV EBVEVBQVQVEADAQEK/CCYKPRAPGCEAPDHLQGLGVPI 6830 1 939 MEPGSVENISIVYRSEDFLVVNIKUMDVIDSKAWRETLTLQKQL RYRPPELADPDTCYFFFCIQLDFSTSGALCVALNKAAAGSAYR CPKERRVTKAYLALLRGHIQESRVTISHAIGRNSTEGRAHTMCI BEGGGCENFKPSLITDLVVLEHIGLVAGDPVSKVLLKPLTGRTHQL RV\HCSALGHPVVGDLTYGERECDFVSKVLLKPLTGRTHQL BEGGGCENFKPSLITDLVLEHIGLVAGDPVSKVLLKPLTGRTHQL RV\HCSALGHPVVGDLTYGERECDFVSKVLKLTAFDPDPE DRGPRESSBALLPGGRPPPPPTKRPETBRQRGPCLQWLSEWT LEPDS  6831 3 1087 SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF NVABKPADISLSSVKLKTADEPRGTILVKSCDGQMVKEKSMILSFD VEDLQQPKFISEVGRBDYGKEISGDBERMINSVVTSADCENL ELQSYSLIGEKLVMEBAKTIVPPHVTDSKRVQKPSALAPPSKWNI SIFKEBFRBDQKQKSILISFDVVDKVYQDFSASSNFASKNITKE SEKPESIILPVESKGSLIJDFSBDRLKKRMONPTSLKISEBETK LRSVSPTEKKDNLENR\SYTL\ABKKVLAEKQNSV\APLELRDS NEIGKTQITIGSRSTBLKSSKADAMPQHFYQNEDYNERPKKIVG SEKRKDEKKKK  6832 1809 412 MGSGLISGPPQDNSGBALKEPERAQEHSLPNPAGGQHFFEYLLV VSLKKKRSEDDYRFIITYQFPRRENLLRGQCEBEBRLLKAIPLF CPPDGMEMASLTFYPRETFSFVLINVDGSKRIGYCRILLPRAGG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPPMQGL REAAFPAPGKTVTLKSFIPDSGTFFISITRPLDSHLEHUDFSSL LHCLSFEQILQI FASAVLEKFITLFLAGGCIFTSJGCTHAAAALLY PFSWANTYIPVVPESILATVCCPTPFMVGVQMRPQQEVMDSPME EVLLVVALGGTFFLMSVGDEKDILPPKLQDDILDSLGGGINSLKT ARQINENVSGPPVQFFVKITJASSITLFLAGGLIFTSJGCTHAAAALLY PFSWANTYIPVVPESILATVCCPTPFMVGVQMRPQQEVMDSPME EVLLVVALGGTFFLMSVGDEKDILPPKLQDDILDSLGGSIFCSFGC ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE VERQKKQ/TETKGKNCEIRAVVMKND FIMTLSQCGGIPGHSHGGHGHGFPVKSTRPGSSDIN VARGEGCGPPQEFTNTLVANYTSNSNGKLLDPADPENPRSGDTVEN	6829	1	782	MRMRAGEAAPPAGAGGRAAGGNGKWVRLNVGGTVFLTTRQTLCR
PKHYYRULQCQEBELTQMVSTMSDGWRFEQLVNIGSSYNYGSED QABFILCVUSKELHSTENGLSSESSKKTSTEGCLBEQOQGBEBY GABFILCVUSKELHSTENGLSSESSKKTSTEGCLBEQOQGBEBY 6830  1 939 MEPGSVENLSIVYRSRDFLVVNKHWDVRIDSKAWRETLTLQKQL RYRFPELADPDTCYGFFFCGQLDFSTGALCVALNKAAAGSAYR RYRFPELADPDTCYGFFFCGQLDFSTGALCVALNKAAAGSAYR RYRFPELADPDTCYGFFFCGQLDFSTGALCVALNKAAAGSAYR RYHCSALGHPVVGDLTYGBVSGREDRPFRWMLHAFYLRIPTDT ECYEVCTPDPFLPSLDACNSPHTLLQSLOQLVQALRATPDPDPB DRGPRPGSPSALLPGBURGPPPPFTKPPETBAQRGPCLQWLSEWT LBPDS  5 LFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF NVABKPADHSLSSVKLKTADBPRGTLVKSCDGOMVKEKSMILSN VEDLQQPKFISEVGREDYGKKEIGGDBERNINSVYTGADGENL ELQSYSLIGEKLVMEBAKTIVPPHVTDSKRVQKPALAPPSKWNI SIFKEBPRBDQKQKSILISFDVVDKVPQQPKSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSBDRLKKEMQNPTSLKISEBETK LRSVSFTEKKDMLENR\SYTL\ABKKLVAEKQNSV\APLELRDS NBIGKTQITIGSSSTRLKESKADAMPQHFYQNEDYNREPKIIVG SEKRKDEKKKK  6832 1809 412 MGSGLISGPPQDNEGBALKEPRAQEHSLPNFAGGQHFFSYLLV VSLKKRSEDDYBFITTYQPPRRENLLAGQQEBBERLIKAIPLF CPPDGNEWASLTTSYPRETFSFVLINVDGSKKIGYGRILLPAGPG PRIPKYVCIISCIGCGLFSKILDBVKKRIQISMAVIYPPMQGL RBAAFPAPGKTVTLKSPIPDSTKEISTFLSHLELDSHLEHVDFSSL LHCLSFEQILQIFASAVLKRKIIFLABGLSTLSQCIHAAAALLY PFSWAHTYLPVVPBSILATVCCPPPFWGVQMRPQQEVMDSPM2 EVILVVNLEBSTFIMSVGDEKDILPPKLQDDILDSIGQGINEKK RBAAFPAPGKTVTLKSPIPDSTLSTRPLDSHLEHVDFSSL LHCLSSTPILMSVGDEKDILPPKLQDDILDSIGGGINCK RBAFPAPGFKVVTLKSPIPGBAEKSKNPPAGYFQQKILE PEWAHTYLPVVBGSILATVCCPPPFWGVQMRPQGEMDSPM2 EVILVNLESGTFIRMSVGDEKDILPPKLQDDILDSIGGGINCKT ABQINEHVSGPPVGFFVKLVGHVASYIKREANGGGHPQESFCK ALTSKTNRFVKKFVKTQLFSLPIQBAEKSKNPPAGYFQQKILE VBEQKKQ/TETRISKNCEIRAVVAKND VAPGEQGPDQETNTLVANYISNGKLKLDPADPENPRSGDTVEV			'	BOKSFLSRLCQGEELQSDRDETGAYLIDRDPTYFGPILNFLRHG
GAEFLCVUSKELHSTPNGLSSESSRKTKSTEEQLEEQOQQBEEV EBYEVEVQVQVADAQEK/CCXKPRAPGCEAPPHLLQGLGVET  6830  1 939 MEPGSVENLS LVYRSEDPLVVNKHWDVR TOSKANWETTLTQKQC RYRFPELADPDTCYGFRFCHQLDFSTSGALCVALNKAAAGSAYR CPKERRVTKAYLALLRGHIQPSRVTISHAIGRNSTEGRAHTMCI EGSQGCENPKPSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHQL RV\HCSALGHPVVDDLTYGEVSGREDRPFRMMLHAFYLRIPTDT ECVEVCTPDPFLPSLDACNSPHTLLQSLDQLVQALRATPDPDPB DRGPRCSPSALLPGPGRPPPPPTRPBTEAQRGPCLQWLSEWT LEPDS  6831 3 1087 SLFFGSSTPDNKVAEQRDLETQPSPSVEKAVTVIDPEGTIPTNP NVABKPADHSLSEVKLKTADEPGRTLVKSGDGGNVKEKSMILSN VEDLQQPKPISEVSREDYGKKEISGDSERNINSVVTSADGENL ELQSYSLIGKKLWMERAKTIVPPHYTDSKRVQEPALAPPSKMIL SIFKEBPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SEKPESILLPVEESKGSLIDFSBORLKKEMQNPTSLKISEETK LERSVSTEKKDNLENR\SYTL\ABKKVLAEKQNSV\APLELRDS NBIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKRKDEKKKK  MCSGLISGPPQDNSGKALKEPERAQEHSLPNPAGGQHFFKYLLV VSLKKKRSEDDYSPIITYQPFRRENLLAGQQEEBERLLKAIPLF CPPDGMEWASLTRVYRSTFSFVLTNVDGSRKIGYCRLLPRAGG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPPMQGL RRAAPPAPGKTVTLKSFIPDSGTKFISLTRPLDSHLEHUDFSSL LHCLSFEQILQIPASAVLERKIIFLAEGLSTLSQCIHAAAALLY PESWAHTYIPVVPRSILATVCCPTFFMVGVQMRPQQEVMDSPMZ EVLLVNLCEGTFILMSVGDEKDILPPKLQDDILDSLGQGINELKT ABQIMEHVSGPFVQFFVKLVGHYASYIKRBANGQGHFQESSFCK ALTSKTNRRFVKKPVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YERQKKQ/TETKGRNCSIRAVVNKND  6833 1 1129 PIMILSQCGGIPGHGHSHGGHCHCHELPRGPRVKSTRPGSSDIN VAPGEGGPDQEETNTLVANTSNSNGLKLDPADPBRPRSGDTVEV				KLVLOKDMAREGVLEEARFYNIGPLIRIIKDRMERKDYTVTQVP
6830 1 939 MBPGSVENLSIVYESRDFLVVNKHUDVRIDSKAMETLITLIQKOL RYRPPELADPDTCYGFFPCHQLDFSTSGALCVALNKAAGSAYR CPKERRVTKAYLALLEGHIQESRVTISHAIGRNSTEGRAHTMCI BGSQGCENPRPSLTDLVVLBHGLYYAGDPVSKVLLKFLTGRTHQL RV\HCSALGHPVVGDLTYGBVSGREDRPFRMILHAFYLRIPTDT ECVEVCTPDFFLPSLDACNSPHTLLQSLDQLVQALRATPDPDPB DRGPRPGSPSALLPGPGRPPPPPTKPPTEAQRGPCLQWLSEWT LEPDS  6831 3 1087 SLFFGSSTPDNKVAEQKDLETQPSPSVEKAVTVIDPEGTIPTNF NVABKPADHSLSEVKLKTADBPRGTLVKSCDGQNVKEKSMILSN VEDLQQPKFISEVSREDYGKKEISGDSERMINSVYTSADGENL EIQSYSLIGBKLVMEEBARTIVPPHTDSKRYQKPALAPPSKWNI SIFKEBPRSDQKQKSLLSFDVVDKVPQQPRSASSNFASKNITKE SEKPESIILPVEBSKGSLIDFSEDRLKKEMQNFFISKISREETK LRSVSPTEKKDNILENR\SYTL\ABKKVLAEKQNSV\APLELRDS NEIGKTQITLGSRSTELKESKADAPQHFYQNEDYMERPKXIVG SEKRKDBKKKK  6832 1809 412 MGSGLISGPDQDNSGBALKEPERAGEHSLPNFAGGQHFFEYLLV CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKHQISMAVIYPFMGGL REAAPPAPGTVTLKSPIPDSGTERISLTSQCHAAAALLY PESWAHTYIPVVPRSILATVCCPTFFMVGVQMRPQGEVMDSPM2 EVLLVNLCBGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT ARQINEHVSGPFVQFFVKIVGHYASYIRREANGQGHFQESSFCK ALTSKTNRRFVKKFVKTQLFSLPIQEARKSKNPPAGYFQQKILE VERQKKQ/TETKGRNCSIRAVVNKND  6B33 1 1129 PIMTLSQCGGTPGHGHSHGGGHCHGLDEKGPRVKSTRPGSSDTN				PKHVYRVLQCQEEBLTQMVSTMSDGWRFEQLVNIGSSYNYGSED
6830 1 939 MEPGSVENLSIVYRSRDFLVVNKHWDVRIDSKAWRETLTLQKQL RYRFPELADPDTCYGFRFCHQLDFSTSGALCVALNKAAAGSAYR CPKERRVTKAYLALLRGHI QBSRVTISHAIGRNSTEGRAHTMCI BGSQGCENPRESLTDLVVLEHIGLYAGDFVSKVLLKFLITGRTHQL RV\HCSALGRPVVGDLTYGGVSGREDRPFRMIHAFYLRIPTDT ECVEVCTFDPFLPSLDACNSPHTLLQSLDQLVQALRATPDDPDEP DRGPRPGSPSALLPGFGRPPPPPTKPPETRAQRGPCLQWLSEWT LEPDS  6831 3 1087 SLFFGSSTPDNKVAEQBDLETQFSPSVEKAVTVIDPEGTIPTNF NVABKPADHSLSEVKLKTADBPRGTLVKSGDGQNVKEKSMILSN VEDLQQPKFISEVSREDYGKKEISGDSERMINSVVTSADGENL EIQSYSLIGBKLVMERAKTIVPPHVTDSKRVQKPAATAPPSKWNI SIFKEBPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE ERSYSPTEKKDNLENR\SYTL\ABKKVLAEKQNSV\APLELRDS NBIGKTQITILGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKRKDEKKK  MGSGLISGPPQDNGGGALKEPERAQEHSLENPAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRQQCEBEERLLKAIPLF CPPDGMEWASLITEYFRETFSFVLINVDGSRRIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPPMQGL RRAAFPAPGKTVTLKSFIPDSGTRFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLBRKIIFLAEGLSTLSQCIHAAAALLY PPSWAHTYIPVVPSSLLATVCCTPFFWVGVQMRPQQEVMDSPMZ LHCLSFEQILQIFASAVLBRKIIFLAEGLSTLSQCIHAAAALLY PPSWAHTYIPVVPSSLLATVCCTPFFWVGVQMRPQQEVMDSPMZ EVLLVNLCBGTFLMSVGDEKDILPPKLQDDLIDSIGQGINELKT ABQINBHVSGPFVQFFVKIVGHYASYIKRBANGQHFPQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE VBEQKKQ/TETKGNCBIRGVHKGDFKGFRVKSTRPGSSDIN VAPGEGCPDQETMTLVANTSNSNGLKLDPADPENPRSGDTVEV		1		QARFI_CVVSKELHSTPNGLSSESSRKTKSTEEQLEEQQQQEEEV
RYRFPELADPDTCYGFRFCHQLDFSTSGALCVALNKAAAGSAYR CREERRYTKAYLALLRGHIQESSTGGARITMCI EGSQGCENPKPSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHQL RV\HCSALGHBVVGDLTYGBVSGREDRPFRMMLHAFYLRI PTDT ECVEVCTPDPFLPSLDACNSPHTLLQSLDQLVQALRATPDPDPB DRGPRGSPSALLPGPGRPPPPPTKPPETRAQRGPCLQWLSEWT LEPDS  5LFPGSSTPDNKVAEQRDLETQPSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVKLKTADBPRGTLVKSGDGQNVKEKSMILSN VEDLQQPKPISEVSREDYGKKSIIGDBERMNINSVYTSADGENL EIQSYSLIGBKLVMBEAKTIVPPHVTDSKRVQKPALAPPSKWNI SIFKEBPRSDQKQKSILSFDVVDKVPQQPKSASSMFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEBETK LKSVSPTEKKDNILENR\SYTL\ABKKVLAEKQNSV\APLELRDS NEIGKTQITIGSRSTELKEKSKADAMPQHFYQNEDYNERPKIIVG SEKRKDSKKKK  6832  1809  412  MGSGLISGPPQDNSGBALKEPERAQEHSLPNPAGGQHFPEYLLV VSLKKKRSEDDYBPIITYQFPRENLLRGQGEBEBRLLKAIPLF CPPPGREWASLTEYPRETFFFVIINVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVKKHQISMAVIYPPMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCTHAAAALLY PPSWAHTYIPVVPESLLATVCPTPFMVGVQMRPQQEVMDSPMS EVILVWILGEGTFLMSVGDEKDLIPPKLQDDLIDSLAGQGINELKT AEQINBHVSGPPVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE VERQKKQ/TETKGKNCEIRAVVKND  6833  1 1129 PIMTLSQCGGIPGHGHSHGGHCKGHGLPKGFRVKSTRPGSSDIN VAPGRQCPDQERTNTLVANTSNSNGLKLDPADPENPRSGDTVEV			ļ .	EBVEVEQVQVEADAQEK/CCYKPBAPGCEAPDHLQGLGVPI
CPKERRVTKAYLALLRGHIQESRVTISHAIGRNSTEGRAHTMCI BGSQGCENPKPSIJTDLVVLLERIGILYAGDPVSKVLLKPLTGRTHQL RV\HCSALGHPVVGGUTYGEVSGREDRPFRMMLHAFYLRIPTDT ECVEVCTPDPFLPSLDACNSPHTLLQSLQQLVQALRATPDPDPB DRGPRPGSPSALLPGPGRPPPPPTKPPETAQRGPCLQWLSEWT LSPDS  1087 SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGQNVKEKSMILSN VEDLQQPKPISEVSREDYGKKEISGDSERNINSVVTSADGENL ELQSYSLIGEKLVMEEAKTIVPPHYTDSKRVQKPAIAPPSKWNI SIFKEBPSDQRQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEEETK LRSVSPTRKKDNLENR\SYTL\ABKKVLABKONSV\APLELRDS NEIGKTQITLGSRSTELKESKADANPQHPYQNEDYNERPKIIVG SEKEKDEKKKK  6832 1809 412 MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFPEYLLV VSLKKKRSEDDYEPIITYQPFPKRENLLRGQGEBEBELLKAIPLF CPPGGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGFG PRLPKVYCIISCIGCTGFLFSKILDBVEKRNQISMAVIYPPMQGL REAAFPAPGKTVTLKSPIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFRQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESILATVCCPTFPMVGVQMRPQQEVMDSPM2 EULLVNLCGGTFLANGVGDEKDILPPKLQDDILDSLGQGINELKT AEQINBHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQGAEKSKNPPAGYFQQKILE VEGKKQ/TETKGKNCEIRAVVNKND VAPGEGGPDZETTNTLVANTSNSGLKLDPADPENPRSGDTVEV	6830	1	939	MEPGSVENLSIVYRSRDFLVVNKHWDVRIDSKAWRETLTLQKQL
EGSQGCENPKPSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHQL RV\HCSALGHPVGDLTYGEVSGREDRPFRMMLHAFYLRIPTDT ECVEVCTPDPFLPSLDACNSPHTLLQSLDQLVQALRATPDPDPD BRGPRPGSPSALLPGPGRPPPPPTKPPETBAQRGPCLQWLSEWT LEPDS  1067 SLFFGSSTPDMKVAEQEDLETQPSPSVEKAVTVTDPEGTIPTNF NVABKPADHSLSEVKLKTADEPRGTLVKSGDGQNVKEKSMILSN VKDLQQPKP1SEVSREDYGKKEISGDSERNNINSVVTSADGENL ELQSYSLIGBKLVMEBAKTIVPPHVTDSKRVQKPALAPPSKWNI SIFKEEPRSDQKQKSILLSFDVVDKVPQQPKSASSNFASKNITKE SKKPESILLPVEESKGSLIDFSEDRLKKEMQNPTSLKISEBETK LRSVSPTBKKDMLENR\SYTL\ABKKVLAEKQNSV\APLELRDS NRIGKTQITLGSRSTBLKESKADANPQHFYQNEDYNERPKIIVG SEKRKDEKKKK  6832 1809 412 MGSGLISGPPQDNSGGBALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYRPIITYQPPKRENLLRQQGEBERLLKAIPLF CPPDGMEWASITEVPRETFSFVLINVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTRFISLTRPLDSHLEHUDFSSL LHCLSFEQILQIFASAVLKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGQWRFQQEVMDSPM2 EVLLVMLCBGTPLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINBHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFTQGEAEKSKNPPAGYFQQKILE VBEQKKQ/TETKGKNCEIRAVVNKND VAPGEGGPDQERTNTLVANTSNSNGLKLDPADPENPRSGDTVEV				RYRFPELADPDTCYGFRFCHQLDFSTSGALCVALNKAAAGSAYR
RV\HCSALGHPVVGDLTYGBVSGREDRPFRMMLHAFYLRIPTDT ECVEVCTPDPFLPSLDACNSPHTLLQSLDQLVQALRATPDPDPB DRGPRPGSPSALLPGPGRPPPPPTKPPBTEAQRGPCLQWLSEWT LEPDS  6831 3 1087 SLFFGSSTPDMKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVKLKTADBPRGTLVKSGDGQNVKEKSMILSN VEDLQQPKPISEVGREDYGKKBISGDSERMINSVVTSADGENL EIQSYSLIGHKLVMEBAKTIVPPHVTDSKRVQKPALAPPSKWNI SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SKKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEETK LRSVSPTEKKDMLENR\SYTL\ABKKVLAEKQNSV\APLELRDS NBIGKTQITIGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKKEBKKKK MGSGLISGPPQDNSGBALKEPERAQEHSLPNPFAGGQHFFEYLLV VSLKKKESEDDYEPIITYQFPKRENLLRGQQEBEBRLLKAIPLF CFPDGNEWASLTEYPRETFSFVLINVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSPIPDSGTKFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGISTLSQCIHAAAALLV PPSWAHTYIPVVPESLLATVCCPTPFMVGQMRFQQEVMDSPM2 EVLLVNLCBGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT ARQINBHVGGPFVQFFVKIVGHYASYIKREANGQGHPQERSFCK ALTSKTNRRFVKKFVKTQHTASYIKREANGQGHPQERSFCK ALTSKTNRRFVKKFVKTPUTGLFSLFIQEAKKSKNPPAGYPQQKILE YEEQKKQ/TETKKKNCEIRAVVNKND  6833 1 1129 PLMTLSQCGGTPGHGSSGGHEKGHGDFKGPRVKSTRPGSSDTN VAPGEQGPDQEFTNTLVANTSNSNGLKLDPADPENPRSGDTVEV				CPKERRVTKAYLALLRGHIQESRVTISHAIGRNSTEGRAHTMCI
BCVEVCTPDPFLPSLDACWSPHTLLQSLDQLVQALRATPDPDPB DRGPRPGSPSALLPGPGRPPPPPTKPPBTBAQRGPCLQWISEWT LEPDS  SLFFGSSTPDMKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGOMVKERSMILSN VEDLQQPKPISEVSREDYGKKEISGDSERMINSVVTSADGENL ELQSYSLIGRKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI SIFKEEPPSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SKEPESIILPVEESKGSLIDFSEDRLKKEMQNEYSLKISEEETK LRSVSPTEKKDMLENR\SYTL\AEKKVLAEKQNSV\APLELRDS NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK  6832  1809  412  MGSGLISGPPQDMSGBALKEPERAQEHSLPNPAGGQHFPEYILV VSLKKKRSEDDVEPIITTQFPRRENLLRGQQEREBERLLKAIPLF CPPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPFMQGL RBAAFPAPGKTVTLKSFIPDSGTKFISLTRPLDSHLEHUDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESILATVCCPTPFMVGVQMRFQQEVMDSPMS EVLLVNLCBGTPLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINBHVGGPPVQFFVKIVGHYASYIRREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQCHTASYIRREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQHTASYIRREANGGGHFQERSFCK ALTSKTNRRFVKKFVKTQHTASYIRREANGGGHFQERSFCK ALTSKTNRRFVKKFVKTQHTASYIRREANGGHFQERSFCK ALTSKTNRRFVKKFVKTQHTASYIRREANGGHFQERSFCK ALTSKTNRRFVKKFVKTQHTASYIRREANGGHFQERSFCK ALTSKTNRRFVKKFVKTQHTASYIRREANGGHFQERSFCK ALTSKTNRRFVKKFVKTQHTASYIRREANGGHFQERSFCK ALTSKTNRRFVKKFVKTQHTASYIRREANGGHFQERSFDÜN VAPGEQGFDQEETNTLVANTSNSNGLKLDPADPENPRSGDTVEV				EGSQGCENPKPSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHQL
DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT LEPDS  1087 SLPFGSSTPDMKVAEQRDLETQPSPSVEKAVTVIDPEGTIPTNP NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGONVKEKSMILSN VEDLQQPKPISEVSREDYGKKEISGDSERMINSVVTSADGENL EIQSYSLIGEKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SKKPESIILPVERSKGSLIDFSEDRLKKRMONPTSLKISEERTK LRSVSPTEKKDNLENR\SYTL\ABKKVLAEKONSV\APLELRDS NRIGKTQITLGSRSTKLKESKADANPQHFYQNEDYNERPKIIVG SEKEKDEKKKK  6832 1809 412 MGSGLISGPPQDNSGEALKEPERAQEHSLPNPAGGQHFPEYLLV VSLKKKRSEDDYBPIITYQFPKRENILRGQQEBEBERLLKAIPLF CPPDGNBMASLTBYPRBTTSFVLINVDGSKRIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRRQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTKFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLEKKIIFLABGLSTLSQCHAAAALLY PFSWAHTYIPVVPBSLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCBGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT ABQINBHVSGPFVQFFVKLVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQKILE VBEQKKQ/TBTKGNNCEIRAVVNKND  6833 1 1129 PLMTLSQCGGIPGHGHSHGGHGKSLPKGFRVKSTRPGSSDIN VAPGEQGPDQERTNTLVANTSNSUGLKLDPADPENPRSGDTVEV		l		RV\HCSALGHPVVGDLTYGEVSGREDRPFRMMLHAFYLRIPTDT
LEPDS  SLFFGSSTPDNKVAEQRDLETQPSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVKLKTADEPRGTILVKSCDGONVKEKSMILEN VEDLQQPKPISEVSREDYGKKEISGDSERMINSVYTSADGENL ETQSYSLIGHKLVMEEAKTIVPPHYTDSKRVQKPAIAPPSKWNI SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEEETK LRSVSPTEKKDNLENR\SYTL\ABKKVLAEKQNSV\APLELRDS NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKRKDEKKKK SEKRKDEKKKK CPPGGNEMASLTEYPRETTSFVLTNYDGSRRIGYCRELLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIPPMGGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCBGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT ABQINEHVSGPFVQFFVKLVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQKILE VEEQKKQ/TETKGNCEIRRAVVNKND  6833 1 1129 PIMTLSQCGGIPGHGHSHGGHGHGHSLPKGSFDTNV		i		ECVEVCTPDPFLPSLDACNSPHTLLQSLDQLVQALRATPDPDPB
6831 3 1087 SLFFGSSTPDNKVAEQRDLETQPSPSVEKAVTVIDPEGTIPTNP NVABKPADHSLSEVKLKTADBPRGTLVKSGDGONVKEKSMILSN VKDLQQPKPISEVSREDYGKKEISGDSERMINSVVTSADGENL EIQSYSLIGBKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI SIFKEEPRSDQKQKSILSFDVVDKVPQQPKSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEEETK LRSVSPTEKKDNLENR\SYTL\ABKKVLAEKQNSV\APLELRDS NBIGKTQITLIGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKBKDBKKKK  6832 1809 412 MGSGLISGPPQDMSGBALKEPERAQEHSLPNPAGGQHFFEYLLV VSLKKKRSEDDYBPIITTQPPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVTYPFMQGL REAAFPAPGKTVTLKSPIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIPASAVLERKIIFLAEGLSTLSQCHHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCBGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT ABQINBHVGGPFVQFFVKLVGHYASYIKRBANGQGHFQERSFCK ALTSKTNRRFVKKFVKTPULFSLFIQEAEKSKNPPAGYFQKLLE YBEQKKQ/TETKGKNCBIRAVVNKND 6833 1 1129 FIMTLSQCGGIPGHSHGGHGHSLPKGPRVKSTRPGSSDIN VAPGEQGPDQERTNTLVANTSNSUGLKLDPADPENPRSGDTVEV		· ·		DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT
NVABKPADHSLSEVKLKTADEPRGTLVKSGDGONVKEKSMILSN VEDLQQPKPISEVSREDYGKKEISGDSERMINSVVTSADGENL ELQSYSLIGEKLVMEEAKTIVPPHYTDSKRVQKPALAPPSKWNI SIFKEEPRSDQKQKKSLLSFDVVDKVPQQPKSASSNFASKNITKE SKKPESIILPVEESKGSLLDFSEDRLKKRMONPTSLKISEEBTK LRSVSPTEKKDNLENR\SYTL\ABKKVLAEKQNSV\APLELRDS NEIGKTQITIGSRSTELKESKADANPQHFYQNEDYNERPKIIVG SEKEKDEKKKK  6832 1809 412 MCSGLISGPPQDNSGEALKEPERAQEHSLPNPAGGQHFFEYLLV VSLKKKRSEDDYRFIITTQFPKRENLLRGQQEBEBRLLKAIPLF CPPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRUDSHLEHVDFSSL LHCLSFEQILQIPASAVLERKIIFLAEGLSTLSQCHAAAALLY PFSWAHTTIPVVPESILATVCCPTFFMVGVQMFPQQEVMDSYM2 EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINBHVGGPFVQFFVKLVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTPUKTQLFSLFJQEAEKSKNPPAGYFQKLLE YEEQKKQ/TETKGKNCEIRAVVNKND 6833 1 1129 FPMTLSQCGGTPGHSHGGHGHSKJPKGFRVKSTRPGSSDIN VAPGEQGPDQEETNTLVANTSNSUGLKLDPADPENPRSGDTVEV		į.		LEPDS
VEDLQQPKPISEVSREDYGKKEISGDSERMNINSVVTSADGENL EIQSYSLIGBKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI SIFKEEPRSDQKQKSILISFDVVDKVPQQPKSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEETK LRSVSPTEKKDNLENR\SYTL\ABKKVLAEKQNSV\APLELRDS NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK  6832 1809 412 MGSGLISGPPQDNGGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYRPIITYQPPKRENILRGQQEEBERLLKAIPLF CFPDGNEWASLTEYPRETPSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPAGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIPASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGGGINELKT AEQINEHVGSPFVQFFVKLVGHYASYIKREANGQGHPQERSFCK ALTSKTNRRFVKKYCTQLFSLFIQEAEKSKNPPAGYFQQKILE YEEQKKQ/TETKGKNCEIRAVVNKND  6833 1 1129 PLMTLSQCGGIPGHGHSHGGHGHSLPKGFRVKSTRPGSSDIN VAPGEQGPDQERTNTLVANTSNSGLKLDPADPENPRSGDTVEV	6831	3	1087	SLFFGSSTPDNKVAEQRDLETQPSPSVEKAVTVIDPEGTIPTNF
VEDLQQPKPISEVSREDYGKKEISGDSERMNINSVVTSADGENL EIQSYSLIGBKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI SIFKEEPRSDQKQKSILISFDVVDKVPQQPKSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEETK LRSVSPTEKKDNLENR\SYTL\ABKKVLAEKQNSV\APLELRDS NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK  6832 1809 412 MGSGLISGPPQDNGGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYRPIITYQPPKRENILRGQQEEBERLLKAIPLF CFPDGNEWASLTEYPRETPSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPAGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIPASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGGGINELKT AEQINEHVGSPFVQFFVKLVGHYASYIKREANGQGHPQERSFCK ALTSKTNRRFVKKYCTQLFSLFIQEAEKSKNPPAGYFQQKILE YEEQKKQ/TETKGKNCEIRAVVNKND  6833 1 1129 PLMTLSQCGGIPGHGHSHGGHGHSLPKGFRVKSTRPGSSDIN VAPGEQGPDQERTNTLVANTSNSGLKLDPADPENPRSGDTVEV				NVABKPADHSLSEVKLKTADBPRGTLVKSGDGONVKEKSMILSN
EIQSYSLIGRKLVMEEAKTIVPPHVTDSKRVQKPATAPPSKWNI SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SEKPESIILIPVEESKGSLIDFSEDRLKKEMONPTSLKISEETK LRSVSPTEKKDNLGERSYSTLLABEKKVLAEKONSV\APIELRDS NBIGKTQITLIGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKRKDEKKKK  6832 1809 412 MGSGLISGPPQDNSGEALKEPERAQEHSLPNPAGGQHFFEYLLV VSLKKKRSEDDYBPIITYQFPKRENILRGQQEBEBERLLKAIPLF CPPDGNBWASLTEYPRETFSFVLINVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPMQGL REAAFPAFGKTVTLKSFIPDSGTRFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT ABQINBHVSGPFVQFFVKLVGHYASYIKREANGQGHFQERSFCK ALTSKTNRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YBEQKKQ/TBTKGNNCEIRAVVNKND 6833 1 1129 PLMTLSQCGGIPGHGHSHGGHGHSLPKGFRVKSTRPGSSDIN VAPGEQGPDQERTNTLVANTSNSGLKLDPADPENPRSGDTVEV		i	1	
SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISERETK LRSVSPTEKKDNILENR\STTL\ABKKVLAEKQNSV\APLELRDS NEIGKTQITLGSRSTELKESKADANPQHFYQNEDYNERPKIIVG SEKRKDEKKKK  6832 1809 412 MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYBPIITYQFPKRENLLRGQQEBEERLLKAIPLF CPPDGNENASLTEYPRETTSFVLITVDGSRRIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRRGJSMAVIPPMQGL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCBGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT ABQINBHVGGPFVQFFVKLVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YEEQKKQ/TETKGKNCEIRAVVNKND  6833 1 1129 PLMTLSQCGGIPGHGHSHGGHGHSLPKGFRVKSTRPGSSDIN VAPGEQGPDQERTNTLVANTSNSUGLKLDPADPENPRSGDTVEV		!	ļ	, <del></del>
SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEEETK LRSVSPTEKKONLENR\SYTL\ABKKVLAEKQNSV\APLELRDS NEIGKTQITLGSRSTELKESKADANPQHFYQNEDYNERPKIIVG SEKRKDEKKKK  6832 1809 412 MCSGLISGPPQDNSGSALKEPERAQEHSLPNPAGGQHFFEYLLV VSLKKKRSEDDYBPIITYQFPKRENLLRGQQEEEERLLKAIPLF CPPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSPIPDSGTFFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLRKXIFLAEGLSTLSQCHHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCBGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT ABQINBHVGGPFVQFFVKLVGHYASYIKRBANGQGHFQERSFCK ALTSKTNRRFVKKFVKTVGLFSLFIQEAEKSKNPPAGYFQQKILE YBEQKKQ/TETKGKNCBIRAVVNKND  6833 1 1129 PLMTLSQCGGIPGHSHGGHGHGHSLPKGFRVKSTRPGSSDIN VAPGEQGPDQERTNTLVANTSNSUGLKLDPADPENPRSGDTVEV				I = ::
LRSVSPTEKKDNLENR\SYTL\ABKKVLAEKQNSV\APLELRDS NBIGKTQITLGSRSTELKESKADANPQHFYQNEDYNERPKIIVG SEKRKDBKKKK  6832 1809 412 MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYBPIITYQPPKRENLLRGQQEBEBERLLKAIPLF CPPDGNEWASLTBYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLBRKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPBSLLATVCCPTPFMVGVQMRPQQEVMDSPME EVILLVNLCBGTFLMSVGDBKDILPPKLQDDILDSLGQGINELKT AEQINBHVSGPPVQFFVKIVGHYASYIKRBANGQGHPQERSFCK ALTSKTNRRFVKKPVKTQLFSLFIQBAEKSKNPPAGYFQQKILE YBEQKKQ/TBIKGKNCBIRAVVNKND  6833 1 1129 PLMTLSQCGGIPGHGSHGGHGHGLPKGPVKSTRPGSSDIN VAPGEQGPDQERTNTLVANTSNSUGLKLDPADPENPRSGDTVEV		ĺ		- · · · · · · · · · · · · · · · · · · ·
NBIGKTQITLGSRSTRLKBSKADAMPQHFYQNEDYNERPKIIVG SEKBKDBKKKK  6832 1809 412 MGSGLISGPPQDMSGBALKEPERAQEHSLPNPAGGQHFFBYLLV VSLKKKBSDDYBPIITYQPPKRENLLRGQQEBEBRLLKAIPLF CPPDGMBWASLTBYPRBTFSFVLINVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVBKRHQISMAVIYPPMQGL RBAAFPAPGKTVTLKSFIPDSGTBFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIPASAVLBRKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPBSLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCBGTFLMSVGDBKDILPPKLQDDILDSLGGGINELKT AEQINBHVGGPFVQFFVKIVGHYASYIKRBANGQGHPQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQBAEKSKNPPAGYFQQKILE YBEQKKQ/TBTKGKNCBIRAVVNKND  6833 1 1129 PLMTLSQCGGIPGHGHSHGGHGHSLPKGPRVKSTRPGSSDIN VAPGEQGPDQBRTNTLVANTSNSGLKLDPADPENPRSGDTVEV		}		
SEKRKDEKKKK  SEKRKDEKKKK  SEKRKDEKKKK  1809  412  MGSGLISGPPQDNSGEALKEPERAQEHSLPNPAGGQHFFEYLLV VSLKKKRSEDDYRPI ITYQFPKRENILRGQQEBEBERLLKAIPLF CPPDGBWASLTBYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCI ISCIGCFGLFSKILDBVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLBRKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPRSLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGGGINELKT AEQINEHVGGPFVQFFVLVGHYASYIKREANGQGHPQERSFCK ALTSKTNRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YBEQKKQ/TBTKGKNCEIRAVVNKND  6833  1 1129  PLMTLSQCGGIPGHGHSHGGHGHSLPKGFVKSTRPGSSDIN VAPGEQGPDQERTNTLVANTSNSUGLKLDPADPENPRSGDTVEV				
6832 1809 412 MGSGLISGPPQDNSGRALKEPERAQEHSLPNPAGGQHFFEYLLV VSLKKKRSEDDYBPITTYQFPKRENLLRGQQEBEERLLKAIPLF CPPDGNEMASLTEYPRETTSFVLITVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPPMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCHHAAAALLY PFSWAHTYIPVVPBSLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCBGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT ABQINBHVSGPFVQFFVKLVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YBEQKKQ/TETKGKNCBIRAVVNKND VAPGEQGPDQEBTNTLVANTSNSGLKLDPADPENPRSGDTVEV	*	1	i	
VSLKKKRSEDDYBPIITYQFPKRENLLRGQQEBEBILLKAIPLF CPPDGNEWASLTBYPRETFSFVLTNVDGSRKIGYCRILLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPFPMQGL REAAFPAPGKTVTLKSPIPDSGTFFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLRKXIFLAEGLSTLSQCHHAAAALLY PFSWAHTYIPVVPRSLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCBGTFLMSVGDBKDILPPKLQDDILDSLGQGINELKT ABQINBHVGGPFVQFFVKLVGHYASYIKRBANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YBEQKKQ/TBTKGKNCBIRAVVNKND FMTLSQCGGIPGHGHSHGGHGHGHSLPKGPRVKSTRPGSSDIN VAPGEQGPDQEBTNTLVANTSNSGLKLDPADPENPRSGDTVEV	6832	1800	472	
CPPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCI ISCIGCFGLFSKILDBVEKRHDISMAVIYPFMQGL REAAFPAFGKTVTLKSFI PDSGTFFISLTRPLDSHLEHVDFSSL LHCLSFEQILQI PASAVLERKI IFLAEGLSTLSQCIHAAAALLY PFSWAHTTIPVVPESILATVCCPTFFMVGVQMRFQQEVMDSPM2 EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINBHVGGPFVQFFVKLVGHYASYIKREANGQGIFPQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKLLE YEEQKKQ/TETKGKNCBIRAVVNKND  6833 1 1129 PLMTLSQCGGIPGHSHGGHGHGHSLPKGFRVKSTRPGSSDIN VAPGEQGPDQEETNTLVANTSNSGLKLDPADPENPRSGDTVEV		1		
PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPPMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIPASAVLERKIIFLAEGLSTLSQCHAAAALLY PFSWAHTTIPVVPESILATVCCPTFFMVGVQMRFQQEVMDSPM2 EVLLVNLEGGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINBHVSGPPVQFFVKLVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YEEQKKQ/TBIKGKNCEIRAVVNKND  1 1129 PIMTLSQCGGTPGHGHSHGGHGHGHZPKGPRVKSTRPGSSDIN VAPGEQGPDQERTNTLVANTSNSGLKLDPADPENPRSGDTVEV		l	1	
REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFWGVQMRFQQEVMDSPME EVILLVNLCEGTFIMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINEHVSGPPVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKPVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YEEQKKQ/TETKGKNCEIRAVVNKND  1 1129 PIMTLSQCGGIPGHGHSHGGHGHGLPKGPRVKSTRPGSSDIN VAPGEQGPDQERTNTLVANTSNSGLKLDPADPENPRSGDTVEV		1	ĺ	
LHCLSFEQILQIPASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFWVGVQMRFQQEVMDSPME EVILLVNILCEGTFLMSVGDEKDILPPKLQDDILDSLGGGINELKT AEQINEHVGGPFVQFFVKIVGHYASYIKREANGQGHPQERSFCK ALTSKTNRFFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YBEQKKQ/TETKGKNCEIRAVVNKND  6833 1 1129 PLMTLSQCGGIPGHGHSHGGHGHSLPKGFRVKSTRPGSSDIN VAPGEQGPDQERTNTLVANTSNSGLKLDPADPENPRSGDTVEV		1	i	•
PFSWAHTYIPVVPBSLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCBGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT ABQINBHVGGPFVQFFVKLVGHYASYIKREANGQGHFQERSFCK ALTSKTNRFFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YBEQKKQ/TBTKGKNCEIRAVVNKND PLMTLSQCGGIPGHGHSHGGHGHGHSLPKGFRVKSTRPGSSDIN VAPGEQGPDQEBTNTLVANTSNSGLKLDPADPENPRSGDTVEV			i	
EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINBHVGGPFVQFFVKLYGHYASYIKREANGQGHPQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YEEQKKQ/TETKGKNCEIRAVVNKND 6833 1 1129 PLWTLSQCGGIPGHGHSHGGHGHGHSLPKGPRVKSTRPGSSDIN VAPGEQGPDQEETNTLVANTSNSUGLKLDPADPENPRSGDTVEV		l		_ · · · · · · · · · · · · · · · · · · ·
AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YEEQKKQ/TETKGKNCEIRAVVNKND  6833 1 1129 PLWTLSQCGGIPGHGHSHGGHGHGHGHCFKGFRVKSTRPGSSDIN VAPGEQGPDQEETNTLVANTSNSHGLKLDPADPENPRSGDTVEV		1		
ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YEEQKKQ/TETKGKNCEIRAVVNKND  6833 1 1129 PIMTLSQCGGIPGHGHGHGHGHGHGFKFFFGSGDIN VAPGEQGPDQEETNTLVANTSNSGLKLDPADPENPRSGDTVEV		l	1	1
YEEQKKQ/TETKGKNCETRAVVNKND  6833 1 1129 PIMTLSQCGGTPGHGHSHGGHGHGHGKFKFFFGSSDTN VAPGEQGPDQEETNTLVANTSNSHGLKLDPADPENPRSGDTVEV		l	1	. = =
6833 1 1129 PIMTLSQCGGIPGHGHSHGGHGHCHGLPKGPRVKSTRPGSSDIN VAPGEQGPDQERTNTLVANTSNSHGLKLDPADPENPRSGDTVEV		1	1	The state of the s
VAPGEQGPDQERTNTLVANTSNSNGLKLDPADPENPRSGDTVEV			<u></u>	
	6833	1.	1129	
QVNGNLVREPDHMELEEDRAGQLNMRGVFLHVLGDALGSVIVVV		1		
		L		QVNGNLVREPDHMELEEDRAGQLNMRGVFLHVLGDALGSVIVVV

SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ľ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
<b></b>	Joques		NALVFYFSWKGCSEGDFCVNPCFPDPCKAFVELINSTHASVYEA
	1	1	GPCWVLYLDPTLCVVMVCILLYTTYPLLKKSALILLQTVPKQID
			IRNLIKELRNVEGVEEVHELHVWQLAGSRIIATAHIKCEDPTSY
	i		MEVAKTIKDVFHNHGIHATTIQPEFASVGSKSSVVPCELACRTQ
ì	1	1	CALKQCCGTLPQAPSGKDAEKTPAVSISCLELSNNLEKKPRRTK
i	j	,	
			AENIPA\VVIEIKN\IPNK\QPESSL
6834	78	1151	AGQERPAPIWRLLWLPTPSVSRKABPAHIPINR*GA*E*RGGLP
	1		LCGSSASAYGWH*RLTPWSPGGS*HM*SSKAPVTQAREVLVAGP
ļ	1		CSKLVLSGARGIVGTTVQVLVEAQQPLLLLFTGVWGLNLRAGEE
1	Į.	1	SRAL+LIBEVTQVRDAHLGNAVVGCAQCLSQGQVGSALAKALLB
]	Į.	1	AAAAVRDCKEVLTVSGDKQQAEVSVRL*VRDVCVERAGCVEFGQ
l	1		AHGRPGLALAKGRGGTNEVEEQVQVDGVQKLVLSAHECHELVAG
[			QQDGEDQAARTRLLQAGAHSVAHGRRQGQAPCRPHQEAGVSCHE
			LQQVVGDAL*ARE*APQIIVLLLLEDVAQLRTGKKA*DLVVDVE
ļ	•		QLLRQL
6835	1	834	GIPAADR\EASLELIKLDISRTFPNLCIFQQGGPYHDMLHSILG
1 0000	1 -		AYTCYRPDVGYVOGMSFIAAVLILNLDTADAFIAFSNLLNKPCQ
\$	}		MAFFRVDHGLMLTYFAAFEVFFEENLPKLPAHFKKNNLTPDIYL
1			IDWIFTLYSKSLPLDLACRIWDVFCRDGERFLFRTALGILKLFB
ŀ	1	1	DILTKMDFIHMAQFLTRLPEDLPABELFASIATIQMQSRNKKWA
ļ			QVLTALQKDSREMREGKSVPPTLRLQREFALGTNQSPMPRPLCC
i	l		FRLTPGOPRRTDAL
5036	1	850	MSCGRPPPDVDGMITLKV\DNLTYRTSPDSLRRVFEKYGRVGDV
6836	1	850	YIPREPHTKAPRGFAFVRFHDRRDAQDAFAAMDGAELDGRELRV
	l .	· ·	QVARYGRRDLPRSRQGRRHAAGPEAA/RYGRRSRSYGRRSRSPR
	Î	İ	RRHRSRSRGPSCSRSRSRSRYRGSRYSRSPYSRSPYSRSRYSRS
1	<b>\$</b>	· ·	PYSRSRYRESRYGGSHYSSSGYSNSRYSRYHSSRSHSKSGSSTS
1	ł	ļ	SRSASTSKSSSARRSKSSSVSRSRSRSRSRSSSMTRSPPRVSKRKS
			KSRSRSKRPPKSPREEGQMSS
6837	1	1369	TOGAAVAGNPGSDYFPGGTAP/GGPRTRRP\SGTSSSGSKASGP
l .		]	PNPPAQGDGTSLSPNYTLESTSGNDGKPVSGGGGRGRRKRDS
i	ł	1	GHVSPGTFFDKYSAAPDSGGAPGVSPGQQQASGAAVGGSSAGET
i	İ	1	RGAPTPHEKALTSPSWGKGAELLLGDQPDLIGSLDGGAKSDSSS
1		)	PNVGEFASDEVSTSYANEDEVSSSSDNPQALVKASRSPLVTGSP
			KLPPRGVGAGEHGPKAPPPALGLGIMSNSTSTPDSYGGGGGPGH
	i	1	PGTPGLEQVRTPTSSSGAPPPDEIHPLBILQAQIQLQRQQFSIS
1			EDQPLGLKGGKKGECAVGASGAQNGDSBLGSCCSEAVKSAMSTI
		1	DLDSLMAKHSAAWYMPADKALVDSADDDKTLAPWKKAKPQNPNS
1	1	I	KEAHDLPANKASASQPGSHLQCLSVHCTDDVGDAKARASVPTWR
l	1	1	SLHSDISNRFGTFVAALT
6838	16	499	LTDTPPPKTHMIHHSISDYKATLRCWALGFYPMBITLTWQQDEB
1	1 ~~		DQTRDMELVETRPAGDGTFQKWAAVVVPSGEE/Q/RYMCHVQHE
1	1	ŀ	GLPKPLTLRWEQSSQPTIPIVGIVAGLVLLGAVVTGAVVSAVMC
1	l	1	RKKNSDRVSYSEAASSDHAQGSDVSLTACKV
- 6030	ļ. <b></b>	1225	AAPAGGGPDPEALSAFPGRHLSGLSWPOVKRLDALLSEPIPIHG
6839	1	1195	
1	ľ	1	RGNFPTLSVQPRQIRAGGPQHPGGAG\IHVHRVRLHGSAASHVL
1			HPESGLGYKDLDLVFRMDLRSEASFQLTKAVVLACLLDFLPAGV
1	1		SRAKITPLTLKEAYVQKLVKVCTDSDRWSLISLSNKSGKNVELK
1		1	FVDSVRRQFRFSIDSFQIILDSLLLFGQCSSTPMSEAFHPTVTG
1		İ	ESLYGDFTBALEHLRHRVIATRSPKEIRGGGLLKYCHLLVRGFR
I	· .	1	PRPSTDVRALQRYMCSRFFIDFPDLVEQRRTLBRYLEAHFGGAD
1	1	1	AARRYACIVTLHRVVNESTVCIMNHERRQTLDLIAALALQALAE
ł	1	1	QGPAATAALAWRPPGTDGVVPATVNYYVTPVQPLLAHAYPTWLP
1	l l	1	CN
6840	4254	2061	ELOGDFSVPDVPKSMAWCENSICVGFKRDYYLIRVDGKGSIKEL
	]	1	FPTGKQLEPLVAPLADGKVAVGQDDLTVVLNEEGICTQKCALNW
	<u> </u>		1

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ΊD	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
-	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ĺ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ī	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	• • • • • • • • • • • • • • • • • • • •	\=possible nucleotide insertion)
<u> </u>		<del></del>	TDIPVAMEHQPPYIIAVLPRYVEIRTFEPRLLVQSIELQRPRFI
l	İ		TSGGSNIIYVASNHFVWRLIPVPMATQIQQLLQDKQFKLALQLA
	j.	ļ	EMKDDSDSEKQQQIHHIKNLYAFNLFCQKRFDESMQVFAKLGTD
1	1	Ì	PTHVMGLYPDLLPTDYRKQLQYPNPLPVLSGAELEKAHLALIDY
1		1	LTQKRSQLVKKLNDSDHQSSTSPIMBGTPTIKSKKKLLQIIDTT
1 .	1		LLKCYLHTNVALVAPLLRLENNHCHIEESEHVLKKAHKYSELII
ĺ			LYPKKGLHEKALQVLVDQSKKANSPLKGHERTVQYLQHLGTENL
İ			HLIFSYSVWVLRDFPRDGLKIFTEDLPEVESLPRDRVLGFLIEN
1			PKGLAIPYLEHIIHVWEETGSRFHNCLIQLYCEKVQGLMKEYLL
I	1		SFPAGKTPVPAGEEEGELGEYRQKLIMFLEISSYYDPGRLICDF
			PFDGLLEBRALLLGRMGKHEQALFIYVHILKDTRMABEYCHKHY
			DRNKDGNKDVYLSLLRMYLSPPSIHCLGPIKLELLEPKANLQAA
1			LQVLELHHSKLDTTKALNLLPANTQINDIRIFLEKVLEENAQKK
			RENOVERNITHABETERA/ÖRBELTFHÖÖAKGIILEBKACMACKKK
į			IGNSAFARYPNGVVHYFCS\KEVNPADT
6841	1	3206	TPSTTGTKSNTPTSSVPSAAVTPINESLQPLGDYGVGSKNSKRA
	_	3200	REKRDSRNMEVQVTQKMRNVSIGMGSSDEWSDVQDIIDSTPELD
			MCPETRLDRTGSSPTQGIVNKAPGINTDSLYHELSTAGSEVIGD
f i			VDEGADLIGEFSCMCKEVGNLLLENSQLIETKNALNVVKNDLIA
) .			KVDQLSGEQEVLRGBLEAAKQAKVKLENRIKELEEELKRVKSKA
1			IIARREPKERAEDVSSYLCTESDKIPMAQRRRFTRVEMARVIME
			RNQYKERLMELQEAVRWTEMIRASREHPSVQEKKKSTIWQFFSR
1			LFSSSSPPPAKRPYPSGNIHYKSPTTAGFSQRRNHAMCPISAG
1			SRPLEFFPDDDCTSSARREQKREQYRQVREHVRNDDGRLQACGW
			SLPAKYKQLSPNGGQEDTRMKNVPVPVYCRPLVEKDPTMKLWCA
] ·	ĺ		AGVNLSGWRPNEDDAGNGVKPAPGRDPLTCDREGDGEPKSAHTS
1 1			PEKKKAKELPEMDATSSRVWILTSTLTTSKVVIIDANQPGTVVD
			QFTVCNAHVLCISSIPAASDSDYPPGEMFLDSDVNPEDPGADGV
			LAGITLVGCATRCNVPRSNCSSRGDTPVLDKGQGEVATIANGKV
1 1			NPSQSTERATEATEVPDPGPSEPETATLRPGPLTEHVFTDPAPT
1 1			PSSGPQPGSENGPEPDSSSTRPEPEPSGDPTGAGSSAAPTMWLG
			AONGWLYVHSAVANWKKCLHSIKLKDSVLSLVHVKGRVLVALAD
		*	GTLAIFHRGEDGOWDLSNYHLMDLGHPHHSIRCMAVVYDRVWCG
			YKNKVHVIQPKTMQIEKSFDAHPRRESQVRQLAWIGDGVWVBIR
			LDSTLRLYHAHTHQHLQDVDIBPYVSKMLGTGKLGFSFVRITAL
	1		LVAGSRLWVGTGNGVVISIPLTETVVLHRGO\LLG\LRANKTSP
	ļ		TSGEG\ARPGG\IIHVYG\DDSSDRAARSFIPYCSMAOAOLCFH
ļ Ē			GHRDAVKFFVSVPGNVLATLNGSVLDSPAEGPGPAAPASEVEGO
l			KLRNVLVLSGGEGYIDFRIGDGEDDETEEGAGDMSQVKPVLSKA
			ERSHIIVWQVSYTPE
6842	3	926	RCQQLSATILTDHQYLERTPLCAILKQKAPQQYRIRAKLRSYKP
<b> </b>			RRLFQSVKLHCPKCHLLQEVPHEGDLDIIFODGATKTPDVKLON
	ĺ		TSLYDSKIWTTKNQKGRKVAVHFVKNNGILPLSNECLLLIBGGT
	ł	,	LSEICKLSNKFNSVIPVRSGHEDLELLDLSAPFLIQGTVHHYGC
İ	1		KQWST*RSIQNLNSLVDKTSWIPSSVARALGIVPLQYVFVMTFT
	İ		LDDGTGVLEAYLMDSDKPPQIPASEVLMDDDLQKSVDMIMDMPC
	ļ		PPGIKIDAYPWLECFIKSYNVTNGTDNQICYQIFDTTVARDVI
6843	2	851	NHRKVLSGAKRYBCNECGKSFAYTSSLIKHRRIHTGERPYBCSE
. !	. 1		CGRSPARNSSLIKHLRVHTGERPYECVECGKSPRRSSSLLQHQR
	į		VHTRERPYECSECGKSFSLRSNLIHHQRVHTGERHECGQCGKSF
	i	ļ	SRKSSLI IHLRVHTGERPYECSDCGKSFAENSSLIKHLRVHTGE
		}	RPYECIDCGKSFRHSSSFRRHQRVHTGMRPYK*SKFWKFSCPGF
		1	LLLQGQRVHTGSRCYECDKWGIFFS*NASFFT*KSAPTEEVPFE
i i		1	CNECEKAPSPLSLVTTIPT
6844	244	642	EHQLAGFELRKTQTSMSLGTTREKTDRVKSTAYLSPQELEDVFY
1	I		QYDVKSEIYSFGIVLWEIATGDIPFQGCNSEKIRKLVAVKRQQE
j	1		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
XD	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
· ·	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *eStop
į.	amino acid	sequence	Codon, /-possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			PLGEDCPSELREIIDECRAHDPSVRPSVDBILKKLSTFSK*CIK
1	1		I
6845	3	1519	VAVRDECYWRHVFWDQDLWMLLFILMCHPETARARLEYRIRTLD
ı	l		GALENAQNLGYQGAKFAWESADSGLEVCPEDIYGVQEVHVNGAV
1			GLAFELYYHTTQDLQLFREAGGWDVVRAVAEFWCSRVEWSPREE
1			KYHLRGVMSPDEYHSGVNNSVYTNVLVQNSLRFAAALAQDLGLP
1	ŀ		IPSQWLAVADKIKVPFDVEQNPHPEFDGYRPGEVVKQADVVLLG
1			YPVPFSLSPDVRRKNLEIYEAVTSPQGPAMTWSMFAVGWMELKD
1	_		AVRARGLLDRSFANMARPFKVWTENADGSGAVNFLTGMGGFLQA
1			VVFGCTGFRVTRAGVTFDPVCLSGISRVSVSGIFYQGNKLNFSF
[			SEDSVTVEVTARAGPWAPHLEAELWPSQSRLSLLPGHKVSFPRS
1			AGRIQMSPPKLPGSSSSEFPGRTFSDVRDPLQSPLWVTLGSSSP
			TESLTVDPASE*SGTGASETSLGPSLWPRLHPPLLGTLLACHPS
			PAARLSGKVHAANPEFKAPCL
6846	213	1258	LYFLKTIK+LNRLAEHP+YENEKLTKLRNTIMEQYTRTEESARG
1			IIFTKTRQSAYALSQWITENEKFABVGVKAHHLIGAGHSSEFKP
[ ]			MTQNEQKEVISKFRTGKINLLIATTVAEEGLDIKECNIVIRYGL
1			VTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDFREKM
			MYKAIHCVQNMKPBEYAHKILBLQMQSIMBKKMKTKRNIAKHYK
			NNPSLITPLCKNCSVLACSGEDIHVIBKMHHVNMTPBFKRLYIV
			RENKTLOKKCADYQINGEIICKCGQAWGIMMVHKGLDLPCLKIR
6847	1450	240	NFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED
1 003/	1450	348	SMCWNSDRLEMPLIDLALILYPPSYVPYTGHLSDDSLSRKYCLT
1			WFEDALNGVL*RAEAIQPHCVNAGDRMEKFRQKYWNKLQTLRQQ
l l			PFAYGTLTVRSLLDTREHCLNEFNFPDPYSKVKQRENGVALRCP PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP
1 1			YFGFEEAKRKLQERPWLVDSYSEWLQRLKGPPHKCALIFADNSG
1			IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTHSESLIVAE
1 1			RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR
j i			ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAKRLG
] }		*	GRLFSVIFKYBVPAE
6848	19	16	AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND
			LKVIIISAEGPVFSSGHDLKELTREQGRDYHAEVFQTCSKVMMH
			IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSPATPGVN
i i			VGLPCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK
1 1	ł		VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA
			YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH
6849	70	821	SLGVDGSCLRQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC
	i		VCVLFASVPDFKEFYSESNINHEGLECLRLLNEILADFDBLLSK
] ]			PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM
	. [		VBPAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ
			YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG
L			VIKVKGKGQLCTYFLNTDLTRTGPPSATLG
6850	2	1235	ARGLINHEWTYEKLROHISRNAQDKQELHLFMLSGVPDAVFDLTD
] [		İ	LDVLKLELIPBAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL
	1	i	RDHLRCLHVKFTDVAEIPAWVYLLKNIRELYLIGNLNSENNKMI
	i		GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT
i 1	j	ļ	KLLVLNSLKKMMNVAELELQNCELERIPHAIPSLSNLQELDLKS
	}	<u> </u>	NNIRTIEEIISPOHLKRLTCLKLWHNKIVTIPPSITHVKNLESL
		j	YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ
			HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ
			LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK
6851	1765		EALNQDINIPPANGI
0031	7,02	660	VSAQVSAREGENCLGWNLADSSQESYKSLEEARDCYPPSLLTLD
		ļ	LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA
			CYCVYKLTIGRDDSEKLEREGEEBWDDDQELDEEEPDIWFDFBT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, P-Phenylalanine, G-Glycine,
ı	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
J.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence .	<u> </u>	\=possible nucleotide insertion)
ı		}	MARPWTEDGDWTEPGAPGGTEDRPSGGGKANRAHPIKQRPFPYE
1	ļ		HKNTWSAQNCKNGSCVLDLSKCLFIQGKLLFAEPKDAGFPFSQD
ł	1	l	INSHLASLSMARNTSPTPDPTVRRALCAFDNLNASIESQGQIKM
f	1	[	YINEVCRETVSRCCNSFLQQAGINLLISMTVINNMLAKSASDLK
			PPLISEGSGCAKVQVLKPLMGLSEKPVLAGELVGAQMLPSPMSL
			PIRNGNRBILLETPAP
6852	1	407	RTRGERTYANFIKHNDGKNIFYAARTPATLFAVMFAMYIISGLT
			GFIGLNSIAVLCNLVMGLALIFLCTWAYVKYSGRFRBIGTVIDQ
l.			IARTLWEQVLKPLGDNLMEBNIRQSVTNSIKAGLTDQVSHHARL
i			KTD
6853	3	469	GDSCAVCIELYKPNDLVRILTCNHIFHKTCVDPWLLEHRTCPMC
1			KCDILKALGIEVDVEDGSVSLQVPVSNEIPNSASSHBEDNRSET
I		ĺ	ASSGYASVQGTYEPPLEEHVQSTNESLQLVNHRANSVAVDVIPH
ł			VDNPTFERDETPNQETAVREIKS
6854	1148	585	HESYIGTFDPGELCVCAAIQWLQDNSASYFLNRKLVYBPSTQAK
1		•	PVKNTPLRMWIYSHHIYQQDLRKKILDVGKRLDVTGFCMTGKPG
Į.			IICVEGFKEHCEBFWHTIRYPNWKHISCKHAESVETEGNGEDLR
j	ļ		LFHSFRELLLEAHGDYGLRNDYHMNLGQFLEFLKKHKSEHVFQI
İ			LFGIESKSSDS
6855	1913	1148	GRVGGRVGRICSPLSGANEY LASTDTLKTERVLLFTDQTDDLAK
i	1.		EEPT3LFQRD9ETKGESGLVLEGDKEIHQIFEDLDKKLALASRP
<b>!</b>			YIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHI
J.	İ		QLTYFSRWSEVEDSCDSDAIKRMYCAPEVGAITEETEACDWWSL
ł	l		GAVLFELLTGKTLVECHPAGINTHTTLNMPRWVSEEARSLIQQL
İ			LQFNPLERLGAGVAGVEDIKSHPFFTPVDWAELMR
6856	1617	• 997	VTQLYVSVDASTKDSLKKIDRPLFKDFWQQFLDSLKALAVKQQR
ł	1	·	TVYRLTLVKAWNVDELQAYAQLVSLGNPDFIEVKGVTYCGESSA
i .			SSLTMAHVPWHEEVVQFVRELVDLIPBYBIACKHEHSNCLLIAH
}			RKFKIGGEWWTWINYNRFQELIQEYEDSGGSKTFSAKDYMARTP
			HWALFGASERGFDPKDTRHQRKNKSKAISGC
6857	1	617	KGPRATAMVCVCSHPNCRQNHIKPSHSAAQTWCGSPTPASAPNH
l			KLMAMEQGKTLPSATEDAKEEGLEAQISRLAKLIGRLESKALWP
ł			DLQQRLSDBDGTNMHLQLVRQEMAVCPEQLSBFLDSLRQYLRGT
ł			TGVRNCFHITAVRLSDGFTFVIYEFWBTEEAWKRHLQSPLCKAF
			RHVKVDTLSQPEALSRILVPAAWCTVGRD
6858	.2	669	RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA
İ	ļ		LRCVQTAKLILEELKLEKKIKIRVEPGIFENTKWEAGKTTPTLM
1	[	· •	SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ
l	<b>[</b>		IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDPAQLVR
	1		KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS
			GN
6859	1	1150	GETMPKKAKTKAKKKPRKRSDSSGGYNLSDI IQSPSSTGLLKSG
			KINSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIR
			AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT
ļ	}		SSASWVAGSPSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT
			VSHGVKLSQKQRKMIALTTKKNNSGMNSMBTVLFTPSKAPKPVN
			AWASSLHSVSSKSFRDFLLBEKKSVTSHSSEDHVKKVSFKGIEN
			SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM
1			VAPVTFASIVEEBLQQEAALIRSREKPLALIQIEEHAIQDLLVF
			YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC
6860	1889	1515	DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ
			DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP
L		!	MGSPVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
6861	1889	1515	DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSBEQKKQLAQ
L I			DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP
			· · · · · · · · · · · · · · · · · · ·

_			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	·	\=possible nucleotide insertion)
			MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
6862	2	471	BEIDREFHNKLKLKEDKLEKQBKPVNGEDKGDSGVDTQNSEGNA
}		1	DEEDPLGPNCYYDKTKSFFDNISCDDNRERRPIWAEERRLNAET
l			FGIPLRPNRGRGGYRGRGGLGFRGGRGGGGGGTFTAPRGFRG
		•	GFRGGRGGREPADFEYRKTTAFGP
6863	2216	487	PQEPALKSEPSQVASNTIPLPLPQPNTCKDNGPCKQVCSTVGGS
1			AICSCFPGYAIMADGVSCEDQDECLMGAHDCSRRQFCVNTLGSF
1	Ì		YCVNHTVLCADGYILNAHRKCVDINECVTDLHTCSRGERCVNTL
i			GSFHCYKALTCEPGYALKDGECEDVDECAMGTHTCQPGFLCQNT
l			KGSFYCQARQRCMDGFLQDPEGNCVDINECTSLSEPCRPGFSCI
ļ	1	}	NTVGSYTCQRNPLICARGYHASDDGTKCVDVNECETGVHRCGEG
1	1		QVCHNLPGSYRCDCKAGFQRDAFGRGCLDVNECWASPGRLCQHT
			CENTLGSYRCSCASGFLLAADGKRCEDVNECEAQRCSQECANIY
			GSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILCTFRCLNVPGS
<u> </u>			YQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGS
j	j		FRCLRFECPPNYVQVSKTKCERTTCHDFLECQNSPARITHYQLN
ļ			POTGLLVPAHIFRIGPAPAFTGDTIALNIIKGNEEGYFGTRELN
İ			AYTGVVYLQRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHIFFT
			TFAL
6864	2	2933	LADSSPSNLQIIIKELLSMHHQPDPALTKEFDYLPPVDSRSSSG
1			FVGLRNGGATCYMNAVFQQLYMQPGLPBSLLSVDDDTDNPDDSV
		•	PYQVQSLPGHLMESKLQYYVPENFWKIPKMWNKELYVRBQQDAY
			EFFTSLIDQMDEYLKKMGRDQIFKMTFQGIYSDQKICKDCPHRY
1		N	ERBEAFMALNLGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK
			EKRITVKRICIKSLPSVLVIHLMRFGFDWBSGRSIKYDBQIRFP
1			WMLNMEPYTVSGMARQDSSSBVGENGRSVDQGGGGSPRKKVALT
ŀ			ENYBLVGVIVHSGQAHAGHYYSFIKDRRGCGKGKWYKFNDTVIB
l .			BFDLNDETLBYECFGGEYRPKVYDQTNPYTDVRRRYWNAYMLFY
ŀ			QRVSDQNSPVLPKKSRVSVVRQEAEDLSLSAPSSPEISPQSSPR
1			PHRPNNDRLSILTKLVKKGEKKGLFVEKMPARIYQMVRDENLKF
			MKNRDVYSSDYFSFVLSLASLNATKLKHPYYPCMAKVSLQLAIQ
			FLFQTYLRTKKKLRVDTEEWIATIEALLSKSFDACQWLVEYFIS
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL
	·		HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL
			LRHSALRHMISFLIGASRONNQIRRWSSAQAREFGNLHNTVALL
			VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM
			SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH
			PIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN
			GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH
		!	wswavqwlqkkmsehywtlqsnvsnetstgktfqrtisaqdtla
			YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGRL
			RSDLDDVDP
6865	1820	1242	DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS
			CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV
			LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ
			DTKAEPLDPEADSHVRVFGDRPEQQLSPIFRNASGQSWFSPPAS
			PFGQSSVQTIQPKRDS
6866	1571	495	DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF
			IIEGMBEAGSVALEBLVEKEKDRFFSGVDYIVISDNLWISQRKP
			AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG
			SLVDSSGHILVPGIYDEVVPLTBEBINTYKAIHLDLEBYRNSSR
			VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV
			IGKF91RLVPHMNVSAVEKQVTRHLEDVF5KRNS5NKMVVSMTL
			GLHPWIANIDDTQYLAAKRAIRTVFGTRPDMIRDGSTIPIAKMF
			QEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLPAAPFL
i			EMAQLH
	7	i	EPPOLITE

022	T 7000 32 -4 - 4		
SEQ ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
l Mo:	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
{	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	
į.	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
6867	2833	1704	\=possible nucleotide insertion)
6867	2033	1704	GTRIMSQPKQKELAGFVRQKMLLDYSVYMGRCVPQESRSPQRSP
Í			LOSAESSPTAGKKLPEVPPSEEBEQEAWVNALLGRIFWDFLGEK
<b>{</b> ·		}	YWSDLVSKKIQMKLSKIKLPYFMNELTLTELDMGVAVPKILQAF
1			KPYVDHQGLWIDLEMSYNGSFLMTLETKMNLTKLGKEPLVEALK
i		ļ	VGEIGKEGCRPRAFCLADSDEESSSAGSSEEDDAPEPSGGDKQL
	İ		LPGAEGYVGGHRTSKIMRFVDKITKSKYFQKATETEPIKKKIBE,
İ			VSNTPLLLTVBVQBCRGTLAVNIPPPPTDRVWYGPRKPPHVELK
	1		ARPKIGEREVTLVHVTDWIEKKLEQEFQKVFVMPNMDDVYITIM
5050	<u> </u>		HSAMDPRSTSCLLKDPPVEAADQP
6868	1	346	RPTRPPTRPEKIKNLILPYISDMNFVQDLCEDFYELFKTDKGFD
1	]		KATFESQMSVMRGQILNLTQALRDGKSPFQLVQIPCVIVERSQG
7070			GSQGRIVHLSNSFTQTVNCRKPFFSSW
6869	3	1619	MYMERMOKRALISFWESVEHLKNANKNEIPOLVGEIYONFFVES
1	[		KEISVEKSLYKEIQQCLVGNKGIEVFYKIQEDVYETLKDRYYPS
1			FIVSDLYEKLLIKEERKHASQMISNKDEMGFRDEAGREAVDDGT
i i	i		NQINEQASFAVNKLREINEKLEYKRQAINSIQNAPKPDKKIVŠK
	Į.		LKDEILLIEKERTDLQLHMARTDWWCENLGMWKASITSGEVTEE
i .			NGEQLPCYFVMVSLQEVGGVETKNWTVPKRLSEFHNLHRKLSEC
	•		VPSLKKDQLPSLSKLPFKSIDHTFMEKPENQLNKFLQNLLSDER LCQSEALYAPLSPSPDYLKVIDVOGKKNSFSLSSFLERLPRDFF
ţ			SHOREETEEDSDLSDYGDDVDGRKDALAEPCFMLIGEIFELRGM .
			FKWVRRTLIALVQVTFGRTINKQIRDIVSNIFSEQMLVYYINIF
			RDAFWPNGKLAPPTTIRSKEQSQETKQRAQQKLLENIPDMLQSL
1			VGQQNARHGIIKIFNALQETRANKHLLYALMELLLIELCPELRV
ŀ	<b>}</b> .		HLDQLKAGQV
6870	1	1566	MAAVVAATRWWQLLLVLSAAGMGASGAPOPPNILLLLMDDMGWG
1	-		DLGVYGEPSRETPNLDRMAAEGLLFPNFYSANFLCSPSRAALLT
l			GRLPIRNGPYTTNAHARNAYTPQEIVGGIPDSEQLLPELLKKAG
ľ			YVSKIVGKWHLGHRPOFHPLKHGFDEWFGSPNCHFGPYDNKARP
Į			NIPVYRDWEMVGRYYBEFPINLKTGEANLTQIYLQEALDFIKRQ
		'	ARHHPFFLYWAVDATHAPVYASKPFLGTSQRGRYGDAVREIDDS
ł			IGKILELLQDLHVADNTFVFFTSDNGAALISAPEQGGSNGPFLC
<u> </u>			GKQTTFEGGMREPALAWWPGHVTAGQVSHQLGSIMDLFTTSLAL
1			AGLTPPSDRAIDGLNLLPTLLQGRLMDRPIFYYRGDTLMAATLG
i			QHKAHFWTWTNSWENFRQGIDFCPGQNVSGVTTHNLEDHTKLPL
1.			IPHLGRDPGERPPLSFASAEYQEALSRITSVVQQHQEALVPAQP
<u></u>			QLNVCNWAVMNWAPPGCEKLGKCLTPPBSIPKKCLWSH
6871	209	1126	RMSLNPPIFLKRSBENSSKFVBTKQSQTTSIASKDPLQNLCLAS
			QEVLQKAQQSGRSKCLKCGGSRMFYCYTCYVPVENVPIEQIPLV
1			KLPLKIDIIKHPNETDGKSTAIHAKLLAPEFVNIYTYPCIPEYE
			EKDHEVALIFPGPQSISIKDISFHLQKRIQNNVRGKNDDPDKPS
1			FKRKRTEEQEFCDLNDSKCKGTTLKKIIFIDSTWNQTNKIFTDE
			RLQGLLQVELKTRKTCFWRHQKGKPDTFLSTIBAIYYFLVDYHT
	<u> </u>		DILKEKYRGQYDNLLFFYSFMYQLIKNAKCSGDKETGKLTH
6872	880	459	FGLLMVVLSL1FMKGNCVREDL1FNFLFKLGLDVRETNGLFGNT
]			KKLITEVFVRQKYLEYRRIPYTEPAEYEFLWGPRAFLETSKMLV
			LRFLAKLHKKDPQSWPFHYLEALARCEWEDTDEDEPDTGDSAHG
			PTSRPPPR
6873	1929	955	DEQAVLCSKDKTYDLKIADTSNMLLFIPGCKTPDQLKKEDSHCN
			IIHTEIFGFSNNYWELRRRRPKLKKLKKLLMENPYEGPDSQKEK
1			DSNSSKYTTEDLLDQIQASEEBIMTQLQVLNACKIGGYWRILEF
ł	•		DYEMKLLNHVTQLVDSESWSFGKVPLNTCLQELGPLEPEEMIEH
			CLKCYGKKYVDEGEVYFELDADKICRAAARMLLQNAVKFNLAEF
		<u> </u>	QEVWQQSVPEGMVTSLDQLKGLALVDRHSRPEIIFLLKVDDLPE
		!	DNQERFNSLFSLREKWTEEDIAPYIQDLCGEKQTIGALLTKYSH
1		1	SSMONGVKVYNSRRPIS

SRO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
6874	1	307	DSIADHVNSAAVNVERGTKNIGKAAKYKLAALPVAGALIGGMVG
		]	
1			GPIGLLAGFKVAGIAAALGGGVLGFTGGKLIQRKKQKMMEKLTS. SCPDLPSQTDKKCS
6875	1688	349	<del>"</del>
""	2000	349	VIGTGERGNSASEKWEIMFNEELGDPFIIIHSISLLNAEEHSIA
i			TLLLRIEKBELDMKGSGFYVSLEWVTISKKNQDNKKYEIIKRDI
1			LRGKSVPHYAAIEPDGNGLMIVSYKSLTFVQAGQDLEKNMDKDI
1			SEKIKEPLYYWQQTEDDLTVTIRLPEDNTKEDIQIQFLPDHINI
1			VLKDHQFLEGKLYSSIDHESSTWIIKESNSLEISLIKKNEGLTW
			PELVIGDKQGELIRDSAQCAAIAERLMHLTSEELNPNPDKEKPP
			CNAQELEECDIFFEESSSLCRFDGNTLKTTHVVNLGSNQYLFSV
	1		IVDPKEMPCFCLRHDVDALLWQPHSSKQDDMWEHIATFNALGYV
			QASKRDKKFFACAPNYSYAALCECLRRVFIYRQPAPMSTVLYNR
1	}		KEGRQVGQVAKQQVASLETNDPILGFQATNERLFVLTTKNLFLI
6876	41	1285	KVNTEN
0076	41	1285	VGENTLINRHLLRPLCLVTSAPRILEMHPFLSLGTSRTSVTKLS
	1		LHTKPRMPPCDFMPERYQVIFLVNSGSBANKLAMLMARAHSNNI
İ			DIISFRGAYHGCSPYTLGLTNVGIYKMELPGGTGCQPTMCPDVF
İ			RGPWGGSHCRDSPVQTIRKCSCAPDCCQAKDQYIEQFKDTLSTS
1			VAKSIAGPPAEPIQGVNGVVQYPKGFLKRAFELVRARGGVCIAN
[	[		PYOTGFGRLGSHFWGFQTHDVLPDIVTMAKGIGNGFPMAAVITT
			PEIAKSLAKCLOHFNTFGGNPMACAIGSAVLEVIKEENLOENSO
1	}		BURGHYMLLKFAKLRDEFEIVGDVRGKGLMIGIEMVQDKISCRPL
Í			PREEVNQIHEDCKHMGLLVGRGSIFSQTFRIAPSMCITKPEVDF
6877	1	778	AVEVERSALTOHMERRAK
1	-	770	GTSPSPARAYAPPTERKRFYQNVSITQGEGGFBINLDHRKLKTP
Î	·		QAKLPTVPSEALAIAVATEWDSQQDTIKYYTMHLTTLCNTSLDN
i			PTQRNKDQLIRAAVKFLDTDTICYRVEEPETLVELQRNEWDPII EWAEKRYGVEISSSTSIMGPSIPAKTREVLVSHLASYNTWALQG
1	ĺ		IRFVAAQLKSMVLTLGLIDLRLTVEQAVLLSRLEREYQIQKWGN
1			IEWAHDYELQELRARTAAGTLFIHLCSESTTVKHKLLKE
6878	931	263	QTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
			LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAP
			BYTWFKDGIRLLENPRLGSQSTNSSYTWNTKTGTLQFWTVSKLD
			TGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVIS
l i			VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSF
1			II
6879	3	845	IRVIGESDIMQRFLSESDRNYNGVSDVELRVALPDGTTVTVRVK
``		# ***	KNSTTDQVYQAIAAKVGMDSTTVNYFALFEVISHSFVRKLAPNE
			FPHKLYIQNYTSAVPGTCLTIRKWLFTTEREILLNDNDLAVTYF
			FHQAVDDVKKGYIKAREKSYQLQKLYEQRKMVMYLNMLRTCEGY
1			NBIIPPHCACDSRRKGHVITAISITHFKLHACTEEGQLENQVIA
l i			FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWVKIFTPYFNYMHE
			CFERVFCBLKWRKEBY
6880	2110	1437	RKONCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS
		~~~	MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLORS
l l			
	İ		NRDQIKNCGFFYGHRAFSVALIFVTAPQGLSVAFILKFLDNMPH
	ľ		VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS
	<b>!</b>		KPQVPEYAPRQERIRDLSGNLWERSSGDGEBLERLTKPKSDESD BDTF
6881	2638	2244	
****	2030	2244	NDSKWEDIHVITGALKMFFRBLPEPLFTFNHFNDFVNAIKQEPR
			QRVAAVKDLIRQLPKPNQDTMQILFRHLRRVIENGEKNRMTYQS
6882			IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR
0004	1	850	GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRPWLVIN
i 1		,	QECNMVTARQBPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT
			TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSQPYRLVHFEPH
Ll			MRPRRPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLEK

	[ Du-3/ 3	Description and	Charles and a second control of the state of the second control of
SEQ ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
<b>\</b>	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	
ł	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
ĺ		sequence	\=possible nucleotide insertion)
i	sequence		KVKATNFRPNIVISGCDVYAEDSWDELLIGDVELKRVMACSRCI
		ì	
l			LTTVDPDTGVMSRKEPLETLKSYRQCDPSERKLYGKSPLFGQYF
C000		2256	VLENPGTIKVGDPVYLLGQ NSKLKLNONLKLFITLTYQVLSLHGWGPGIHLOKEGAFPVTONR
6883	2794	2236	ALOLLYDLRYLNIVLTAKGDEVKSGRSKPDSRIBKVTDHLEALI
ł		4	DPFDLDVFTPHLMSNLHRLVQRTSVLFGLVTGTENQLAPRSSTF
<b>.</b>		1	
i		ĺ	NSQEPHNILPLASSQIRFGLLPLSMTSTRKAKSTRNIETKAQYD ANC
6884	2	99	BFBRVTABAVKPRETSBPRAAAQRFCRKFPFL
6885	297	1554	STGQFWHVTDLHLDPTYHITDDHTKVCASSKGANASNPGPFGDV
1		1	LCDSPYQLILSAFDFIKNSGQRASFMIWTGDSPPHVPVPELSTD
<b>!</b>	1	1	TVINVITNMTTTIQSLFPNLQVFPALGNHDYWPQDQLSVVTSKV YNAVANLWKPWLDBEAISTLRKGGFYSQKVTTNPNLRIISLNTN
Í		[	——————————————————————————————————————
l	Į.	[	LYYGPNIMTLNKTDPANQFEWLBSTLMNSQONKEKVYIIAHVPV
	1	1	GYLPSSONITAMREYYNEKLIDIFOKYSDVIAGOFYGHTHRDSI MVLSDKKGSPVNSLFVAPAVTPVKSVLEKOTNNPGIRLFOYDPR
		l	DYKLLDMLQYYLNLTEANLKGESIWKLEYILTQTYDIEDLQPES
l		i	LYGLAKOFTILDSKOPIKYYNYFFVSYDSSVTCDKTCKAPQICA
i			IMNLDNISYADCLKOLYIKHNY
6886	<del> </del>	1341	OCGGIPGREGGSSRPLEEGTGSSPACVRGAAPGSEDAFYPTRAK
0000		1341	QARVSQBLKKAAKRTVSISEGPDTLGDGMRERRETLALAPEPEP
Į		1	LEKEACEKWKRPFRSASATSLTLSHCVDVVKGLLDFKKRRGHSI
ŀ			GGAPEQRYQIIPVCVAARLPTRAQDVLDAHLSEVNAVREGPNSS
	•		LLATGGADRLIHLWNVVGSRLEANOTLEGAGGSITSVDFDPSGY
1	ĺ	}	QVLAATYNQAAQLWKVGRAQSKETLSGHKDKVTAAKFKLTRHQA
Ī		j	VTGSRDRTVKEWDLGRAYCSRTINVLSYCNDVVCGDHIIISGHN
			DQKIRFWDSRGPHCTQVIPVQGRVTSLSL9HDQLHLLSCSRDNT
ŀ		[	LKVIDLRVSNIROVFRADGFKCGSDWTKAVFSPDRSYALAGSCD
			GALYIWDVDTGKLESRLQGPHCAAVNAVAWCYSGSHMVSVDQGR
ļ	}		KVVLWQ
6887	1047	116	WTARPSOKPFWRAGAVPGDPLSTGCSQAQLGGCCPRGPWGPQHG
1	1	1	GOORAAGPTLPRGERGGPOOSGPGLAAOTPPTSKOVAWRAFLTG
1	İ	<u> </u>	TYRSQSPRSPAGPFRGGTGWWPEPAVCLCVAVGPQRLSSPGLVY
1		}	NASGSEHCYDIYRLYHSCADPTGCGTGPDARAWDYQACTEINLT
			FASHNUTDMPPDLPFTDELRQRYCLDTWGVWPRPDWLLTSFWGG
	į.	ļ	DLRAASNIIFSNGNLDPWAGGGIRRNLSASVIAVTIQGGAHHLD
			LRASHPEDPASVVEARKLEATIIGEWVKAARREQQPALRGGPRL
l	1	1	SL
6888	1	992	FVAYVKKBIPHIVVTHCLLNPHALVIKTLPTKLRDALFTVVRVI
ĺ	1	]	NFIKGRAPNHRLFQAFFEEIGIEYSVLLFHTEMRWLSRGQILTH
	1	1	IFEMYER INQPLHHKSSNLVDGFENKEFKIHLAYLADLFKHLNE
l	1	1	LSASMORTOMNTVSAREKLSAFVRKFPFWQKRIEKRNFTNFPFI
		1	BELIVSDNEGIFIAAEITLHLQQLSNFFHGYFSIGDLNEASKWI
	1	}	LDPFLFNIDFVDDSYLMKNDLAELRASGQILMEFETMKLEDFWC
	l	l	AQFTAFPNLAKTALEILMPFATTYLCELGFSITFTFQNKVPRAA
			LILSDDTRVAISKKVPSFLGHH
6889	1	1534	LTLENQIKERREQDNSESPNGRTSPLVSQNNEQGSTLRDLLTTT
	_	)	AGKLRVGSTDAGIAFAPVYSMGAPSSKSGRTMPNILDDIIASVV
	ł	1	ENKIPPSKTSKINVKPBLKEBPEBSIISAVDENNKLYSDIPHSW
	<b>\</b>	ł	ICEKHILWLKDYKNSSNWKLPKECWKQGQPAVVSGVHKKMNISL
	1	1	WKAESISLDFGDHOADLLNCKDSIISNANVKBFWDGFEEVSKRO
	l	Į	KNKSGETVVLKLKDWPSGEDFKTMMPARYEDLLKSLPLPEYCNP
	1	1	EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI
	1	l	EVSDVVNILVYVGIAKGNGILSKAGILKKFEEEDLDDILRKRLK
i	ì	1	DSSETPGALWHIYAGKDVDKIRRFLOKISKEQGLEVLPEHDPIR
			DOSWYVNKKLRORLIBEYGVRTWTLIQFLGDAIVLPAGALHQVQ
		<u> </u>	L

	T		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning mucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
i	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
j	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	seddence	\=possible mucleotide insertion)
<b>-</b>	DUJUULUU		NPHSCIQVTEDFVSPRHLVESFHLTQELRLLKKEINYDDKLQVK
}	ļ		NILYHAVKEMVRALKIHEDEVDDMEEN
6890	3	667	THACGMWIPLYLHRALVVHKTAETCNSPPCGAKDSLIFGAITCF
1000	]	007	TGFLGVDTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFV
į			AAKSSIVGAYICIFVGBTLLFSNWAITADILMYVVIPTRRATAV
i	1		ALQSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYA
ł	ł		LMLCPFVVVLGGMFFLATALFFVSDRARAEQQVNQLAMPPASVK
l			V V V V V V V V V V V V V V V V V V V
6891	1980	1262	LRIHQBLLSKELKLLRGITIESIIHIGLAAGKEOFMODASNVMO
	1		LLLKTQSHLYNMEDNNPEVRQAAAYGLGVMAQFGGDDYRSLCSE
1			AVPLLVKVIKRAHSKTKKNVIATENCISAIGKILKFKPNCVNVD
•	1		EVLPHWLSWLPLHEDKEEAIQTLSFLCDLIESNHPVVIGPNNSN
į į			LPKIISIIAEGKINETINYEDPCAKRLANVVRQVQTSEDLWLEC
			VSQLDDBQQRALQELLNFA
6892	3	876	RSVAAASGPGAWGTDHYCLELLRKRDYEGYLCSLLLPAESRSSV
<b>f</b>			FALRAFNVELAQVKDSVSEKTIGLMRMQFWKKTVEDIYCDNPPH
			QPVAIELWKAVKRHNLTKRWLMKIVDEREKNLDDKAYRNIKELB
]			NYAKNTOSSILYLTLEILGIKDLHADHAASHIGKAOGIVTCLRA
			TPYHGSRRKVFLPMDICMLHGVSQEDFLRRNQDKNVRDVIYDIA
1			SQAHLHLKHARSFHKTVPVKAFPAFLQTVSLEDFLKKIQRVDFD
			IPHPSLQQKNTLLPLYLYIQSWRKTY
6893	1	842	DGERKSMSVERTFSBINKAEEQYSLCQELCSBLAQDLQKKRLKG
1	·		RTVTIKLKNVNFEVKTRASTVSSVVSTABBIFAIAKELLKTEID
			ADFPHPLRLRLMGVRISSPPNEEDRKHQQRSIIGFLQAGNQALS
<b>(</b>			ATECTLEKTOKOKFVKPLEMSHKKSFFOKKRSERKWSHQDTFKC
1			EAVNKQSFQTSQPFQVLKKKMNENLEISENSDDCQILTCPVCFR AQGCISLEALNKHVDECLDGPSISENFKMFSCSHVSATKVNKKB
i I			NVPASSLCBKODYEAH
6894	1742	1463	TTLCKPLVPREHQFYETLPAEMRKFTPQYKGKSQLLEGLPHWRG
		1103	DVRDRGHGRPWQPSLBPSLPPTLCFPSLSSFSSWPSAQHLTPS
l			VENDA
6895	2379	478	VTYVELCDLASPTALLIMRTVLDLIVEDLQSTSEDKEQQYTSQT
			TRLLALLYALASHKACKLAYLHLINGTIKGDERYAEIPQDLLAL
			VRSPGDSVIRQQCVBYVTSILQSLCDQDIALILPSSSEGSISEL
			EQLSNSLPNKELMTSICDCLLATLANSBSSYNCLLTCVRTMMFL
			AEHDYGLPHLKSSLRKNSSALHSLLKRVVSTFSKDTGKLASSFL
			EFMRQILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAARLKQLL
			QSKERSPENLFLELEKLVLEHSKDDDNLDSLLDSVVGLKQMLES
			SGDPLPLSDQDVBPVLSAPESLQNLFNNRTAYVLADVMDDQLKS
		ŀ	MWFTPFQAEEIDTDLDLVKVDLIELSEKCCSDFDLHSELERSFL
			SEPSSPGRTKTTKGFKLGKHKHETPITSSGKSEYIEPAKRAHVV
1	ľ		PPPRGRGGGGGGGGRPHDIFRQRKQNTSRPPSMHVDDFVAAES
			KEVVPQDGIPPPKRPLKVSQKISSRGGFSGNRGGRGAFHSQNRF
	İ	ļ	FTPPASKGNYSRREGTRGSSWSAQNTPRGNYNESRGGQSNFNRG
	ļ		PLPPLRPLSSTGYRPSPRDRASRGRGGLGPSWASANSGSGGSRG
6896	<del></del>		KFVSGSGRGRHVRSFTR
0000	1	. 555	GNIVIQKKKYNKQHIIPLENVTIDSIKDEGDLRNGWLIKTPTK8
		-	FAVYAATATEKSEWMNHINKCVTDLLSKSGKTPSNEHAAVWVPD
			SEATVCMRCQKAKFTPVNRRHHCRKCGFVVCGPCSEKRFLLPSQ
. [			SSKPVRICDFCYDLLSAGDMATCQPARSDSYSQSLKSPLNDMSD
6897			DDDDDDSSD
0051	3	920	GDGLMHRVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY
1			AGYEQUTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLPSVL
- 1			SLANGFIADVDLESEKYRRIGEMRFTLGTFLRLAALRTYRGRLA
			YLPVCRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDB
			DPVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
4	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ.	веquence		\=possible nucleotide insertion}
			LRLFLAMBKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGE
]		<u> </u>	IMVSEAVQGQVHPNYFWMVSGCVEPPPSWKPQQMPPPBEPL
6898	919	346	QKTVTAVASLLKGRQGIYTENERRMGAVIKIRFFKIMLVLIICW
i	ł		LSNIINESLLFYLEMQTDINGGSLKPVRTAAKTTWFIMGILNPA
1	İ	1	QGFLLSLAFYGWTGCSLGFQSPRKBIQWESLTTSAAEGAHPSPL
1		1	MPHENPASGKVSQVGGQTSDEALSMLSEGSDASTIBIHTASESC
1	ļ		NKNEGDPALPTHGDL
6899	120	827	MKVRKNNDAYLLDKNKINMDCFISCPFKKMLTTLMFSHSGILSL
			LENGREYTPSLPCAYARSILTVPWVELGGKVSVNCAKTGYSASI
1			TFHTKPFYGGKLHRVTAEVKHNITNTVVCRVQGEWNSVLEFTYS
1	1	1	NGETKYVDLTKLAVTKKRVRPLEKQDPFESRRLWKNVTDSLRES
l	ĺ	[	EIDKATEHKHTLRERORTBERHRTETGTPWKTKYFIKEGDGWVY
İ		İ	HKPLWKIIPTTQPAE
6900	3	451	TRVLGSKGIHELRSSTSALHHALBESASLLTMFWRAALPSTHIP
		l	VLPGKVGESTERELLELETKVSQQEQLLQSTTEHLKNANQQKES
i			MEOFIVSOLTRIHDVLKKARINLEVRKLLHQSEAPSLSPIHHHP
l l	}	}	LADLVGDSWPALRFOEK
6901	<del> </del>	201	DDNMVQRLBTDFKMTLQQQSTLEQWAAWLDNVMMQALKPYEGRP
0501	^	1	SFPKAARQFLLKWSFYRYHLGFS
6902	2	267	GAPPPPPSOPPROPPOAAPSSHPHSDLTFNPSSALEGOAGAOGA
0502	^	207	SDMPRPSLDLLPRLTNPDELLSYLDPPDLPSNSNDDLLSLFENN
6903	1 i	149	RINOVYROGPTGIHILVIDOMVQNFQDESCFLFSTVKAESSDGI
0503	<b>1</b>	147	HILK
6904	464	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVQATQKK6GNPDLLLC
6904	404	2092	VCNFFGSTODAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA
<b>!</b>	ļ	Į.	DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF
l .		į.	3PKDVSSLRMMLCTTSQFKGVDILLTSPWPKCVGNFGNSSGEVD
ì	Ì	1	TKKCGSALVSSLATGLKPRYHFAALRKTYYERLPYRNHIILQEN
į.			ACHATRFIALANVGNPEKKKYLYAFSIVPMKIMDAAELVKQPPD
1 .			VTENPYRKSGORASIGKQILAPVEBSACOFFFDINEKQGRKRSS
1	·	}	TGRDSKSSPHPKOPRKPPOPPGPCWFCLASPKVEKHLVVNIGTH
l	1	t .	CYLALAKGGLSDDHVLILPIGHYQSVVBLSAEVVEEVEKYKATL
		1	RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF
1	1	1	ITOAQEQQIRLLEIPEHSDIKQIAQPGAAYFYVELDTGEKLIFHR
1	1	1	IKKNPPLOFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR
1	1	ĺ	TRANFPIQFGREVIASEATION VEDRSDWRQCQTSREDBETDARR
L-000-	ļ	- 336	VSKTGRAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI
6905	1	226	VSKIGKAETITSHILFALGVIKTBILFNWIWRIHFEGFFDLIAI
C025	<del> </del>	611	SYDDHNGHIDFITAASNIRAKMYSIBPADRFKTKRIAGKIIPAI
6906	3	POTT	•
1	1	1	ATTTATVSGLVALEMIKVTGGYPFKAYKNWFLNLAIPIVVFTET
	I	1	TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE
1		i	PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV
	<u> </u>	L	SFAPDIDGDEDLPGPPVRYYFSHDTD
6907	2	2228	LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS
1	1	1	SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS
1	1	{	DAHTSYYSESLVHESWFPPRESLEELHGDANWGEDLRVRRRRGT
1	1	1	GGSESSRASGLVGRKATEDFLGSSSGYSSBDDYVGYSDVDQQSS
1	<b>S</b>	<b>{</b>	SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWNAGTTWYRLTTAA
1	1	1	SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ
1	1	]	TFHPALVSWWAAKDSRRADEGNEARDSSPHFQAEQRVMSRVHSL
1	1	}	ERRLEALAAEFSSNWQKRAMRLERLELRQGAPGQGGGGGLSHED
[	i	1	TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE
1	i	1	DLYKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE
	Į.	ļ	DQLAGLQQBLAALALKQSSVABEVGLLPQQIQAVRDDVESQFPA
		1	WISOFLARGGGGRVGLLQREEMQAQLRELESKILTHVAEMQGKS
	<u> </u>	<u> </u>	

CRO Dwedieted Dwedieted 3	
	containing signal peptide
	eine, D=Aspartic Acid, E=
	henylalanine, G=Glycine,
location corresponding H=Histidine, I=Isol	
	onine, N=Asparagine,
to first amino acid P=Proline, Q=Glutan	
amino acid residue of SeSerine, TeThreoni	
	rosine, X=Unknown, *=Stop
	nucleotide deletion,
sequence \≈possible nucleoti	
, , , , , , , , , , , , , , , , , , , ,	GVTEEQVHHIVKQALQRYSEDRIGLA
	Tyetktallslfg1plwyhsqsprv1
	PAVVRLSARIRPTAVTLEHVPKALSP
	DLQQEGTLLGKFTYDQDGBPIQTFHF
1. I	NGHPEYTCIYRFRVHGEPAH
f 1	GLGSRLGLQGCFGAARLLYPRFQSRG
	IPKIYTKTGDKGFSSTFTGERRPKDD
QVFEAVGTTDELSSAIGFA	ALELVTEKGHTFABELQKIQCTLQDV
GSALATPCSSAREAHLKY	TTFKAGPILKLEQWIDKYTSQLPPLT
1 1	AVCRRAKRRVVPLVQMGETDANVAKF
	egnqekiykkndpsaesegl
1 I I	eqellvqdatpvsnsllpekafsdip
	QDQDDRRTWDGRPLTMAATFDDCLYA
1	iaimteepelspaylisramrrsrms
LYC	<u> </u>
6910 1 1068 LVPVVV1DSYYYGKLV1A	PLNIVLYNIFTPHGPDLYGTEPWYFY
1	LPLTSLMBYLLQRFHVQNLGHPYWLT
,	erflffvypliclcgavalsalqhsf
1 1 1	ytvtsnwlalgtvflfgllsfsrsva
	ATDPTIHTVPEGRPVNVCVGKEWYRF
, , , , , , , , , , , , , , , , , , , ,	PRGQLPKPFAEGPLATRIVPTDMNDQ
	DLDTMRETPREPKYSSNKERWISLAY
f f l	PFLSDQYTVYVNYTILKPRKAKQIRK
KSGG	
1 1	PGSSPSGLLRKSPGGGREEEEGEESG
PBAABPGQICCDKPVLRD	
i i =	TGSALKAQSYEDAYRCIKSSILLGSI
3 (	VYKGEIQARNIGMAVRAWNEEGKAVW
	FWNDENGNKYRKAYFSKFPGIWAHGD
1 1	GTINPNGVRFGSSEIYNIVESFEEVE
	FLKMASGHAFQPDLVKRIRDAIRMGL
1 1	lngkkvevavkqiiagkaveqggafs
NPRTLDLYRDIPELQGF	er of needeb
6913 1643 . 1558 KKSHKESHKBELSYGAQAS 6914 1251 615 ELAARCKSAGYPGTLIPYS	
, .,	RCDLSNEEDILSMFSAIRSQHSGVDI SGWKDMFNVNVLALSICTREAYOSMK
1	RVLPLSVTHFYSATKYAVTALTEGLR
	VVETOFAFKLHDKDPEKAAATYEOMK
CLKPEDVAEAVIYVLSTP	
CO1E 254 CD CDCY CDVMDY TIME TOTAL	FOOTTHITOWNANL DOOL AULANYOLL
6915 254 652 GRSLSPKTPLIWVLISTY(	רים עמוג זעה. זים פוניערונים זים פולותוא. זים ביו או או או
ALILTBLIMVALTVRTWH	NLMVVARFLSLGCYVSSLAFLNEYFD
ALILTELLMVALTVRTNH VAFITTVTFLWKVSALTVV	vsclplyvlkylrrklsppsycklas
ALILTELLMVALTVRTNHH VAFITTVTFLWKVSAITVV 6916 254 652 GRSLSFKTFLIWVLISIY(	vsclplyvlkylrrklsppsycklas QGGILMYGALVLFESEFVHVVA18FT
ALILTELLMVALTVRTNH VAPITTVTFLWKVSAITVV 6916 254 652 GRSLSPKTFLIWVLISIY( ALILTELLMVALTVRTWH	vsclpi.yvlkylrrklsppsycklas Qggilmygalvlpesepvhvva18PT Wlmvvarplslgcyvsslafinbyfd
ALILTELLMVALTVRTNEN VAPITTVTFLWKVSALTVV 6916 254 652 GRSLSFKTFLIWVLISIY( ALILTELLMVALTVRTWEN VAPITTVTFLWKVSALTVV	vsci.pi.yvlkylrrki.sppsycklas Qggilmygalvlfpsepvhvvai.bpt Wlmvvabplslgcyvsslaflneypd Vsci.plyvlkylrrki.sppsycklas
ALILTELLMVALTVRTNRN VAPITTVTFLWKVSALTVV 6916 254 652 GRSLSPKTFLIWVLISIY( ALILTELLMVALTVRTWHW VAPITTVTFLWKVSALTVV 6917 254 652 GRSLSPKTFLIWVLISIX(	vsci.pi.yvlkylrrki.sppsycklas Qggiimygalvlfesefvhvvaisft Wlmvvabplslgcyvsslaflneyfd Vsci.plyvlkylrrki.sppsycklas Qggiimygalvlfesefvhvvaisft
ALILTBLLMVALTVRTNEN VAPITTVTFLMKVSAITV  6916 254 652 GRSLSPETFLIWVIJSIY( ALILTBLLMVALTVRTWH) VAPITTVTFLMKVSAITV  6917 254 652 GRSLSPETFLIWVIJSIY( ALILTBLLMVALTVRTWH) ALILTBLLMVALTVRTWH)	vsci.plyvlkylrrkisppsycklas Qggilmygalvlfesepvhvvaisft Wlmvvabplslgcyvsslaflneyfd Vsci.plyvlkylrrkisppsycklas Qggilmygalvlfesepvhvvaisft Wlmvvabflslgcyvsslaplneyfd
ALILTBLIMVALTVRTNEN VAPITTVTFLMKVSAITVV 6916 254 652 GRSLSPETFLIWVLISIY ALILTBLIMVALTVRTWEN VAPITTVTFLMKVSAITVV 6917 254 652 GRSLSPETFLIWVLISIY ALILTBLIMVALTVRTWEN VAPITTVTFLWKVSAITVV VAFITTVTFLWKVSAITVV	vsclplyvlkylrrklsppsycklas Qggilmygalvlpesepvhvvaispt Wlmvvarplslgcyvsslaflneypd vsclplyvlkylrrklsppsycklas Qggilmygalvlpesepvhvvaispt Wlmvvarplsigcyvsslaflneypd Vsclplyvlkylrrklsppsycklas
ALILTBLIMVALTVRTNEN VAFITTVTFLMKVSAITVV 6916 254 652 GRSLSFRTFLIWVLISIY( ALILTBLIMVALTVRTNEN VAFITTVTFLMKVSAITVV 6917 254 652 GRSLSFRTFLIWVLISIY( ALILTBLIMVALTVRTNEN VAFITTVTFLWKVSAITVV VAFITTVTFLWKVSAITVV 6918 28 921 PEAGTRSWREPDPEDLRRI	VSCLPLYVLKYLRRKLSPPSYCKLAS QGGILMYGALVLPESEPVHVVAISPT WLMYVARPLSLGCYVSSLAFLNEYPD VSCLPLYVLKYLRRKLSPPSYCKLAS QGGILMYGALVLFESEPVHVVAISFT WLMYVAEPLSLGCYVSSLAFLNEYFD WSCLPLYVLKYLRRKLSPPSYCKLAS FILSAACRSPPQWLPGGGGGQVSSCS
ALILTELLMVALTVRTNEN VAPITTVTFLWKVSAITVV 6916 254 652 GRSLSPKTFLIWVLISIY( ALILTELLMVALTVRTWEN VAPITTVTFLWKVSAITVV 6917 254 652 GRSLSPKTFLIWVLISIY( ALILTELLMVALTVRTWEN VAPITTVTFLWKVSAITVV VAFITTVTFLWKVSAITVV 6918 28 921 PEAGTRSWREPDPEDLRRI DTDVPYLLLAVKSEPGRFF	VSCLPLYVLKYLRRKLSPPSYCKLAS QGGILMYGALVLFESEFVHVVAISFT WLMVVARPLSLGCYVSSLAFINEYFD VSCLPLYVLKYLRRKLSPPSYCKLAS QGILMYGALVLFESEFVHVVAISFT WLMVVAEFLSLGCYVSSLAFLNEYFD VSCLPLYVLKYLRRKLSPPSYCKLAS FILSAACRSPPQWLFCGGGGQVSSCS AERQAVRETWGSPAPGIRLLFLLGSP
ALILTELLMVALTVRTNEN VAFITTVTFLNKVSAITVV 6916 254 652 GRSLSFKTFLIWVLISIY( ALILTELLMVALTVRTWEN VAPITTVTFLWKVSAITVV 6917 254 652 GRSLSFKTFLIWVLISIY( ALILTELLMVALTVRTWEN VAFITTVTFLWKVSAITVV VAFITTVTFLWKVSAITVV 6918 28 921 PEAGTRSWREPDPEDLREN DTDVPYLLLAVKSEPGRFF VGRAGPDLDSLVAWESRRY	VSCLPLYVLKYLRRKLSPPSYCKLAS QGGILMYGALVLFESEFVHVVAISFT WLMVVARPLSLGCYVSSLAFINEYFD VSCLPLYVLKYLRRKLSPPSYCKLAS QGGILMYGALVLFESEFVHVVAISFT WLMVVABFLSLGCYVSSLAFLNEYFD VSCLPLYVLKYLRRKLSPPSYCKLAS FLLSAGCRSFPQWLPGGGGQVSSCS AERQAVRETWGSPAPGIRLLFLLGSP YSDLLLWDFLDVPFNQTLKDLLLLAW
ALILTELLMVALTVRTNEN VAFITTVTFLNKVSAITVV 6916 254 652 GRSLSFKTFLIWVLISIY( ALILTELLMVALTVRTWEN VAFITTVTFLWKVSAITVV 6917 254 652 GRSLSFKTFLIWVLISIY( ALILTELLMVALTVRTWEN VAFITTVTFLWKVSAITVV VAFITTVTFLWKVSAITVV 6918 28 921 PEAGTRSWREPDPEDLREN DTDVPYLLLAVKSEPGRFF VGEAGPDLDSLVAWESRRY LGRHCPTVSFVLRAQDDAN	VSCLPLYVLKYLRRKLSPPSYCKLAS QGGILMYGALVLFESEFVHVVAISFT WLMVVARPLSLGCYVSSLAFLNEYFD VSCLPLYVLKYLRRKLSPSYCKLAS QGGILMYGALVLFESEFVHVVAISFT WLMVVAEFLSLGCYVSSLAFLNEYFD VSCLPLYVLKYLRRKLSPPSYCKLAS FFLSAGCRSFPQWLPGGGGGQVSSCS AERQAVRETWGSPAPGIRLLFLLGSP YSDLLLWDPLDVPPNQTLKDLLLLAW FFVHTPALLAHLRALPPASARSLYLGE
ALILTBLLMVALTVRTMEN VAPITTVTFLMKVSAITV 6916 254 652 GRSLSPKTFLIWVIJSIY( ALILTBLLMVALTVRTWEN VAPITTVTFLMKVSAITVI 6917 254 652 GRSLSPKTFLIWVIJSIY( ALILTBLLMVALTVRTWEN VAPITTVTFLMKVSAITVI 6918 28 921 PEAGTRSWREPDPEDLRRE DTDVPYLLLAVKSEPGRFA VGRAGPDLDSLVAWESRRY, LGRHCPTVSFVLRAQDDAE VFTQAMPLRKPGGPFFVPE	VSCLPLYVLKYLRRKLSPPSYCKLAS QGGILMYGALVLPESEPVHVVA18PT MILMVVARPILSIGCYVSSLAFLNEYPD VSCLPLYVLKYLRKLSPPSYCKLAS QGGILMYGALVLPESEPVHVVA15PT MILMVVABPLSIGCYVSSLAPLNEYPD VSCLPLYVLKYLRRKLSPPSYCKLAS FILISAACRSPPQWLPGGGGQVSSCS AERQAVRETWSPAPGITLIFLIGSP VSCLLLWDPLDVPPNQTLKDLLLLAW FYNTPALLAHLRALPPASARSLYLGE ESPFEGGYPAYASGGGYVIAGRLAPW
ALILTELLMVALTVRTMEN VAPITTVTFLMKVSAITV  6916 254 652 GRSLSPKTFLIWVIJSIY( ALILTELLMVALTVRTWEN VAPITTVTFLMKVSAITVI  6917 254 652 GRSLSPKTFLIWVIJSIY( ALILTELLMVALTVRTWEN VAPITTVTFLWKVSAITVI  6918 28 921 PEAGTESWREPDPEDLREE DTDVPYLLLAVKSEPGRFA VGRAGPDLDSLVAWESRRY) LGRHCPTVSFVLRAQDDAE VFTQAMPLRKPGGPFFVPE	VSCLPLYVLKYLRRKLSPPSYCKLAS QGGILMYGALVLPESEPVHVVAISPT WLMVVARPLSLGCYVSSLAFLNEYPD VSCLPLYVLKYLRKLSPPSYCKLAS QGGILMYGALVLPESEPVHVVAISFT WLMVVARFLSLGCYVSSLAFLNEYPD VSCLPLYVLKYLRRKLSPPSYCKLAS FILSAACRSPPQWLPGGGGQVSSCS AERQAVRETWGSPAPGIRILFLLGSP VSDLLLWDPLDVPPNQTLKDLLLLAW FYNTPALLAHLRALPPASARSLYLGE ESPFEGGYPAYASGGGYVIAGRLAPW GLCIRALGLVPQAHPGFLTAWPADRT

		T 8 37 3	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
[	amino acid	sequence	Codon, /=possible nucleotide deletion,
	Bequence		\=possible mucleotide insertion)
6919	850	41	QGRRELSGSVFCPFIQQEPKEMLTLSEYHBRVRSQGQQLQQLQA
1	İ		ELDKLHKEVSTVRAANSERVAKLVFQRLNEDFVRKPDYALSSVG
j .	<u> </u>		ASIDLQKTSHDYADRNTAYFWNRFSFWNYARPPTVILEPHVFPG
Į.	1		NCWAFEGDQGQVVIQLPGRVQLSDITLQHPPPSVEHTGGANSAP
1			RDFAVFFLLSFFTHQGLQVYDETEVSLGKFTFDVEKSEIQTFHL
Į.			QNDPPAAFPKVKIQILSNWGHPRFTCLYRVRAHGVRTSEGAEGS
ł	j		AQGPH
6920	1418	591	EAQGPSKVHLTLKKKK
6921	2	1711	MNATRSBEQFHVINHABQTLRKMENYLKBKQLCDVLLIAGHLRI
1			PAHRLVLSAVSDYFAAMFTNDVLEAKQEBVRMEGVDPNALNSLV
1	1	1	QYAYTGVLQLKEDTIESLLAAACLLQLTQVIDVCSNFLIKQLHP
1	1	1	SNCLGIRSPGDAQGCTELLNVAHKYTMEHFIEVIKNQEFLLLPA
1	1	l	NEISKLLCSDDINVPDEETIFHALMQWVGHDVQNRQGELGMLLS
1	1	1	YIRLPILPPOLLADLETSSMFTGDLECQKLLMEAMKYHLLPERR
ŀ	1	i	SMMQSPRTKPRKSTVGALYAVGGMDAMKGTTTIEKYDLRTNSWL
]	1	1	HIGTMNGRRLQFGVAVIDNKLYVVGGRDGLKTLNTVKCFNPVGK
ì		1	INTVMPPMSTHRHGLGVATLEGPMYAVGGHDGWSYLNTVERWDP
ł	1		EGRQWNYVASMSTPRSTVGVVALNNKLYAIGGRDGSSCLKSMEY
1			PDPHTNKWSLCAPMSKRRGGVGVATYNGFLYVVGGHDAPASNHC
ļ			SRLSDCVRRYDPKGDSWSTVAPLSVPRDAVAVCPLGDKLYVVGG
1	}	l	YDGHTYLNIVESYDAQRNEWKEEVPVNIGRAGACVVVVKLP
6922	1075	369	LTPPAGIRHEVROREREREREREREKFPLDSTGSELKONIHSIT
1			GLPPAMQKVMYKGLAPEDKTLREIKVTSGAKIMGGGSTINDVLA
1	ļ		VNTPKDAAQQDAKABENKKEPLCRQKQHRKVLDKGKPEDVMPSV
	İ		KGAQKRLPTVPLSGMYNKSGGKVRLTFKLEQDQLWIGTKERTEK
Í			LPMGSIKNVVSEPIEGHEDYHMMAFQLGPTEASYYWVYWVPTQY
1		†	VDAIKDTVLGKWQYF
6923	2469	1660	LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWARAECQRQQ
			LPVTYGNKQKVLGKALSLIRFPLMTIEEFAAGPAQSGILSDREV
l.	ļ		VNLFLHFTVNPKPRVEYIDRPRCCLRGKECCINRFQQVBSRWGY
ļ		l	SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQVNIQIIEYEKK
j			QTLGQNDTGFSCDGTANTFRVMFKEPIBILPNVCYTACATLKGP
ŀ			DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIKDGQIP
1		}	BIIFYT
6924	2210	1235	PEERVICEVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP
1	1	1	KORVKPKRTASRSPASCHEHPMADDPSKSYKLRFVARQVSHHPP
1	1	1	ISCFYCECERARLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE
			HGREYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF
Į.	1	ł	HTKPFYGGKVHRVTABVKHNPINTIVCKAHGEWNGTLEFTYNNG
}	1		BTKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI
}	1		DAATEQKRHLBEKQRVEKRKRENLRTPWKPKYFIQEGDGSGILQ
ļ			SPLESTLMGLEVQSFPV
6925	2	1653	RGGAAGAAMBPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL
1	_		SCLOSMPSVRCLOISNGTSSVIVSRKRPSEGNYQKEKOLCIKYF
1			DOWSESDOVEFVEHLISRMCHYOHGHINSYLKPMLQRDFITALP
	Į.		EQGLDHIAKNILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI
1	1 .		ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI
1	1	Į.	IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG
l	1		LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS
ŀ	1		TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV
1	1		WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW
1		1	STSTCEFVRTINGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC
ł	ł	1	GACLRVLEGHERLYRCIRFDNKRIVSGAYDGKIKVWDLQAALDP
1			
1	1		RAPASTLCLRTLVBHSGRVFRLQFDBFQIISSSHDDTILIWDFL
6006	<del>                                     </del>		NVPPSAQNETRSPSRTYTYISR SGRVAMDGLGLOFPEOGFPAGPPLLPPHMGGHYRDCQSLGAPPL
6926	11	733	POKANTIOPORAL NEGAL NACASTPA SULPCOUT KRC/STOWS ST

670	Two-streets	1 m 12 m 1 m 1	
SEQ ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
L	sequence		\~possible nucleotide insertion)
İ			DGYPLPTPDTSPLDGVDPDPAFFAAPMPGDCPAAGTYSYAQVSD
1			YAGPPEPPAGPMHPRLGPEPAGPS I PGLLAPPSALHVYYGAMGS
ŀ			PGAGGGRGFQMQPQHQHQHQHQHHPPGPGQPTPPPRALPCRDGT
Į.	1		DPSQPABLLGEVDRTEFEQYLHFVCKPEMGLPYQGHDSGVNLPD
6927	2		SHGATSSVVSDASSAVYYCNYPDV
6927	<b>_</b>	1484	LTLCGDIQLMLAQNANNRAAHLEEFHYQTKEDQEILHSLHRESS
í	İ		CQGFAWATDLSTDLESQLSVSCKCYBAANBILQFRDLKSQNPRH YVQVLKRMGNIRNBIGVFYMNQAAALQSBRLVSKSVSAABQQLW
1	ļ		KKSPSCFEKGIHNFESIEDATNAALLLCNTGRLMRICAQAHCGA
1			GDELKREFSPEEGLYYNKAIDYYLKALRSLGTRDIHPAVWDSVN
]			WELSTTYFTMATLQQDYAPLSRKAQEQIEKEVSEAMMKSLKYCD
İ			VDSVSARQPLCQYRAATIHHRLASMYHSCLRNQVGDEHLRKQHR
1			VLADLHYSKAAKLFQLLKDAPCKLLRVQLERVAFAEFQMTSQNS
1			NVGKLKTLSGALDIMVRTEHAFQLIQKELIEEFGQPKSGDAAAA
			adaspsinreevmkilsiyesrisylilqsikilsstkkktsnn
ł			IEDDTILKTNKHIYSQLLRATANKTATLLERINVIVHLLGQLAA
			GSAASSNAVQ
6928	1086	777	EAIDLINNLLQVKMRKRYSVDKTLSHPWLQDYQTWLDLRELECK
			IGERYITHESDDLRWEKYAGEQGLQYPTHLINPSASHSDTPETE
6929	1749	607	ETEMKALGERVSIL RDORGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG
""	1/45	607	NLHQHDPQDLRHNGNVVVAGRPSCSRGPRRAIQKPQPAGGRRSG
			RGPAAGGLCLQPPDGGTCVPEEPPVPPMDWEALEKHLAGLQFRE
			QEVRNQGQARTNSTSAQKNERESIRQKLALGSFFDDGPGIYTSC
i ·			SKSGKPSLSSRLQSGMNLQICFVNDSGSDKDSDADDSKTRTSLD
1 .			TPLSPMSKQSSSYSDRDTTEEESESLDDMDFLTRQKKLQABAKM
1			ALAMAKPMAKMQVEVEKQNRKKSPVADLLPHMPHISECLMKRSL
			KPTDLRDMTIGQLQVIVNDLHSQIESLNEELVQLLLIRDELHTE
(000			QDAMLVDIEDLTRHAESQQKHMABKMPAK
6930	131	545	FKDTANVFVSLFQMRNNFRHYF1BPSQLKLFYDVITWIVTQVAI
i i		i	SYTVVPPVLLSIKPSLTFYSSWYYCLHILGILVLLLLPVKKTQR
1			RKNTHENIQLSQSKKFDEGENSLGQNSFSTTMNVCNQNQELASR HSSLKO
6931	2	659	PVERLPNRPACLLVASGAAEGVSAQSPLHCFTMASTAPNLQVAT
	-	<b>4.33</b>	PGGKAMEFVDVTESNARWVQDFRLKAYASPAKLESIDGARYHAL
[			LIPSCPGALTDLASSGSLARILQHPHSESKPICAVGHGVAALCC
]			ATNEDRSWVFDSYSLTGPSVCELVRAPGFARLPLVVEDFVKDSG
			ACFSASEPDAVHVVLDRHLVTGQNASSTVPAVQNLLFLCGSRK
6932	2	1131	FVDSPGQGEQAEEEEGGIQMNSRMRAHSPAEGASVESSSPGPKK
			SDMCBGCRSLAAGHPGYISHDKETSIKYVSHQHPSHPQLFSIVR
}			QACVRSLSCEVCPGREGPIFFGDEQHGFVFSHTFFIKDSLARGF
	ŀ		QRWYSIITIMMDRIYLINSWPFLLGKVRGIIDBLQGKALKVPEA
	ļ		EQFGCPQRAQRMNTAFTPFLHQRNGNAARSLTSLTSDDNLWACL
	]		HTSFAWLLKACGSRLTEKLLEGAPTEDTLVQMRKLADLERESES
	•	_	WDNSEAEREEKAPVLPESTEGRELTQGPAESSSLSGCGSWQPRK
		•	LPVFKSLRHMRQVGGRGTAHHRLRRRANHGLCLPTRLASGPSTL
6933	1431	a on	KTLQRVTDSLLGGWLMAQGVGGII
,,,,,	+377	890	SLNLHCTLPPPPHQYPAGYPSDKBGKKPKGQSKKQPSGTTKRPI
			SDDDCPSASKVYKASDSAKAIRAFQLTPQQQHLIRBDCQNQKLW
	}		DEVLSHLVEGPNFLKKLEQSFMCVCCQELVYQPVTTECFHNVCK DCLQRSFKAQVFSCPACRHDLGQNYIMIPNEILQTLLDLFFPGY
	l		SKGR
6934	3030	2588	DRDHSQCGGIRRVALARVSSVKLISKAKIRTVKMTPIIVLAFIV
			CWTPPFPVQMWSVWDANAPKBASAPIIVMLLASLNSCCNPWIYM
			LFTGHLFHELVQRFLCCSASYLKGRRLGETSASKKSNSSSFVLS
	İ	ļ	HRSSORSCSQPSTA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:			
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	]	\=possible nucleotide inscrtion)
6935	886	543	NSALYVAGGNDGTSCLNSVBRYSPKAGAWESVAPMNIRRSTHDL
1			VAMDGWLYAVGGNDGSSSLNSIBKYNPRTNKWVAASCMFTRRSS
	1		VGVAVLELLNFPPPSSPTLSVSSTSL
6936	1347	567	RSHRROFLSRALLEFFGKSHPPPHRLFRKSLNVGLHYSHIPFLT
I	İ		TCLHFLRKRLQKGEVGLSVETSKPQVPVGGLSRKKVPQEPWATV
i		İ	MEKRLQEAQLYKEEGNQRYREGKYRDAVSRYHRALLOLRGLDPS
			LPSPLPNLGPQGPALTPEQENILHTTQTDCYNNLAACLLQMBPV
ļ			NYERVREYSOKVLEROPDNAKALYRAGVAFFHLODYDOARHYLL
l	l		AAVNROPKDANVRRYLOLTOSELSSYHRKEKOLYLGMFG
6937	<del>                                     </del>	727	AVEFRCCPGRDPACFARGWRLDRVYGTCFCDQACRFTGDCCFDY
"""	1 *	l <i>'*'</i>	DRACPARPCFVGEWSPWSGCADQCKPTTRVRRRSVQQEPQNGGA
1	1	l	PCPPLEERAGCLEYSTPQGQDCGHTYVPAFITTSAFNKERTRQA
İ	1		TSPHWSTHTEDAGYCMBFKTBSLTPHCALENRPLTRWMQYLRBG
I	i	ļ	
1	1		YTVCVDCQPPAMNSVSLRCSGDGLDSDGNQTLHWQAIGNPRCQG TWKKVRRVDOCSCPAVHSFIFI
-	<del></del>		
6938	3	719	NSRKLELAERVOTOFMQLKKRRQSSEKENDSGTLDTVGAVVVDH
l .	i		BGNVAAAVSSGGLALKHPGRVGQAALYGCGCWARNTGAHNPYST
1		•	AVSTSGCGEHLVRTILARECSHALQAEDAHQALLETMONKFISS
į			PFLASEDGVLGGVIVLRSCRCSAEPDSSQNKQTLLVEFLWSHTT
1			RSMCVGYMSAQDGKAKTHISRLPPGAVAGQSVAIEGGVCRLGBP
			SELTLQAECEASQRHFRT
6939	3	810	KVTAPRRPQRYSSGHGSDNSSVLSGELPPAMGRTALFHHSGGSS
1			Gyeslrrdseatgsassapdsmsesgaaspgartrslkspkkra
1 .			TGLQRRRLIPAPLPDTTALGRKPSLPGQWVDLPPPLAGSLKEPF
		·	BIKVYBIDDVERLQRPRPTPREAPTQGLACVSTRLRLAERRQQR
İ	1		LREVQAKHKHLCEBLAETQGRLMLEPGRWLEQFEVDPELEPESA
t			EYLAALERATAALEQCVNLCKAHVMMVTCFDISVAASAAIPGPQ
			BADA
6940	1188	496	GRMAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMENDTQ
1 .			VVKGSSPLGPAGLGAREPAAGPQLPSWLQPERCAVFQCAQCHAV
1	,		LADSVHLAMDLSRSLGAVVFSRVTNNVVLKAPFLVGIEGSLKGS
J	}		TYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLL
			KTKAIVNASEMDIQNVPLSEKIABLKEKIVLTHNRLKSLMKILS
L			RVTPDQSKPEN
6941	1	713	SLSRADSDPHGPHTCGHVLNVIIGSNVLALAEAQRQABALGYQA
l			VVLSAAMQGDVKSMAQFYGLLAHVARTRIJPSMAGASVERDAQI.
1			HBLAABLQIPDLQLBRALBTMAWGRGPVCLLAGGBPTVQLQGSG
	1		RGGRNQELALRVGAELRRNPLGPIDVLFLSGGTDGQDGPTEAAG
]			AWYTPRLASQAAAEGLDIATFLAHNDSHTFFCCLQGGAHLLHTG
l	i		MTGTNVMDTHLLFLRPR
6942	1	246	GDYVERYDPKTDTWTMGAPLSMPTNAVGGCLLGDRLYADGGYDG
1			QTYLNTMBSYDPQTNBWTQMASLNIGRAGACVVVIKQP
6943	. 1	739	PMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLG
	_	· = <del>-</del>	HSPAGGSITETLVQGDKTEYLLTALEPKPTYIICMVTMETTNAY
			VADETPVCAKAETADSYGPTTTLNQEQNAGPMASLPLAGIIGGA
1			VALVFLFLVLGAICWYVHQAGELLTRERAYNRGSRKKDDYMESG
1	<b>j</b>		TKKDNSILEIRGPGLOMLPINPYRAKEBYVVHTIFPSNGSSLCK
1			ATHTIGYGTTRGYRDGGIPDIDYSYT
6944	960	156	VANILLNGVKYBSBLTGSSERAEQPLSVGRLCSTICNMPKALRT
1 0 2 2 2	70U	130	LCVNHFLGWLSPEGMLLFYTDFMGEVVFQGDPKAPHTSEAYQKY
1			
			NSGVIMGCWGMCIYAFSAAFYSAILEKLEEFLSVRTLYFIAYLA
			FGLGTGLATLSRNLYVVLSLCITYGILFSTLCTLPYSLLCDYYQ
			SKKPAGSSADGTRCMGVDISLLSCQYPLAQILVSLVLGPLTSA
1			VGSANGVMYFSSLVSFLGCLYSSLFVIYEIPPSDAADEKHRPLL
I	1		LNV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6945	2067	179	EGEDRGLPRTMGAALGTGTRLAPWPGRACGALPRWTPTAPAQGC
Ì	Ì		HSKPGPARPVPLKKRGYDVTRNPHLNKGMAFTLKERLQLGIHGL
}	ļ		IPPCFLSQDVQLLRIMRYYBRQQSDLDKYIILMTLQDRWEKLFY RVLTSDVEKFMPIVYTPTVGLACQHYGLTFRRPRGLFITIHDKG
1	1	Ì	HLATMINSWPEDNIKAVVVTDGERILGLGDLGCYGMGIPVGKLA
Į.	l		LYTACGGVNPOOCLPVLLDVGTNNEBLLRDPLYIGLKHQRVHGK
1	}	}	AYDDLLDBFMQAVTDKFGINCLIQFBDFANANAFRLLNKYRNKY
1	ł		CMFNDDIQGTASVAVAGILAALRITKNKLSNHVFGFQGAGRAAM
}		}	G\IAHLLVMALE\KEGVPKA\EATRKIW\MVDF\KGLIVQGRDH
			INHEKEMFAQD\HPEVNSLEBVVRLVKPTAIIGVAAIABA\FTB
ļ	l		QILRDMASFHERP\IIFALSNPTSKAECTA\EKCYRVTEGPRGF
	i	į	FAS\GSPF*GVLIWEMGKTFIPGGRGNNA*RVPRGWQLGVHSPG
ļ	Į		GDPGHIP\DEIFLPDSRAKLPQEVSEQHLSQGRLYP\PLST\IR
]			NVFLRIAIKVFD*GYKHNLV\SYYPEPKD\KEAFCKIPG8YTPD
			YDSFYT/VDSYIWAQGKAMNVQTV
6946	133	2551	SCEYSGITVAPGDPCPGVAHLLAPSMASDTPRSLMALCTDFCLR
}	-	ł	NLOGTIGYLLDKETLRLHPD1FLPSB1\CDRLVNEYVELVNAAC NF\EPHE\SFFNPLFRDPRKOPASRR1HL\RBD\LVQD\QD\LE
1			AIRKODL\VEL\YLTN\CEKLSAKSLQTLRSPSHTLGVP*AFFG
j	l		C\TNILLERKENPGGL/CEDEYLFNPTCQVLVKDFTFEGFSRLR
	}		P\LKLGRMIDWVPVBS\LLRPLNSLAALDLSGIQTSDAA\FLTQ
ļ	l	1	WKDSL\VSLVL\YMMDLSDDHIR\VIVQLHKLRHLDISRDRLSS
ļ	ļ.	ļ	YYKFKLTREVLSLFVQKLGNLMSLDISG\HMILENCSISKIGKR
l	ł		EAGQTSI\EPSK\SSIIPFRGFEGGPLQF\LGVF*GIFCGRLTH
	Į.		IPAYKVSGDKNEEQVLNAIKAYTEHRPEITSRAINLLFDLARIE
		ŀ	RCNQLLRALKLVITALKCHKYDRNIQVTGSAALFYLTNSEYRSE
ľ			QSVKLRRQVIQVVLNGMESYQEVTVQRNCCLTLCNFSIPEELEF
]	j		QYRRVNELLLSILNPTRQDESIQRIAVHLCNALVCQVDNDHKEA
	ł		VGKMGFVVTMLKLTQKKLLDKTCDQVMEFSW\SALWNITDETPD
	1		NCEMPLNFNGMKLFLDCINEFPEKQBLHRNMLGLLGNVAEVKEL
	ļ ·		RPOLMTSOFISVFSNLLESKADGIEVSYNACGVLSHIMFDGPEA WGVCEPOREEVEERMWAAIOSWDINSRRNINYRSFEPILRLLPO
}	}		GISPVSQHWATWALYNLVSVYPDKYCPLLIKEGGMPLLRDIIKM
l	1	ł	ATARQETKEMARKVIEHCSNFKEENMDTSR
6947	<del>  2</del>	1682	TSVSTIPRGLASARPOSRSWRCCPVWRRSPGRARGRGLKMLNVP
031,	1		SQSFPAPRSQQRVASGGRSKVPLKQGRSLMDWIRLTKSGKDLTG
ł	ł		LKGRLIEVTEBELKKHNKKDDCWICIRGFVYNVSPYMEYHPGGE
			DELMRAAGSDGTBLFDQVHRWVNYESMLKECLVGRMAIKPAVLK
[	Į	[	DYRBEEKKVLNGMLPKSQVTDTLAKEGPSYPSYDWFQTDSLVTI
l	ł	}	/EHIY*TEGYQFRLNNS*SSB*FLYSRNNY*GLLISYTYW/R*A
1			MRFRKIPLCGL/CESVGKIEIVLQKKENTSWDFLGHPLKNHNSL
}	}		IPRKDTGLYYRKCQLISKEDVTHDTRLFCLMLPPSTHLQVPIGQ
İ			HVYLKLPITGTRIVKPYTPVSGSLLSEFKEPVLPNNKYIYFLIK
1	1		IYPTGLPTPELDRLQIGDFVSVSSPEGNPKISKFQELEDLFLLA
1			ASTGFTPMVKILNYALTDIPSLRKVKLMFFNKTRDDIIWRSQLE
1	i e		KLAPKOKRLOVEFVLSAPISEWNGKQGHISPALLSEFLKRNLOK
			SKYLVCICGPVPFTEQGVRLLHDLNFSKNRIHSFTA
6948	104	58	PDGAHSFPPDEYFTCSSLCLSCGVGCKKSMNHGKEGVPHEAKSR CRYSHQYDNRVYTCKACYERGEEVSVVPKTSASTDSPWMGLAKY
}	1		AWSGYVIECPNCGVVYRSRQYWPGNQDPVDTVVRTEIVHVWPGT
,	l		DGFIKDNNNAAQRLLDGMNFMAQSVSRLSLGPTKAVTSWLTDQI
Ī			APAYWRPNSOILSCNKCATSPKDNDTKHHCRACGEGFCDSCSSK
1			TRPVPERGWGPAPVRVCDNCYEAR/TRPVSCYRGTSGR*RRRRT
]			OETVB
6949	152	4656	GLRICLSRPLTRPGDDSVGGSAMASGAGGVGGGGGGKIRTRRCH
]		}	QGPIKPYQQGRQQHQGILSRVTESVKNIVPGWLQRYFNKNEDVC
L	<u> </u>	L	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alamine, C=Cysteine, D=Aspartic Acid, E=
	nucleotide		
NO:	1	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=beucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
<del></del>		· · · · · · · · · · · · · · · · · · ·	SCSTDTSEVPRWPENKEDHLVYADEESSNITDGRITPEPAVSNT
ł	1		REPSTTSTAST\YPDVLTRVSLYRSHLNFSMLESPALHCQPSTS
1			1
J			SAPPIGSSGPSLVKEIKDSTSQHDDDNISTTSGFSSRASDKDIT
1			VSKNTSLPPLNSPEARRSHSLSQHTATSSKKPAFNLSAFGTLSP
Į.	ļ		SLGNSSILKTSQLGDSPFYPGKTTYGGAAAAVRQSKLRNTPYQA
l	i ·		PVRRQMKAKQLSAQSYGVTSSTARRILQSLEKMSSPLADAKRIP
İ	i		SIVSSPLNSPLDRSGIDITDFQAKREKVDSQYPPVQRLMTPKPV
i			SIATNRSVYPKPSLTPSGEFRKTNQRIDKKCSTGYEKNMTPGQN
1			REQRESGFSYPNFSLPAANGLSSGVGGGGGKMRRERHAFVASKP
1			LREEEMEGPVLPKISLPITSSSLPTFNFSSPEITTSSPSPINSS
ı	Ì		QALTNKVQMTSPSSTGSPMFKPSSPIVKSTRANVLPPSSIGFTP
1	ì		SVPVAKTAKLSGSSSTLEPIISSSAHHVITVNSTNCKKTPPEDC
1		l	BGPFRPARILKEGSVLDILKSPGFASPKIDSVAAQPTATSPVVY
1	l	l	TRPAISSFSSGIGFGRSLKAGSSWOCDTCLLONKVTDNKCIAC
1		[	
l			QAAKLSPRUTAKQTGIBTPNKSGKTTLSASGTGFGDKFKPVIGT
ì	]		WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET
į.			MTASSSSCTVTTGTLGPGDKFKRPIGSNECSVCCVSNNAEDNKC
			VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPRGIWDC
i			BLCLVONKADSTKCLACKSAKDGTKSGFKGFDTSSSSSNSAASS
l	ŀ		SPKFGVSSSSSGPSQTLTSTGNFKPGDQGGPKIGVSSDSGYINP
ļ			MSEGF*FSKHIVGFKFGVSSESKPREVKKDSKNDNFKFGLSFGL
ł.	ļ	ļ.	SNPVFLTPPQFGVSNLGQBBKKBBLLKSSCAGFRFGTGVINSTR
			VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA
ł	}	}	TKGGFSFGNVEPASLPSASVFVLGRTEBKQQBPVTSTSLVFGEG
ŀ	ĺ	1	KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE
1			SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS
\	}		AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTABSST
<b>†</b> '		ŀ	SOSILFSODSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG
1	]	}	ATTTSSSAGSSFVFGTGPSAPSASPAFGANQTPTFGQSQGASQP
1	ţ	ļ	NPPGFGSISSSTALFPTGSQPAPPTFGTVSSSSQPPVFGQQPSQ
i		1	SAFGSGTTPNSSSAFQPGSSTTNFNFTNNSPSGVFTFGANSSTP
<b>j</b> .	)	<b>)</b> '	
į.	Į.	Į.	AASAQPSGSGFPFNQSPAAFTVGSNGKNVFSSSGTSFSGRKIK
			TAVRRRK
6950	2585	411	PRPGSRSGLCRRAGERGAVRAGGLSRRTRAE+IMDELHYQDTDS
ı	]	Ī	DVPEQRDSKCKVKWTHEKDEQLRALVRQFGQQDWKFLASHFPNR
1	1	}	TDQQCQYRWLRVLNPDLVKGPWTKEEDQKVIELVKKYGTKQWTL
j		}	IAKHLKGRLGKQCRERWHNHLNPEVKKSCWTEEEDRIICEAHKV
i	I	ŀ	LGNRWABIAKMLPGRTDNAVKNHWNSTIKRKVDTGGFLSESKDC
1		)	KPPVYLLLELEDKDGLQSAQPTEGQGSLLTNWPSVPPTIKEKEN
1		ł	SEEELAAATTSKEQEPIGTDLDAVRTPEPLEEFPKREDQEGSPP
1	1	ł	ETSLPYKWYVEAANLLIPAVGSSLSEALDLIESDPDAWCDLSKF
1	<u> </u>	1	DLPEEPSAEDS INNSLVQLQASHQQQVLPPRQPSA\LVPSVTEY
1	]		RLDGHTISDLSRSSRGELIPISPSTEVGGSGIGTPPSVLKRORK
1	1	1	RRVALSPYTENSTSLSFLDSCNSLTPKSTPVKTLPFSPSQFLNF
(	į.		
1	1	•	WNKQDTLRLESPSLTSTPVCSQKVVVTTPLHRDKTPLHQKHAAF
1	<b>\</b>	f ·	VTPDQKYSMDNTPHTPTPFKNALEKYGPLKPLPQTPHLEEDLKE
		1	VLRSBAGIBLIIEDDIRPEKQKRKPGLRRSPIKKVRKSLALDIV
1	1	1	DEDMKLMMSTLPKSLSLPTTAPSNSSSLTLSGIREDNSLLNQGF
1	ł	4	LQAKPEKAAVAQKPRSHFTTPAPMSSAWKTVACGGTRDQLFMQE
1		1	KARQLLGRLKPSHTSRTLILS
6951	1940	239	AGPDDTMKRSLQALYCQLLSPLLILALTEALAFAIQEPSPRESL
1	1		QVLPSGTPPGTMVTAPHSSTRHTSVVMLTPNPDGPPSQAAAPMA
i	Į.		TPTPRAEGHPPT\TPSPPSLRQ*PPPILKAP/SSTGPAPAAMAT
1	1	1	TSSKPEGRPRGOAAPTILLTKPPGATSRPTTAPPRTTTRRPPRP
	ĺ	I	
İ	1	1	PGSSRKGAGNSSRPVPPAPGGHSRSKEGORGRNPSSTPLGQKRP
L	<u></u>	<u> </u>	LGKIFQIYKGNFTGSVBPEPSTLTPRTPLWGYSSSPQPQTVAAT

SEQ Predicted predicted end beginning nucleotide location nucleotide location corresponding to first amino acid residue of amino acid segment containing signal per (A=Alanine, C=Cysteine, D=Aspartic Acid, Glutamic Acid, F=Phenylalanine, G=Glycin H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Sequence Codon, /=possible nucleotide deletion, \_=possible nucleotide insertion)  TVPSNTSWAPTTTSIGPAKOKPGLRRAAGGGGSTFTSQGGTAASGAPVSP/PSCPSAFSAPPPR*PTGCPVLSPGWYPGTTHPSKVSESTISGAKKETVA\PSP*PTGCPVLSPGWYPGTTTPATGPTPTGCPVLSPGWYPGTTTPATGPTPTGCPVLSPGWYPGTTTPATGPTPTGCPVLSPGWYPGTTTPTGCPVLSPGWYPGTTTPTGCPVLSPGWYPGTTTPTGCPVLSPGWYPGTTTTPTGCPVLSPGWYPGTTTTPTGCPVLSPGWYPGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	, E= ne,
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence code sequence code code code code code code code co	ne,
location corresponding to first amino acid residue of amino acid sequence  location corresponding to first amino acid residue of amino acid sequence  corresponding to first amino acid residue of amino acid sequence  codon, /=possible nucleotide deletion, location, location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location	
corresponding to first amino acid residue of amino acid residue of amino acid sequence  Sequence  Codon, /=possible nucleotide insertion)  TVPSNTSWAPTTTSLGPAKDKPGLRRAAGGGSTFTSQGGTAATGPTPAAFDTSVSAPSQGIPQGASTT	Stop
to first amino acid residue of sequence P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, amino acid sequence Codon, /=possible nucleotide deletion, =possible nucleotide insertion)  TVPSNTSWAPTTTSLGPAKDKPGLRRAAGGGSTFTSQGGTAASGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYCYSRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTT	Stop
amino acid residue of sequence S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=S (Codon, /=possible nucleotide deletion, t=possible nucleotide insertion)  TVPSNTSWAPTTSLGPAKDKPGLRRAAGGGSTFTSQGG TAASGAPVSP/PSCPSAFSAPPRR*PTGWPQP**LLAYCY SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTT	Stop
residue of amino acid sequence Codon, /=possible nucleotide deletion, (=possible nucleotide deletion)  TVPSNTSWAPTTTSLGPAKDKPGLRRAAGGGSTFTSQGC  TAASGAPVSP/PSCPSAFSAPPPR*PTGWPQP***LLAYCY SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTT	Stop
amino acid sequence Codon, /=possible nucleotide deletion, sequence \text{\text{\text{-possible nucleotide insertion}}} \\ \text{TVPSNTSWAPTTTSLGPAKDKPGLRRAAQGGSTFTSQGC} \\ \text{TAASGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYCS} \\ \text{SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTS} \\ \text{SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTS} \\ \text{TABSGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYCS} \\ \text{SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTS} \\ \text{TABSGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYCS} \\ \text{SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTS} \\ \text{TABSGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYCS} \\ \text{SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTS} \\ \text{TABSGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYCS} \\ \text{SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTS} \\ \text{TABSGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYCS} \\ \text{SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTS} \\ \text{TABSGAPVSP/PSCPSAFSAPPPR*PTGWPQP***LLAYCS} \\ \text{SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTS} \\ \text{TABSGAPVSP/PSCPSAFSAPPPR*PTGWPQP***LLAYCS} \\ \text{SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTS} \\ \text{TABSGAPVSP/PSCPSAFSAPPPR*PTGWPQP****LAYCS} \\ \text{SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTS} \\ TABSGAPVSP/PSCPSAFSAPPPR*PTGWPQP***********************************	JUD
sequence   \=possible nucleotide insertion     TVPSNTSWAPTTTSLGPAKDKPGLRRAAQGGSTFTSQGG   TAASGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYCS   SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTT	
TVPSNTSWAPTTTSLGPAKDKPGLRRAAQGGGSTFTSQGG TAASGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYC'SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGAST	
TAASGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYCY SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTY	TPDA
SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTT	
· · · · · · · · · · · · · · · · · · ·	•
	-
STAWSPPGPGSLGQQCTSPMWPRGTNRSTEPPSA*ARWIS	
WPSACPSPP\LCPADGVLHEBBEEDRQPGEQPEAYGNNTF	
TFQQAC\RGAAFGBIPVPLKPLRTQLSRPRSPANGDYRD1	
c	
6952 658 304 PESEGESGEMTDRYTIHSQLEHLQSKYIGT\ATPTPPSGS	CVCK
PTPRLVLLLHGPLRPSQLLRHCGE*EQSASPLQLDGKDAS	-
ASRQARGELELCLITTAVRGTSPSVSPVCQSS	
6953 1512 349 NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRET	CODES
FSPHFRGKMGGVV\KLBKELENTEQPVGGNEG*KHEVTGN	_
PLLBLCQCPLCQLDCGSREQLIAHVYQHTAAVVSAKSYM	
GRALSSPGSLGRHLLIHSEDORSNCAVCGARFTSHATFNS	
BVLNMBSLPTVHNEGPSSARGKDIAPSPPVYPAGILLVC	
YRKLLEAGTPSVRKWALRRQNEPLEVRLGRLERERTAKKS	SRRDN
ETPREREVRRMRDREAKRLQRMQETDEQRARRLQRDREAM	IRLKR
AIETPEKRQARLIREREAKRLKRRLEKMDMMLRAQFGQDE	AMAR
ALAAEMNFFQLPVSGVELDSQLLGKMAFEEQNSSSLH	
6954 819 1 PPPPFIIPSHPREAGT+AG+KRSGDSECSPFVEQ+A+TRA	AAAQN
*PQR*RWTEGNSPQASAVATPGQGASPAAPRCTP*PSRRI	IRRLP
PGARPPAG*AAPAPTKPWLAGPASAPQPGAAPLSPPAPPI	IRTR
*CAGAAARGRPRRDRSPRPTPGGCSWSEPRTPPAVSASA	AQTPS
DAG*AGGR*GQRQRPSTGR*PPGVGGAGRSHRREGTIPGN	<b>IPHPR</b>
AS*RAGWQR*PGP/REWGL*EPQGEEMSGPGGAPPNC	2VGSS
VMQAMSTGI	
6955 1968 782 PPGRRQVRAQVAGAPVGHWGTRARQVKTGGRRRARRTMPF	7LGQD
WRSPGWSWIKTEDGWKRCESCSQKLERENNHCNISHSIII	
GEIFNNEEHBYASKKRKKDHFRNOINTQSFYREKWIYVH	
BRHGYCTLGEAFNRLDFSSAIQDIRRFNYVVKLLQLIAKS	
LSGVAQKNYFNILDKIVQKVLDDHENPRLIKDLLQDLSST	
/N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*AS	
LTLSDLPLHMLNNILYRFSDGWDIITLGQVTPTLYMLSEI	
KKLCQYHFABKQFCRHLILSBKGHIBWKIMYFALQKHYPA	
GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHF1	DPLK
<u> </u>	20000
DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVS	
PEISPKVCPAASTVVSPAVPSVVSPASSAVLPAVSLRVPI TSPKASPVTSPAAAPPTASPANKDVSSFLRTTADVREITG	
ASGSGDVMRRRIATPREVRLPLQHGWRREVRIKKGSHRWQ	
YYGPCGKRMKOPPEVIKYLSRNVVHSVRREHFSFSPRMPU	
EERDTPEGLOWVOLSAERIPSRIOAITGKRGRPRNTEKAR	
PKVKRGRGPPKVKITELLNKTDNRPLKKLRAOKTLNERC	
AKSKKKMRQKVQRGBCQTTIQGQARNKRKQBTKSLKQKEA	
KARKEKGKTKOEKLKEKVKREKKEKVKMKEKEEVTKAKPA	
XTLATORRLRERQRQOMILEEMKKPTEDMCLTDHOPLPDF	
GLTLPSCAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVL	
LCQGDSIGEVODILVRLIKAALHDPGFPSYCQSLKILGEN	
PLTRDNVSEILRCFLMAYGVEPALCDRLRTQPFQAQPPQQ	
LAFLVHBLNGSTLIINEIDKTLESMSSYRKNKWIVEGRLR	
1 1	
VLAKRTGRSEVEMEGPEECLGRRRSSRIMEVTSGMEEERE AAVDCDDCCDDCCEUDATAGGTDDLEDGTEGT CKDOLEER	
AAVPGRRGRDGEVDATASSIPELERQIEKLSKRQLFFRK	
SSQMLRAVSLGQDRYRRRYNVLPYLAGIFVBGTEGNLVPE KRTDSLKVAAHASLNPALFSMKMELAGSNTTASSPARARG	
RETURNERVANDAMENTALISMENTALISMETALISMENT   RETURNERVANDAMENTALISMENT   RETURNERVANDAMENTALISMETALISMENT   RETURNERVANDAMENTALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALISMETALI	KPKK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ı	sequence		\=possible nucleotide insertion)
			TKPGSMQPRHLKSPVRGQDSEQPQAQLQPEAQLHAPAQPQPQLQ
1			LQLQSHKGFLEQEGSPLSLGQSQHDLSQSAFLSWLSQTQSHSSL
1	1		LSSSVLTPDSSPGKLDPAPSQPPEEPEPBPBAESSPDPQALWFNI
1			SAQMPCNAAPTPPPAVSEDQPTPSPQQLASSKPMNRPSAANPCS
ŀ			PVQFSSTPLAGLAPKRRAGDPGKMPQSPTGLGQPKRRGRPPSKF
<b>.</b>	]		PKQMBQRYLTQLTAQPVPPEMCSGWWW1RDPBMLDAMLKALHPR
1	!		GIREKALHKHLNKHRDFLQEVCLRPSADPIFEPRQLPAFQEGIM
	j ,		SWSPKEKTYETDLAVLQWVEBLEQRVIMSDLQIRGWTCPSPDST
			REDLAYCEHLSDSQEDITWRGRGREGLAPQRKTTNPLDLAVMRL
			AALEQNVERRYLREPLWPTHEVVLEKALLSTPNGAPEGTTTEIS
			YEITPRIRVWRQTLERCRSAAQVCLCLGQLERSIAWEKSVNKVT
			CLVCRKGDNDEFLLLCDGCDRGCHIYCHRPKMEAVPEGDWFCTV
			CLAQQVEGEFTQKPGPPKRGQKRKSGYSLNFSEGDGRRRRVLLR
1			GRESPAAGPRYSEEGLSPSKRRRLSMRNHHSDLTPCEIILMEME
			SHDAAWPFLEPVNPRLVSGYRRIIKNPMDFSTMRERLLRGGYTS SEEFAADALLVFDNCQTFNEDDSEVGKAGHIMRRFFE\SRWBEP
			YQGKQGQSVRQGRWGVTLWHLPPTFQTKTCHFHLLMLPWVQTQV
1			RYMPDF
6957	82	3514	HLIVAMPEPTKKKENEVPAPAPPPEEPSKEKBAGTTPAKDWTLV
1 1			ETPPGEEQAKQNANSQLSILFIEKPQGGTVKVGEDITFIAKVKA
			EDLSEKPTINGSRKWMDLASKAGKHLQLKETFERHSRVYTFEMQ
			IIKAKONFAGNYRCEVTYKOKFOSCSFOLEVHESTGTTPNIDIR
1 1			SAPKRSGEGQEDAGELDFSGLLKRREVKQQEEEPQVDVWELLKN
[ ·			TKPSEYEKIAFQYESPTCSGMLKRLKRSIREEKKSAAFAKILDP
1			VYQVDKGGRVRFVVELADPKLKVKWNKNGQKLRPSTKYIFEDTR
1 1			CQSILNIDNCQMTDDSBYYVTAGDBKCSTKLLVREPPIMVTKQL
1 1	·		RDTTDYCGERVELECEVSEDDAQVKWPKWGEEIILVQTRYRIRV
1 [			EGKKHILIIEGATKADAADYSVMTTGGQSSAKLSVDLKPLKILT
1	ŀ		PLTDQTVNLGKEICLKCEISENIPGKWTKNGLPVQESDRLKVVH
1 1			KGRIHKLVIDHALTEDEGDYVFAPDAYNVTLPAKVHVIDPPKII LDGLDADNTVTVIAGNKLRLEIPISGEPPPKAMNSRGDKAIMEG
]			SGRIRTESYPDSSTLVIDIAERDDSGVYHINLKNEAGRAHASIK
1 1			VKVVDFPDPPVAPTVTEVGDDWCIMNWEPPAYDGGSPILGYFIE
			RKKKQSSRWMRLNFDLCKETTPBPKKMIEGVAYEVRIPAVNA\+
	· ]		RKKKQSSRWMRLNFDLCKETTFEPKKMIEGVAYEVRIPAVNA\I GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI
<u> </u>			GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI
			GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFBGSTSAKQSDBNGBAAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVKAVNAAGASBPKYYSQPILVKB
			GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDBNGBAAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVKAVNAAGASBPKYYSQPILVKB IIBPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPELTWKKD
			GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDBNGEAAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVKAVNAAGASBPKYYSQPILVKB IIBPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPBLTWKKD GABIDKNQINIRNSETDTIIFIRKABRSHSGKYDLQVKVDKFVB
			GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDENGERAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVAVNAAGASBPKYYSQPILVKE IIBPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPELTWKKD GABIDKNQINIKNSETDTIIFIKKAERSHSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT
			GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDENGEBAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVKAVNAAGASBPKYYSQPILVKE IIBPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKRPREHTWKND GABIDKNQINIRNSETDTIIFIRKABRSHSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIEDVWGRNVALIWTPPKDDGNAAIT GYTIQKADKKSMEWLRVIEHIIEPVPHTRLVIGNEYYFRVFSEN
			GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDENGEAAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVKAVNAAGASBPKYYSQPILVKE IIBPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPELTWKKD GABIDKNQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIBDVWGRNVALTWTPPKDDGNAAIT GYTIQKADKKSMEWLRVIEHIIEPVPHTRLVIGNEYYFRVFSEN MCGLSEDATMTKESAVIARDGKIYKNPVYEDPDFSEAPMFTQPL
			GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDENGEAAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVKAVNAAGASEPKYYSQPILVKE IIEPPKIHSPKHLKQTYIRRVGDRVILVIPFOGKPRELTWKKD GABIDKNQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIBDVWGRNVALTWTPPKDDGNAAIT GYTIQKADKKSMEWLRVIEHIIEPVPHTELVIGNEYYFRVFSEN MCGLSEDATMTKESAVIARDGKIYKNPVYEDPDFSEAPMFTQPL VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPRYRMFS
6959	274		GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDBNGEAAYDLPAEDWIVANKD LIDKTKFTTTGLPTDAKIFVRVKAVNAAGASBPKYYSQPILVKE IIBPPKIHSPKHLKQTYIRRVGDRVILVIFFGGKPRPELTWKKD GABIDKNQINIRNSETDTIIFIKAERSHSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT GYTIQKADKKSMEWLRVIEHIIEPVPHTRLVIGNEYYFRVFSEN MCGLSEDATMTKESAVIARDGKIYKNPVYEDPDFSEAPMFTQPL VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPRYRMFS NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ
6958	274	1663	GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDENGERAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVVKAVNAAGASBEKYYSQPILVKE IIBPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPBLTWKKD GABIDKNQINIRNSETDTIIFIRKABRSHSGKYDLQVKVDKFVB TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT GYTIQKADKKSMEWLRVIEHIIEPVPHTELVIGNBYYFRVFSEN MCGLSEDATMTKESAVIARDGKIYKNPVYBDPPFBEAPMFTQPL VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPRYRMFS NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ PRTSRVKTEGSQGSSAMDFSVKVDIEKEVTCPICLELLTBPLSI
6958	274	1663	GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDENGERAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVAVNAAGASBPKYYSQPILVKR LIDRYKHSPKHLKQTYIRRVGDRVILVIPFQGKPRPBLTWKKD GABIDKNQINIKNSETDTIIFIRKABRSBSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT GYTIQKADKKSMEWLRVIEHIIEPVPHTELVIGNBYYFRVFSEN MCGLSEDATMTKESAVIARDGKIYKNPVYEDPDFBEAPMFTQPL VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPRYRMPS NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ PRTSRVKTEGSQGSSAMDFSVKVDIEKEVTCPICLELLITBFISL DCGHSFCQACITAKIKESVIISRGESSCPVCQTRFQPGNLRPNR
695B	274	1663	GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDENGERAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVKAVNAAGASBPKYYSQPILVKR LIDRYKHSPKHLKQTYIRRVGDRVILVIPFQGKPRPELTWKKD GABIDKNQINIRNSETDTIIFIRKABRSHSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT GYTIQKADKKSMEWLRVIEHIIEPVPHTRLVIGNEYYFRVFSEN MCGLSEDATMTKESAVIARDGKIYKNPVYEDFDFSEAPMFTQPL VNRLCHSGYMATLNCSVKGNPKPKITWMKNKVAIVDDPRYRMFS NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ PRTSRVKTEGSQGSSAMDFSVKVDIEKEVTCPICLBLLTRPISL DCGHSFCQACITAKIKESVIISRGESSCPVCQTRPQPGNLRPNR HLANIVERVKEVKMSPQEGQKRDVCKHHGKKLQIPCKEDGKVIC
6958	274	. 1663	GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDENGEAAYDLPAEDWIVANKD LIDKTKFFTTGLPTDAKIFVRVKAVNAAGASBPKYYSQPILVKE IIBPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPELTWKKD GABIDKNQINIRNSETDTIIFIRKABRSHSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIBDVWGRNVALITWTPPKDDGNAALT GYTIQKADKKSMEWLRVIEHILEPVPHTRLVIGNBYYFRVFSEN MCGLSEDATMTKESAVIARDGKIYKNPVYEDPDPSEAPMFTQPL VRRLCHSGYMATLNCSVRGNPRPKITWMKNKVAIVDDPRYRMPS NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ PRTSRVKTEGSQGSSAMDFSVKVDIBKEVTCFICLELLTBPLSL DCGHSFCOACITAKIKBSVIISRGESSCPVCQTRFQPGNLRPNR HLANIVERVREVKMSPQEGQREDVCKHHCKKLQIFCKEDGKVIC WVCELSQEHQGHQTPRINBVVKBCQEKLQVALQRLIKENQEARK
695B	274	1663	GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDENGEAAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVKAVNAAGASBPKYYSQPILVKE IIBPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPELTWKKD GABIDKNQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAATT GYTIQKADKKSMEWLRVIEHILEPVPHTELVIGNBYYFRVFSEN MCGLSEDATMTKESAVIARDGKIYKNPVYEDFDPSEAPMFTQPL VNRLCHSGYMATLNCSVRGNPRPKITWMKNKVAIVDDPRYRMFS NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ PRTSRVKTEGSQGSSAMDFSVKUDIEKEVTPICLELLITBPLSI DCGHSFCQACITAKIKESVIISRGESSCFVCQTRFQPGNLRPNR HLANIVERVREVMSPQEGQKRDVCKHHGKKLQIPCKEDGKVIC WVCELSQEHQGHQTFRINEVVKECQBKLQVALQRLIKENQRAEK LEDDIRQERTAWKNYIQIERQKILKGFNENRVILDNEEQRBLQK
6958	274	1663	GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDENGERAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVVKAVNAAGASBYKYYSQPILVKE LIBPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPBLTWKKD GABIDKNQINIRNSETDTIFIRKABRSHSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAALT GYTIQKADKKSMEWLRVIEHILEPVPHTELVIGNBYYFRVFSEN MCGLSEDATMTKESAVIARDGKIYKNPVYEDPPFSEAPMFTQPL VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPRYRMFS NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ PRTSRVKTEGSQGSSAMDFSVKVDIEKEVTCPICLELLTBPLSL DCSHSFCOACITAKIKBSVIISRGESSCPVCQTRFQPGNLRPNR HLANIVERVREVKMSPQEGQKRDVCBHHCKKLQIFCKEDGKVIC WVCBLSGEHQGHOTPRINBVVKECQBKLQVALQRLIKENQEABK LEDDIRQERTAWKNYIQIERQKILKGPWEMRVILDNEEQRBLQK LEEGEVNVLDNLAAATDQLVQQRQDASTLISDLQRRIRGSSVEM
6958	274	1663	GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDENGERAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVVKAVNAAGASPKYYSQPILVKE ITBPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPBLTWKKD GABIDKNQINIRNSETDTIIFIRKABRSBSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT GYTIQKADKKSMEWLRVIEHIIEPVPHTELVIGNEYYFRVFSEN MCGLISEDATMTKESAVIARDGKIYKNPVYEDPDFSEAPMFTQPI VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPRYRMFS NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ PRTSRVKTEGSQGSSAMDFSVKVDIBKEVTCPICLELLTEPISI DCGHSFCQACITAKIKESVIISRGESSCPVCQTRFQPGNLRPNR HLANIVERVKEVKMSPQEGQKRDVCKHHGKKLQIFCKEDGKVIC WVCELSQEHGCHQTFRINBVVKBCQBKLQVALQRLIKENQERBLQK LEDDIRQERTAWKNYIQIERQKILKGFNEMRVILDNEEQRBLQK LEBGEVNVLDNLAAATDQLVQQRQDASTLISDLQRRLRGSSVEM LQDVIDVMKRSESWTLKKPKSVSKKLKSVFNVPDLSGMLQVIKE
6958	274	1663	GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDENGERAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVVRAVNAAGASPKYYSQPILVKE ITBPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPBLTWKKD GABIDKNQINIKNSETDTIIFIRKABRSHSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIBDVWGRNVALTWTPPKDDGNAAIT GYTIQKADKKSMEWLRVIEHIIEPVPHTELVIGNBYYFRVFSEN MCGLISEDATMTKESAVIARDGKIYKNPVYEDPDFSEAPMFTQPI VNRLCHSGYMATLNCSVRGNPKPKITWKNKVAIVDDPRYRMFS NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ PRTSRVKTEGSQGSSAMDFSVKVDIBKEVTCPICLELLITEPISI DCGHSFCQACITAKIKESVIISRGESSCPVCQTRFQPGNLRPNR HLANIVERVKEVKMSPQEGQKRDVCKHHGKKLQIPCKEDGKVIC WVCELSQEHQCHQTFRINBVVKBCQBKLQVALQKLIKENQEABK LEDDIRQERTAWKNYIQIBRQKILKGFNEMRVILDNEEQRBLQK LEBGEVNVLDNLAAATDQLVQQRQDASTLISDLQRRLRGSSVEM LQDVIDVMKRSESWTLKKPKSVSKKLKSVFRVPDLSGMLQVIKE LTDVQYYWDVMLNPGSATSNVAISVDQRQVKTVRTCTFKNSNP
6958	274	1663	GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDENGERAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVKAVNAAGASBPKYYSQPILVKR LIDKTKFTITGLPTDAKIFVRVGDRVILVIPFQGKPRPELTWKKD GABIDKNQINIRNSETDTIIFIRKABRSHSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT GYTIQKADKKSMEWLRVIEHIIEPVPHTRLVIGNEYYFRVFSEN MCGLSEDATMTKESAVIARDGKIYKNPVYEDFDFSEAPMFTQPL VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPRYRMPS NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ PRTSRVKTEGSQGSSAMDFSVKVDIEKEVTCPICLELLTRPISL DCGHSFCQACITAKIKESVIISRGESSCPVCQTRFQPGNLRPNR HLANIVERVKEVKMSPQEGQKRDVCBHHGKKLQIFCKEDGKVIC WVCGLSQEHQCHQTTRINBVVKBCQBKLQVALQRLIKENQEABK LEDDIRQERTAWKNYIQIRQKILKGFMEMRVILDNEBQRBLQK LEGSEVNVLDNLAAATDQLVQQRQASTLISDLQRRLRGSSVEM LQDVIDVMKRSESWTLKKPKSVSKKLKSVFRVPDLSGMLQVLKE LTDVQYYWDVMLMPGSATSNVAISVDQRQVKTVRTCTFKRSNP CDFSAFGVFGCQYFSSGKYYWEVDVSGKIAWILGVHSKISSLNK
695B	274	1663	GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDENGERAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVVRAVNAAGASPKYYSQPILVKE ITBPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPBLTWKKD GABIDKNQINIKNSETDTIIFIRKABRSHSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIBDVWGRNVALTWTPPKDDGNAAIT GYTIQKADKKSMEWLRVIEHIIEPVPHTELVIGNBYYFRVFSEN MCGLISEDATMTKESAVIARDGKIYKNPVYEDPDFSEAPMFTQPI VNRLCHSGYMATLNCSVRGNPKPKITWKNKVAIVDDPRYRMFS NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ PRTSRVKTEGSQGSSAMDFSVKVDIBKEVTCPICLELLITEPISI DCGHSFCQACITAKIKESVIISRGESSCPVCQTRFQPGNLRPNR HLANIVERVKEVKMSPQEGQKRDVCKHHGKKLQIPCKEDGKVIC WVCELSQEHQCHQTFRINBVVKBCQBKLQVALQKLIKENQEABK LEDDIRQERTAWKNYIQIBRQKILKGFNEMRVILDNEEQRBLQK LEBGEVNVLDNLAAATDQLVQQRQDASTLISDLQRRLRGSSVEM LQDVIDVMKRSESWTLKKPKSVSKKLKSVFRVPDLSGMLQVIKE LTDVQYYWDVMLNPGSATSNVAISVDQRQVKTVRTCTFKNSNP
6958	274	1663	GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLBYCFEGSTSAKQSDENGERAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVKAVNAAGASBYKYYSQPILVKR LIDKTKFTITGLPTDAKIFVRVKAVNAAGASBYKYYSQPILVKR GABIDKNQINIRNSETDTIIFIRKABRSHSGKYDLQVKVDKFVR TASIDIRIIDRPGPPQIVKIEDVWGRNVALITWTPYKDDGNAAIT GYTIQKADKKSMEWLRVIEHIIEPVPHTRLVIGNEYYFRVFSEN MCGLSEDATMTKESAVIARDGKIYKNPVYEDPDPSEAPMFTQPL VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPRYRMPS NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ PRTSRVKTEGSQGSAMDFSVKVDIBKEVTCPICLBLLTBPLSL DCGHSFCOACITAKIKESVIISRGESSCPVCOTTROPGNLRPNR HLANIVERVKEVKMSPQEGQKRDVCKHHGKKLQIPCKEDGKVIC WVCBLSQEHQGHOTPRINEVVKBCQBKLQVALQRLIKENQEABK LEDDIRQERTAWKNYIQIERQXILKGPNEWRVILDNEBQRBLQK LEEGEVNVLDNLAAATDQLVQQRQDASTLISDLQRRLRGSSVEM LQDVIDVMKRSESWTLKKPKSVSKKLKSVFRVPDLSGMLQVLKE LTDVQYYWDVMLNPGSATSNVAISVDQRQVKTVRTCTFKNSNP CDFSAFGVFGCQYFSSGKYYWEVDVSGKIANILGVHSKISSLNK RKSSGFAFDPSVNYSKVYSRYRPQYGYWVIGLQNTCEYNAPEDS

C 455	1 7	Predicted end	Daving and assembly contide giornal contide
SEQ	Predicted	nucleotide	Amino acid segment containing signal peptide (A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	beginning	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		to first	L=Leucine, M=Methionine, N=Asparagine,
<u> </u>	corresponding to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ſ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	1	Codon, /=possible nucleotide deletion,
İ	1	sequence	\=possible nucleotide insertion)
	sequence	<u> </u>	
	1		LQPQTPGLNQSSHLSLLSSRDYRMLSSFNEWFWQDRFWLPPNVT
1			WTELEDROGRVYPHPQDLLAALPLALVLLAMRLAFERFIGLPLS
ŀ	Į.	ŀ	RWLGVRDQTRRQVKPNATLEKHFLTEGHRPKEPQLSLLAAQCGL
		Ì	TLQQTQRWFRRRRNQDRPQLTKKFCRASWRFLFYLSSFVGGLSV
			LYHESWLWAPVMCWDRYPNQLTLSCPAADSEA\SLYWWYLLELG
1			FYLSLLIRLPFDVKRKGGGPSSIKPRPHYDPPSTA\DFKEQVIH
		i	HPVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLRACKMVNYMQ
	ļ	ł	YQQVCDALFLIFSFVFFYTRLVLFPTQILYTTYYRSISNRGPFF
į.	1		GYYFFNGLIMLIQLIHVFWSCLILRMLYSFMKKGOMBKDIRSDV
1			EESDSSEBAAAAQBPLQLKNGTAGGPRPAPTDGPRSRVAGRLTN
			RHTTAT
6960	387	2068	AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS
ł		Ì	HLEPREKQALKRLVEBEPLKMQVDEAASREDKLDLTKKGKRPPT
		,	PCSDPRRKRFRFNSBSESGSEASSPDYFGPPAKNGVASRSHTHP
}			KBENPRRA\SKAVEESSDEKRORDLPAORGKESSEKKKKGYKGK
		Ì	TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTAKKVEGN KGTKSLKESEQESEEEILAQKKEQREEEVEEEKEEDEEKGDWK
1		1	PRTRSNGRRKSAREERSCKOKSQAKRLLGDSDSEKEQKEAASSG
]			<b>1</b> • • • • • • • • • • • • • • • • • • •
1			DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTA KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS
1		}	SRKGRTRSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIR
1			ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCR
			ALKEQREBAAEVASLDVANIISGSGRPRRRTAWNPLGEAAPPGB
		1	LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN
6961	340	1646	RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL
0 201	340	1040	NOESPOLALLEEVWSEODFOYLROKLSPTYPAAHHFRSGIIGSG
		Ì	LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL
			SGMVLNAYVTHIHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK
ł		ł	ADVVLLCODLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG
		l	NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET
			TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS
ŀ		1	PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL
ĺ		1	LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG
		İ	LYRAOAKLOHVLGRAREAODLGPEPQLYALL\LGQQEGDRTKEQ
6962	340	1646	RPWS8PTMKPNFSLRLRIFNLNCWG1PYLSKHRADRMRRLGDFL
0302			NOESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG
1	ĺ		LCVPSKHPIOELTOHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL
l			SGMVLNAYVTHLHABYNRQKDIYLAHRVAQAWELAQFIHHTSKK
			ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG
	Į.	1	NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET
			TTGFDPHRGTPLSDHRALMATLFVRHSPPQQNPSSTHGP\AERS
Į.	1	İ	PL/MCVCLKEALDGSLGLGMA\QARWWA\TPA\SYVIGLGL\LL
[	1	1	LALLCYLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQBVNG
ł	1	1	LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ
6963	374	2618	RVTPLILKILKKPKTAENQKASEENEITQPGGSSAKPGLPCLNF
			BAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN
	1	1	LHNFSNSVLETLNEORNRGHFCDVTVR IHGSMLRAQRCVLAAGS
}	ł	1	PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA
ł		1	LOILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG
· ·		[	TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE
1		1	RSPYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL
1	ľ	[	STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ
			ILERNESEECTEDIDQAEGTESEPKGESFDSGVSSSIGTEPDSV
			EOOFGPGAARDSOAKPTOPEOAAKAPAEGGPQTNQLETGASSPE
l	1	1	RSNEVEMOSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR
1		I	QTETLTSNLRMPLTLTSNTQVIGTAGNTYLPALFTTQPAGSGPK
L	1	<u> </u>	Kunner mint mint and a to transfer trees of the support

WO 01/53312

PCT/US00/34263

SEQ Predicted beginning nucleotide location nucleotide location corresponding to first amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence	cic Acid, B= G=Glycine, sine, ragine, ine, ine, hown, *=Stop letion, PAPOPLASSAGH FVHTGEKPHQCSI CRFTQKSSLNVHM SASNGTPPAGTPP QFNDHMRMHVSDG
No: nucleotide location corresponding to first amino acid residue of amino acid sequence counce councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence councillate and sequence	G=Glycine, sine, ragine, ine, ine, hown, *=Stop letion, PAPOPLASSAGH FVHTGEKPHQCSI GRFTQKSSLNVHM SASNGTPPAGTPP QFNDHMRMHVSDG
location corresponding to first amino acid residue of amino acid sequence    Percline, Q=Glutamine, N=Aspan   Percline, Q=Glutamine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=V	sine, ragine, ine, , nown, *=Stop letion,  PAPOPLASSAGH FTOKSSLNVHM SASNGTPPACTPP PFNDHMRMHVSDG
corresponding to first amino acid amino acid residue of amino acid sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code, sequence code,	ragine, ine, , nown, *=Stop letion,  PAPOPLASSAGH FURTGEKPHCCSI GRFTOKSSLNVHM BASNGTPPAGTPP PFNDHMRMHVSDG
to first amino acid residue of amino acid residue of amino acid sequence  P=Proline, Q=Glutamine, R=Argini S=Serine, T=Threonine, V=valine, W=Tryptophan, Y=Tyrosine, X=Unkn Codon, /=possible nucleotide del \=possible nucleotide insertion)  PFLFSLPQFLAGQOTQFVTVSQPGLSTFTAQI STASGQGEKKPYECTLCNKTFTAKQNYVKNME CWRSFSLKDYLIK\HMVTHTGVRAYQCSICNK RLHRGEKSYBCYICKKKFSHKTLLERHVALHS GARAGPPGVVACTEGTTYVCSVCPAKFDQISQ  1 178 SGRPFFFFSNTDVYFIKKVTNRWTAGSSYKM QIPIG\NCSMFVLVI SGSLGYNLPQNH\GLIGRNTLVLLGQMRRISP PQRKVEVSQLQKA\QAMSFLYDVLQQVFNFSH PGPTPHFTSSAAGTPGDLLGAGDGRRRSWCQW	ine, nown, *=Stop letion, DPAPOPLASSAGH TVHTGEKPHQCSI RRFTQKSSLNVHM BASNGTPPAGTPP QFNDHMRMHVSDG
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unkm Codon, /=possible nucleotide del \  -possible nucleotide insertion	nown, *=Stop Letion, 
residue of amino acid sequence Codon, /=possible nucleotide del sequence PFLFSLPQPLAGOOTOFVTVSQPGLSTFTAGI STASGQEKKPYECTLCNKTFTAKONYVKHME CWRSFSLKDYLIK\HMVTHTGVRAYQCSICNK RLHRGEKSYECYICKKRFSHKTLLERHVALHS GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQ OF 1 178 SGRPFFFFFSNTDVYFIKKVTNRWTAGSSYKM QIFIG\NCSMFVLVI  6965 757 208 NVFIERRIQGFMKTSAHPGQKHPDFSMGLLFF GGSLGYNLPQNH\GLLGRNTLVLLGQMRRISP PQRKVEVSQLQKA\QAMSFLYDULQQVFNFSH PGPTPHFTSSAAGTPGDLLGAGDGRRRSWCQW	nown, *=Stop Letion, PAPOPLASSAGH FVHTGEKPHQCSI CRFTQKSSLNVHM SASNGTPPAGTPP QFNDHMRMHVSDG
amino acid sequence Codon, /=possible nucleotide del   -possible nucleotide insertion)   PFLFSLPQPLAGQOTQFVTVSQPGLSTFTAQI     STASGGEKKPYECTLCNKTFTAKQNYVKINE     CWRSFSLKDYLIK,HMVTHTGVRAYQCSICNK     RLHRGEKSYBCYICKKKFSHKTLLBRHVALHS     GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQ     G964 1 178 SGRPFFFFFSNTDVYFIKKVTNRWTAGSSYKM     QIFIG\NCSMFVLVI     G965 757 208 NVFIERRIQGFMKTSAHPGQKHPDFSMGLLFF     SGSLGYNLPQNH\GLLGRNTLVLLGQMRRISP     PQRKVEVSQLQKA\QAMSFLYDULQQVFNFSH     PQRKVEVSQLQKA\QAMSFLYDULQQVFNFSH     PGPTPHFTSSAAGTPGDLLGAGDGRRRSWCQW	Letion,  PAPOPLASSAGH  FVHTGEKPHQCSI  GRFTQKSSLNVHM  EASNGTPPAGTPP  QFNDHMRMHVSDG
Sequence   Sequence   Sequence   Sequence   STASSQGERRPYETTLCNKTFTAKONYVKHME   STASSQGERKPYECTLCNKTFTAKONYVKHME   CWRSFSLKDYLIK\HMVTHTGVRAYQCSICNK   RLHRGEKSYRCYICKKKFSHKTLLERHVALHS   GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQ   GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQ   GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQ   GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQ   GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQ   GARAGPPGVVFIKKVTNRWTAGGSYKM   QIPIG\NCSMFVLVI   QUPIG\NCSMFVLVI   GASGLGYNLPQNH\GLLGRNTLVLLGQMRRISP   GGSLGYNLPQNH\GLLGRNTLVLLGQMRRISP   PQRKVEVSQLQKA\QAMSPLYDVLQQVFNPSH   PGPTPHFTSSAAGTPGDLLGAGDGRRRSWCQW	LPAPOPLASSAGH FVHTGEKPHOCSI GRFTOKSSLNVHM BASNGTPPAGTPP OFNDHMRMHVSDG
PFLFSLPQPLAGQQTQFVTVSQPGLSTFTAQI STASGQGBKRPYECTLCNKTFTAKQNYVKHMF CWRSFSLKDYLIK\HMVTHTGVRAYQCSICNK RLHRGEKSYBCYICKKRFSHKTLLERHVALHS GARAGPPGVVACTEGTTYVCSVCPAKFDQIBQ 6964 1 178 SGRPFFFFSNTDVYFIKKVTNRWTAGSSYKM QIPIG\NCSMPVLVI 6965 757 208 NVFIEPRIQGFMKTSAHPGQKHPDFSMGLLFF SGSLGYNLPQNH\GLLGRNTLVLLGQMRRISP PQRKVEVSQLQKA\QAMSFLYDVLQQVFNPSH PGPTPHFTSSAAGTPGDLLGAGDGRRRSWCQW	LPAPQPLASSAGH FVHTGEKPHQCSI CRFTQKSSLNVHM SASNGTPPAGTPP QFNDHMRMHVSDG
STASGQGEKRPYECTLCNKTFTAKONYVKHME CWRSPSLKDYLIK\HMVTHTGVRAYQCSICNK RLHRGEKSYBCYICKKKPSHKTLLERHVALHS GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQ 6964 1 178 SGRPFFFFSNTDVFIKKVTNRWTAGSSYKM QIPIG\NCSMFVLVI 6965 757 208 NVFIEPRIQGFMKTSAHPGQKHPDFSMGLLFF SGSLGYNLPQNH\GLLGRNTLVLLQQMRRISP PQRKVEVSQLQKA\QAMSPLYDVLQQVFNPSH PGPTPHFTSSAAGTPGDLLGAGDGRRRSWCQW	TVHTGEKPHQCSI CRFTQKSSLNVHM BASNGTPPAGTPP QFNDHMRMHVSDG
CWRSFSLKDYLIK\HMVTHTGVRAYQCSICNK RLHRGEKSYBCYICKKKFSHKTLLERHVALHS GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQ 6964 1 178 SGRPFFFFSNTDVYFIKKVTNRWTAGSSYKM QIPIG\NCSMFVLVI 6965 757 208 NVFIEPRIQGFMKTSAHPGQKHPDFSMGLLFF SGSLGYNLPQNH\GLIGRNTLVLLGQMRRISP PQRKVEVSQIQKA\QAMSFLYDVLQQVFNFSH PGPTPHFTSSAAGTPGDLLGAGDGRRRSWCQW	CRPTOKSSLNVHM BASNGTPPAGTPP OFNDHMRMHVSDG
RLHRGEKSYBCYICKKKFSHKTLLERHVALHS GARAGPPGVVACTEGTTYVCSVCPAKFDQIBQ 6964 1 178 SGRPFFFFSNTDVYFIKKVTNRWTAGSSYKM QIPIG\NCSMFVLVI 6965 757 208 NVFIEPRIQGFMKTSAHPGQKHPDFSMGLLFF SGSLGYNLPQNH\GLLGRNTLVLLQQMRRISH PQEKVEVSQLQKA\QAMSFLYDVLQQVFNFSH PGPTPHFTSSAAGTPGDLLGAGDGRRRSWCQW	SASNGTPPAGTPP OFNDHMRMHVSDG
GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQ 6964 1 178 SGRPFFFFFSNTDVYFIKKVTNRWTAGSSYKM QIFIG\NCSMFVLVI 6965 757 208 NVFIEBRIQGFMKTSAHPGQKHPDFSMGLLFF SGSLGYNLPQNH\GLLGRNTLVLLQQMRRISP PQRKVEVSQIQKA\QAMSFLYDVLQQVFNFSH PGFTPHFTSSAAGTPGDLLGAGDGRRRSWCQW	PNDHMRMHVSDG
6964 1 178 SGRPFFFFSNTDVYFIKKVTNRWTAGSSYKM QIFIG\NCSMFVLVI 6965 757 208 NVFIEPRIQGPMKTSAHPGQKHPDFSMGLLFF SGSLGYNLPQNH\GLLGRNTLVLLGQMRRISP PQEKVEVSQLQKA\QAMSFLYDVLQQVFNPSH PGPTPHFTSSAAGTPGDLLGAGDGRRSWCQW	
QIFIG\NCSMFVLVI 6965 757 208 NVFIEPRIQGPMKTSÄHPGQKHPDPSMGLLFP SGSLGYNLPQNH\GLLGRNTLVLLGQMRRISP PQEKVEVSQLQKA\QAMSFLYDVLQQVFNPSH PGPTPHFTSSAAGTPGDLLGAGDGRRSWCQW	ACTION 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
6965 757 208 NVFIEPRIQGFMKTSAHPGQKHPDPSMGLLFP SGSLGYNLPQNH\GLLGRNTLVLLGQMRRISP PQEKVEVSQLQKA\QAMSFLYDVLQQVFNPSH PGPTPHFTSSAAGTPGDLLGAGDGRRSWCQW	TTRMKSTGKTILL
SGSLGYNLPQNH\GILGRNTLVLLGQMRRISP PQRKVEVSQLQKA\QAMSPLYDVLQQVFNPSH PGPTPHFTSSAAGTPGDLLGAGDGRRRSWCQW	
PQEKVEVSQLQKA\QAMSFLYDVLQQVFNPSH PGPTPHFTSSAAGTPGDLLGAGDGRRRSWCQW	
PGPTPHFTSSAAGTPGDLLGAGDGRRRSWCQW	
1 1 I I I	•
· · · · · · · · · · · · · · · · · · ·	IVIEGSTLALKRY
FQESISTLE 6966 820 1867 IITALGVRGMPGCPCPGCGMAGPRILIFITALA	T DT T ON T O O O
6966 820 1867 IITALGVRGMPGCPCPGCGMAGPRLLFLTALA ALRSRGTATACRLDNKESESWGALLSGERLDT	
LSGVFPLLVIPLEMGTMLRSEAGANRLKOLLS	
HLLPRAWAYTCSASPGGEGQSLQQQQQLGLWV	
/HVPGQQGGGDQPGPQQRPHCCCRRAQWRPLS	
GP\DIKVSGYLNLLANTIDNFTHGLAVAASFL	
ILLIBIPHEVGDPAILLRAGFDRWSAAKLQLS	
ICTQSPKGVBETAAWVLPPTSGGFLYIALVNV	
6967 162 633 GPLPFKYWILDLSASSRMETDCNPMKLSSMSG	
TOMKOMRLKABAVVNOVLFAVNNMFVSKSLRC	
ERNRYCLELTEAGLKUVGYAFDQVDDHLQTPY	
SPAYREAFGKR\LLQRLEALKRDGQS	
6968 1 2265 RGGGGGRGGPGARERERPGEPERTMEAAAGGR	GCFOPHPGLOKT
LEQPHLSSMSSLGGPAAFSARWAQEAYKKESA	KEAGAAAVPAPV
PAATEPPPVLHLPAIQPPPPVLPGPFFMPSDR	STERCETVLEGE
TISCFVVGGBKRLCLPQILMSVLRDFSLQQIM	AVCDELHIYCSR
CTADQLEILKVMGILPFSAPSCGLITKTDAER	LCNALLYGGAYP
PPCKKELAASLALGLELSERSVRVYHE\CFGK	CKGL/LVPBLYS
SPSAACIQCLD\CRIMYPPHKFVVHSHKALRN	
	FDYGNKYKRRVP
RVSSEPPASIRPKTDDTSSQSPAPSRKDKPSS	
LGCVHPRQRLSAFRPWSPAVSASBKBLSPHLP	
PETAVAPNVALAPPAQQKVVSSPPCAAAVSRA	
RKLTVDTPGAPETLAPVAAPBKDKDSRAKVEV	
LSSPSPTSSSSAKDLGSPGARALPSAVPDAAA	
EHLRQALEGGLDTKRAKEKFLHEVVKMRVKQE	
LHQELEPLRVAKKEKLREATEAKRNLRKEIER;	
NESRLRLKRBLEQARQARVCDKGCEAGRLRAK	
QHAEADREQLRADILLREREAREHLEK\VVK\E	T-CEAT-MAKWAKAB
AAGSEG\AAELEP	Churchttrouge
6969 1855 118 AGTMHGRLKVKTSEEQAEAKRLEREQKLKLYQ	
GKLDESVLELTSQILGANPDFATLWNCRREVLO AALVKAELGFLESCLRVNPKSYGTWHHRCWLLO	
RICARPLEVDERNPHCWDYRRPVATOAAVPPAI	
NFSNYSSWHYRSCLLPOLHPOPDSGPQGRLPBI	
NFSNISSWHYRSCLLDPQLHPQPDSGPQGKDPBI APFTDPNDQSAWFYHRWLLGRADPQDALRCLHY	7 1
l 1 ·	
SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRI	
AASLNDQLPQHTFRVIWTAGDVQKECVLLKGR(	
QLPRCKLSVEKSTVLQSELESCKELQELEPENT	
RALDPLLYEKETLQYFQTLK\AWDPKRATY\Li VLKMBYABVRVLHLAHKDLTVLCHLEQLLLVTI	
· · · · · · · · · · · · · · · · · · ·	
PPALAALRCLEDPPPRT\VLQASDNAIESLDG\	_
)	1 TOTAL DOLL A 101 1 1
CNNRLQQPAVLQPLASCPRLVLLNLQGNPLCQA PSVSSVLT	AVGILEQLARLL

			and the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second o
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
110	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6970	3	1528	SPPPLLSSPSAVGEGKVAVAAPCPGRSECARAKMAYIQLEPLNE
			GFLSRISGLLLCRWTCRHCCQKCYESSCCQSSEDEVEILGPFPA
l		ļ	QTPPWLMASRSSDKDGDSVHTASKVPLTPRTNSPDGRRSSSDTS
		*	KSTYSLTRRISSLESRRPSSPLIDIKPIEFGVLSAKKEPIQPSV
	<u> </u>	}	LRRTYNPDDYFRKFEPHLYSLDSNSDDVDSLTDEBILSKYQLGM
ļ			LHFSTQYDLLHNHLTVRVIEARDLPPPISHDGSRQDMAHSNPYV
l	1		KICLLPDQKNSKQTGVKRKTQKPVPEERYTFEIPFLEAQRRTLL
Į.			LTVVDFDKFSRHCVIGKVSVPLCEVDLVKGGHWWKALIPSSQNE
	}	1	VELGELLLSLNYLPSAGRLNVDVIRAKQLLQTDVSQGSDPFVKI
ľ	ļ	Ì	QLVHGLKLVKTKKTSFLRGTIDPFYNRSFSFKVPQBELENASLV
ļ	i		FTVFGHNMKSSNDFIGRIVIG\QYSSGP\SEPNHWRRMLNTHRT
l	1		AVEQWHSLRSRAECDRVSPASLEVT
6971	37	3702	ACFYVPGSRSFKLIPRHGLVNMGRSGKLPSGVSAKLKRWKKGHS
, /			SDSNPATCRHRQAARSRFFSRPSGRSDLTVDAVKLHNELQSGSL
	İ	ļ	RIGKSRAPETPMEERABLVLTEKSSGTFLSGLSDCTNVTFSKVQ
i		1	RFWBSNSAAHKBICAVLAAVTEVIRSQGGKETETEYFAALIRKA
			AOHGVCSVLKGSEFMFEKAPAHHPAAISTAKFCIQBIBKSGGSK
	Ì		BATTTIHMLTLLKDLLPCPPEGLVKSCSBTLLRVMTLSHVLVTA
			CAMOAFHSLFHARPGLSTLSAELNAQIITALYDYVPSENDLQPL
ĺ			LAWLKVMEKAHINLVRLQWDIGIGHLPRFFGTAVTCLLSPHSQV
i			LTAATQSLKEILKECVAPHMADIGSVTSSASGPAQSVAKMFRAV
	{		EEGLTYKFHAANSSVLQLLCVFFBACGRQAHPVMRKCLQSLCDL
		j	RLSPHFPHTAALDQAVGAAVTSMGPEVVLQAVPLEIDGSBETLD
l			FPRSWLLPVIRDHVQETRLGFFTTYFLPLANTLKSKAMDLAQAG
	<b>}</b>		STVESKIYDTLQWQMWTLLPGFCTRPTDVAISPKGLARTLGMAI
			SERPDLRVTVCQALRTLITKGCQAEADRAEVSRFAKNFLPILFN
		1	LYGQPVAAGDTPAPRRAVLETIRTYLTITDTQLVNSLLEKASEK
I			VLDPASSDFTRLSVLDLVVALAPCADEAAISKLYSTIRPYLESK
		'	AHGVQKKAYRVLEEVCASPQGPGALFVQSHLEDLKKTLLDSLRS
İ		1	TSSPAKRPRLKCLLHIVRKLSABHKEFITALIPBVILCTKEVSV
			GARKNAFALLVEMGHAFLRFGSNQBBALQCYLVLIYPGLVGAVT
ł			MVSCSILALTHLLFEFKGLMGTSTVEQLLENVCLLLASRTRDVV
1			KSALGFIKVAVTVMDVAHLAKHVQLVMEAIGKLSDDMRRHFRMK
į			LRNLFT\KF1PK\FGILTWGKKAVGPKEYHRVLVN1RKARARAK
	1	1	RHRALSQAAVEERBEEEEBBEPAQGKGDSIBEILADSEDBEDNE
1	1		EEERSRGKEORKLARORSRAWLKEGGGDEPLNFLDPKVAORVLA
ſ	1		TQPGPGRGRKKDHSPKVSADGRLIIREEADGNKMEEEEGAKGED
Î	l	1	EEMADPMEDVIIRNKKHQKLKHQKEABEBELEIPPQYQAGGSGI
		1	HRPVAKKAMPGABYKAKKAKGDVKKKGRPDPYAYIPLNRSKLNR
1	}	1	RKKMKLQGQFKGLVKAAQRGSQVGHKNRRKDRRP
6972	2179	973	PGGAILLPLWRRTRPREATVPRGAAQRGRARSAEGRIPSSQSPS
		1	PARAGGATRSPPPRPPRPARPPGPSAPPLLRSDAGPGATVSAAA
ļ			AAATBRARRGATMGAQLSTLGHMVLPPVWFLYSLLMKLFQRSTP
}	J.	1	AITLESPDIKYPLELIDEBIISHDTERFEFALPSPQHILGLPVG
	ļ	ŀ	QHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKDTHPK
	!	1	FPAGGKMSQYLRSMQIGDTIEFRGPSGLLVYQGKGKFAIRPDKK
1		1	SNPIIRTVKSVGMIAGGTGITPMLQVIRAIMKDPDDHTVCHLLF
]	1	1	ANQTEKDILLRPELEELRNKHSARFKLNYTLDRAPBANDYGQG\
1	1		FVNREMIRDHLPPPE\EBPLVLMCGPPPMIQYACLPNL\DHVGH
1	1	}	PTERCFYF
6973	1	1964	LOPRCAHRGLRAQKCGRPAPGVDAMVLCPVIGKLLHKRVVLASA
} ~~~			SPRROBILSNAGLRFEVVPSKFKEKLDKASFATPYGYAMBTAKQ
1			KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILBKPVDKQDAY
	<b>!</b>		RMLSRYE/SGREHSVFTGVAIVHCSSKDHQLDTRVSBFYEBTKV
ł	ľ	1	KFSELSERLLWEYVHSGEPMDKAGGYGIQALGGMLVBSVHGDFL
		1	NVVGFPLNHFCKQLVKLYYPPRPEDLRRSVKHDSIPAADTFRDL
L	L	L	MAAGEEDMECUXHAVIITEEKEDNIKOAKIDOITIEDIEBDB

PCT/US00/34263

	* *		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
٠,	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	eednence	Codon, /=possible nucleotide deletion,
<u> </u>	веquencе		\=possible nucleotide insertion)
1	ì	i	SDVEGGGSEPTORDAGSRDEKAEAGEAGQATARABCHRTRETLP
J		<u> </u>	PFPTRLLBLIEGFMLSKGLLTACKLKVFDLLKDRAPQKAADIAS
1			KVDASACGMERLLDICAAMGLLEKTEQGYSNTETANVYLASDGE
j			YSLHGPIMHNNDLTWNLFTYLEFAIREGTNOHHRALGKKAEDLF
l		}	QDAYYQSPETRLRFMRAMHGHTKLTACQVATAFNLSRFSSACDV
1	1		GGCTGALARELAREYPRMQVTVFDLPDIIBLAAHFQPPGPQAVQ
1	1		IHFAAGDFFRDPLPSAELYVLCRILHDWPDDKVHKLLSRVAESC
į.		ł	KPGAGLLLVETLLDBEKRVAQRALMQSLNMLVQTEGKERSLGEY
- 2004		22.77	QCLLBLHGFHQVQVVHLGGVLDAIL\PPKWPPBAQAACSL
6974	3082	2172	RSCAAFASFASRPPLELPAPPGSHRSPPGRGVATSAQCALSVRK
1	1		LLAARPGLGTKYQATMVYKTLFALCILTAGWRVQSLPTSAPLSV
1		[	SLPTNIVPPTTIWTSSPONTDADTASPSNGTHNNSVLPVTASAP
1	1	1	TELLPKNISIESREERITSPGSNWEGTNTDPSPSGFSSTSGGVH
1	1	1	LTTTLEBHSLGTPBAGVAATLSQSAAEPPTLISPQAPASSPSSL
1	1	1	STSPPEVFSASVTTNHSSTVTSTQPTGAPTAPESPTERSSSDHT PTSHATAEPVPOEKTPPTTVSGKVMCELIDMET\PPPFPG
6975	2	500	RPRPTVHCCKWALKLETAMETLINVFHAHSGKEGDKYKLSKKEL
1 05.5	_	1	KELLQTELSGFLDVKELML*ATRALKTFEEA*KSPIIQCSSSRS
Ì			SLPPAPOPPPYL*LSAVPFP1HLPLPPDAOKDVDAVDKVMK
1	Į.		BLDENGDGEVDFQBYVVLVAALTVACNNFFWENS
6976	1216	970	GCQL*VAYGTTENSPVTFAHPPEDTVEQKAESVGRIMPHTEARI
		1	MNMEAGTLAKLNTPGBLCIRGYCVMLGYWGEPQKTERAVDQDKW
ı	'		YWTGDVATMNEQGFCKIVGRSKDMIIRGGENIYPAELEDFFHTH
l	ļ ·		PKVQEVQVVGVKDDRMGEEICACIRLKDGRETTVKEIKAFCKGK
			ISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL+IKQQ
}	1 3	ļ	ACPGRLA
6977	1298	588	SLFINTNLLSNQIRKTSFGMCSEPISDNTKDQKGKLKTPDFA*R
i			ANKKSKHHVNGNRTVBPFPBGTQMAVFGMGCFWGARRKFWVLKG
ł		ł	VYSTQVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVYQPEHMSFE
i .	ł		BLLKVFWENHDPTQGMRQGNDHGTQYRSAIYPTSAKQMEAALSS
1	1		KENYQKVLSEHGFGPITTDIREGQTFYYAKDYHQQYLSKNPNGY
	<u> </u>		CGLGGTGVSCPVGIKK
6978	3	242	SFPFRDSRRCGCCKGSSLRHTAVAMVKLSKRAKQRLQQLFKGSQ
			PAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG
6979	3917	1146	DEARVRGEAVAAAILSRCRHWSGPPPFPPSPPDRKGLRGTEPWE
1	1	[	AGPGSGATPGARAMDVRRLKVNBLRERLQRRGLDTRGLKTELAE
]	ł	1	RLQAALEABEPDDERBLDADDEPGRPGHINEEVETEGGSELEGT
1		ĺ	AQPPPPGLQFHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE
	1		NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP
	1		DRQQFQSRKRPYEENRGRGYPEHREDRRGRSPQPPAKEDEDDFD
Ī	{		DTIVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL
}			
1	į .		GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFRIOKEALGGOALYPHVLVKNCAVEFNF
Í .	· .		GORAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV
			GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR
1			NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR
ŀ	1		RKMRPFEGFORKAIVICPTDEDLKDRTIKRTDEBGKDVPDHAVL
1			EMKANFTLPDVGDFLDEVLFIELOREEADKLVROYNEEGRKAGP
]	<b>J</b>		PPEKRFDNRGGGGFRGRGGGGGFQRYENRGPPGGNRGGFQNRGG
1	[		GSGGGGYRGGFNRSGGGYSONRWGNNNRDNNNSNNRGSYNRA
1			PQQQPPPQQPPPPQPPPQQPPPPPSYSPARNPPGASTYNKNSNI
			PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ
]	1		GYTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY
1	ļ		NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTQGGTSTQ
6980	1	420	GTRGRKTGRVAAPSTRRRTGNMOKLOTRSPAMSLSDPGLGYHPT
	<u> </u>		The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s

SBO	Predicted	Predicted end	Amino agid goment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /-possible nucleotide deletion,
1	sequence	sequence	\=possible nucleotide insertion)
	bequence		("possible nucleotide insertion)
		İ	CWTLRWPPLCSLHALHVFHCLFSSRLGTPVSPRLAMDPNCSCEA
			GGSCACAGSCKCKKCKCTSCKKSCCSCCPLGCAKCAQGCICKGA
6981	10		SEKCSCCA
0301	10	1054	PERGFRRASIRPAFAARGVFQGGLGQAKQARTRACAALPTPHPS
			APRILEPQGVFSLFPPPPGPWPNMILTKAQYDRIAQCLVSVPPT
	ł		ROSLRKLKORFPSOSOATLLSIFSOBYOKHIKRTHAKHHTSKAI
			BSYYQRYLNGVVKNGAAPVLLDLANKYDYAPSLMARLILERFLQ
			RHEETPPSKSIINSMLRDPSQIPDGVLANQVYQCIVNDCCYGPL
			VDCIKHAIGHEHEVLLRDLLLEKNLSFLDEDQLRAKGYDKTPDF
			ILQVPVAVEGHIIHWIESKASFGDECSHHAYLHDQFWSYWNRFG
6982	153	1000	PGLVIYWYGFIQBLDCNRERGILLKACPPTNIVTLCHSIA
0302	153	1285	FPQQDCSAPAAPGLAGSEPRRLRAYRRRRQRARGLKRVAWLAPP
			PSLLQGLQGWAQAPVDGTLGPEDSRASSPMIQNSRPSLLQPQDV
	ļ		GDTVBTLMLHPVIKAFLCGSISGTCSTLLFQPLDLLKTRLQTLQ
	,		PSDHGSRRVGMLAVLLKVVRTESLLGLWKGMSPSIVRCVPGVGI
			YFGTLYSLKQYFLRGHPPTALESVMLGVGSRSVAGVCMSPITVI
			KTRYESGKYGYESIYAALRSIYHSEGHRGLFSGLTATLLRDAPF
	j		SGIYLMFYNQTKNIVPHDQVDATLIPITNFSCGIPAGILASLVT
	1	•	QPADVIKTHMQLYPLKFQWIGQAVTLIFKDYGLRGFFQGGIPRA
6983			LRRTLMAAMANTVYBEMMAKMGLKS
6983	82	773	BMSFLQDPSPFTMGMWSIGAGALGAAALALLLANTDVPLSKPQK
	<b>!</b>		AALEYLEDIDLKTLEKEPRTPKAKELWEKNGAVIMAVRRPGCPL
	1		CREEAADLSSLKSMLDQLGVPLYAVVKKHIRTEVKDFQPYPKGK
			IFLDEKKKPYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLE
	1		GEGFILGGVPVVGSGKQGILLEHRKKEFGDKVNLLSVLEAAKMI
6984	7.045	1200	KPOTLASEKK
0.704	1845	1282	GGRSAYSLPAGSLPRVPATAAAKMASGVQVADEVCRIFYDMKVR
	<b>!</b>		KCSTPEEIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTIT
	)		DPFKHFVGMLPEKDCRYALYDASFETKESRKEBLMPFLWAPELA
			PLKSKMIYASSKDAIKKKPQGIKHECQANGPEDLNRACIAEKLG
6985	1887	7777	GSLIVAFEGCPV
0703	100/	1324	RRTAGIYPCFPKPGRTRHALCSVVLLLLTGQLAFDDFQESCAMM
			WQKYAGSRRSMPLGARILFHGVFYAGGFAIVYYLIQKFHSRALY
	]		YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLK
	j l		IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFK
6986	642	1250	LSGENGDEVKKE
0300	0%4	1350	YHLYFKMGDPNSRKKQALNRLRAQLRKKKESLADQFDFKMYIAF
			VFKEKKKSALFEVSEVIPVMTNNYEENILKGVRDSSYSLESSL
			ELLQKDVVQLHAPRYQSMRRDVIGCTQBMDFILWPRNDIBKIVC
			LLFSRWKESDEPFRPVQAKFEFHHGDYEKQFLHVLSRKDKTGIV
			VNNPNQSVFLFIDRQHLQTPKNKATIFKLCSICLYLPQEQLTHW
6987	1000	- 345	AVGTIEDHLRPYMPE
078/	1623	341	LEAAEKASRAPKESQRQTDSKNYETENWSPQKSQRRYDMYNTAC
			FLGBIKVGLYTIQILQLTPFFHKENKLSKKHMVQFLSGKWTIPP
	1		DPRNBCYLALSKFTSHLKNIQSDLKRCFDFFIDYMVLLKMRYTQ
ĺ	ľ		KEIABIMLSKKVSRCFRKYTELFCHLDPCLLQSKESQLLQRENC
			RKKLBALRADRFAGLLEYLNPNYKDATTMESIVNBYAFLLQQNS
	1		KKPMTNEKQNSILANIILSCLKPNSKLIQPLTTLKKQLREVLQF
			VGLSHQYPGPYFLACLLFWPENQELDQDSKLIEKYVSSLNRSFR
			GQYKRMCRSKQASTLFYLGKRKGLNSIVHKAKIEQYFDKAQNTN
ł	l		SLWHSGDVWKKNEVKDLLRRLTGQAEGKLISVEYGTEEKIKIPV
			ISVYSGPLRSGRNIERVSFYLGFSIEGPPGL
6988	3	689	TQLLRRPAVFVGSAASGIRSGLWSASSGHWCAPAAGRAHAPVPR
	į		LVRGLGAASTAAPQDAQTGPQPMPRADCIMRHLPYFCRGQVVRG
	į	ł	PGRGSKQLGIPTANFPEQVVDNLPADISTGIYYGWASVGSGDVH
			KMVVSIGWNPYYKNTKKSMBTHIMHTFKEDFYGRILNVAIVGYL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j .	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /-possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			RPEKNFDSLESLISATQGDIBEAKKRLELPEHLKIKEDNFFQVS
1	j		KSKIMNGH
6989	2	1118	LMPSDRPLSPSTHASAGSHCHAPPTTARRAFPIPFGSKSNMATL
1	<b>\</b>	<b>,</b>	KDQLIYNLLKEEQTPQNKITVVGVGAVGMACAISILMKDLADEL
	1		ALVDVIEDKLKGEMMDLQHGSLFLRTPKIVSGKDYNVTANSKLV
			IITAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPNCKLLIV
1	1		SNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGV
i	l	1	HPLSCHGWVLGRHGDSSVPVWSGMNVAGVSLRTLHPDLGTDKDK
1		1	EQWKEVHKQVVESAYEVIKLKGYTSWAIGLSVADLAESIMKNLR
1	J	1	RVHPVSTMIKGLYGIKDDVFLSVPCILGQNGISDLVKVTLTSEE
1	1	}	EARLKKSADTLWGIQKELQF
6990	719	258	THASGMASVVLALRTRTAVTSLLSPTPATALAVRYASKKSGGSS
l			KNLGGKSSGRRQGIKKMEGHYVHAGNIIATQRHFRWHPGAHVGV
l	1	1	GKNKCLYALEEGIVRYTKEVYVPHPRNTBAVDLITRLPKGAVLY
į .	Į.		KTFVHVVPAKPBGTFKLVAML
6991	169	451	RESSOPHNPGFLSRPVSLEBNIHHQVICSTKNKRRNPKKIAYLL
1			SSLLMTNLNPNESTENOPVDAYWAFTLDQEFLTYACVEGTGCLF
1	· ·	1	CGRHVH
6992	944	510	ROAPGCSSLALROVROVYCGLVRAPQVQTRPLSSRFVERRGALY
1			RSPMNQRNPPPYPGPGPTAPYPPYPPQPMGPGPMGGPYPPPQGY
ŀ		1	PYQGYPQYGWQGGPQBPPKTTVYVVEDQRRDELGPSTCLTACWT
İ			ALCCCCLWDMLT
6993	1	374	QWCVTCPQHNARQGPAVPPGIQAYGAAPFEDLQVDFTEMSKCRG
	_		DRVWIKNWNVASLCPLWKGPQTVVLSPPTAVKVEGIPAWIHHSH
<u>ا</u>		}	VKPAARSTWEARPSPONPFRVTLKKTTSPAPVTPGS
6994	346	1100	QWPEKDPVMAASSISSPWGKHVFKAILMVLVALILLHSALAQSR
	Į		RDFAPPGQQKREAPVDVLTQIGRSVRGTLDAWIGPETMHLVSES
ſ			SSQVLWAISSAISVAFFALSGIAAQLLNALGLAGDYLAQGLKLS
i	1		PGQVQTFLLWGAGALVVYWLLSLLLGLVLALLGRILWGLKLVIF
		1	LAGFVALMRSVPDPSTRALLLLALLILYALLSRI/TGSRASGAQL
i		ł	EAKVRGLERQVEELRWRQRRAAKGARSVEEE
6995	144	1346	GSVAVGLSGIMAAQKDLWDAIVIGAGIQGCFTAYHLAKHRKRIL
1	I	}	LLEQFFLPHSRGSSHGQSRIIRKAYLEDFYTRMMHECYQIWAQL
1	1	Į.	BHEAGTQLHRQTGLLLLGMKENQELKTIQANLSRQRVEHQCLSS
1	1	ł	BELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQLG
1			GIVRDGEKVVBINPGLLVTVKTTSRSYQAKSLVITAGPWTNQLL
}	}	}	RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH
			HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL
1		<b>{</b>	SSFVRDHLPDLKPBPAVIESCMYTNTPDBQFILDRHPKYDNIVI
	ł		GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG
Į.		ļ	KAHL
6996	543	1942	BTANABAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDBE
			MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAKNEVLLQKLR
1	1	1	EESRAVFLQRKSRELLDNEBLQNLWFLLDKHQTPPMIGERAMIN
1	İ		YENPLKVGKKAGAKCKQFFTAKVFAKLLHTDSYGRISIMQFFNY
1	1	}	VMRKVWLHQTRIGLSLYDVAGQGYLRESDLENYILELIPTLPQL
ì		ł	DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD
	1	1	LLELRDEELSKESQETNWFSAPSALRVYGQYLNLDKDHNGMLSK
			ERLSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDFVLALEN
	j	ļ	RKEPAALQXIFKLLDIENKGYLNVFSLNYFFRAIQELMKIHGQD
ĺ	1		PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTTILIDL
	1		NGFWTYENREALVANDSENSADLDDT
6997	370	1104	AMELTIFILELATYILTPPLYLLNYIGLWSWICKKWPPYFLVRF
""	370	*10*	TVIYNEQMASKKRELFSNLQEFAGPSGKLSLLEVGCGTGANFKF
l		· ·	YPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAAGENMH
	I .	1	TEACKATOTDEMEMENTED THE STREET AND THE STREET

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence	·	\=possible nucleotide insertion)
			QVADGSVDVVVCTLVLCSVKNQERILREVCRVLRPGGAFYFMEH
ł			VAAECSTWNYFWQQVLDPANHLLFDGCNLTRESWKALERASFSK
	}		LKLQHIQAPLSWELVRPHIYGYAVK
6998	2	616	FVSRALLRVRSRRHPABERAAPGRPEDAPIECPGATNCPEPLWC
į .	ĺ		SHLPVPYAPPTMESRGKSASSPKPDTKVPQVTTEAKVPPAADGK
1	İ		APLTKPSKKRAPAEKQQPPAAPTTAPAKKTSAKADPALLNNHSN
1	1		LKPAPTVPSSPDATPBPKGPGDGAEEDEAASGGPGGRGPWSCEN
	İ		FNPLLVAGGVAVAAIALILGVAFLVRKK
6999	14	1591	GRAGACSRRDTAMSIBLESSDVIRLIMQYLKENSLHRALATLQE
	I	l	RTTVSLNTVDSIRSFVADINSGHWDTVLQAIQSLKLPDKTLIDL
1	1	j	YEQVVLELIKLRELGAARSLLRQTDPMIMLKQTQPERYIHLENL
	1	1	LARSYFDPRKAYPDGSSKEKRRAAIAQALAGEVSVVPPSRLMAL
	· ·		LGQALKWQQHQGLLPPGMTIDLFRGKAAVKDVEEEKFPTQLSRH
ļ	1	Į.	IKFGQKSHVECARFSPDGQYLVTGSVDGFIEVWNFTTGKIRKDL
1	1		KYQAQDNFMMMDDAVLCMCFSRDTEMLATGAQDGKIKVWKIQSG
1		{	QCLRRFERAHSKGVTCLSFSKDSSQILSASFDQTIRIHGLKSGK
1		<b> </b>	TLKBFRGHSSFVNRATFTQDGHYIISASSDGTVKIWNMKTTECS
]	]	ļ	NTFKSLGSTAGTDITVNSVILLPKNPRHFVVCNRSNIVVIMNMQ
i			GQIVRSFSSGKREGGDFVCCALSPRGEWIYCVGEDFVLYCFSTV
		1	TGKLERTLTVHEKDVIGIAHHPHQNLIATYSEDGLLKLWKP
7000	2	827	GPGVVFLELMESEGPPESERSEFFSQRERENEEERAQEPEETGP
1	Ì	ļ	KNPLLQPALTGDVEGLQKIFEDPENPHHEQAMQLLLKEDIVGRN
l .		1	LLYAACMAGQSDVIRALAKYGVNLNEKTIRGYTLLHCAAAWGRL
l .			ETLKALVELDVDIEALNFREERARDVAARYSQTECVEFLDWADA
	1		RLTLKKYIAKVSLAVTDTEKGSGKLLKEDKNTILSACRAKNEWL
ľ			ETHTEASINELFEQRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH
1			DQKRSQDDTSN
7001	2056	844	RRCLIIAFLKGCFIFIYFIFIFETEFLSCCPGWSAVAQSRLIAN
1			FASQVQAIPILPKDSQVGPDVKSEAAPKRALYESVFGSGEICGP
			TSPKRLCIRPSEPVDAVVVVSVKHDPLPLLPKANGHRSTNSPTI
	ļ	<b>,</b>	VSPAIVSPTOUSRPNMSRPLITRSPASPLNNQGIPTPAQLTKSN
1	[	1	APVHIDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQ
1		1	HYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQL
ŀ	1		QPMLLBMERWKQDRETGRPSRPCECLVVRVAPDLGERITLSGDK
1	1	1	SLIBEVFPEIGDVMCNSVNAGWNHDSTHVIRFPLNGYCHLNSVQ
1	[		VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI
	•		RIKQEPLD
7002	1043	498	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP
1		1	TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS
1	-	1	SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV
ļ		1	PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA
]	ļ	1	RGAEVC
7003	818	61	QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP
		Ì	GSVADKRKNPPWIRRRPVVVBPISDEDWYLFCGDTVEILBGKDA
1	1	1	GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP
ł		1	LLHRQVKLVDPMDRKPTEIBWRFTEAGERVRVSTRSGRIIPKPE
i		1	FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMRAM
İ		1	GIKETR\NTRRSIGIEPGABQLLPNFCPSLEG
7004	121	2285	FLLPVLTSRSLRQPAVPHARLGGVRPAAMKSARAKTPRKPTVKK
		1	G\PKRTLKTQLG/YYCRVRPLGFPDQECCIEVINNTTVQLHTPE
1			GYRLNRNGDYKETQYSFKQVFGTHTTQKRLFDVVANPLVNDLIH
		1	GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF
1		1	QAKRYVFKSNDRNSMDIQCKVDALLERQKREAMPNPKTSSSKRQ
		1	VDPEFADMITVQBFCKAREVDBDSVYGVFVSYIBIYMNYIYDLL
			BEVPFDPINPNLHNLNCPVKIKNHNMYVAGCTEVEVKSTERAFE
	1	1	VFWRGQKKRRIANTHLNRESSRSHSVFNIKLVQAPLDADGDNVL
i	E .	.1_	

PCT/US00/34263

	I w	[ <del></del>	Taring and annual garages assumt weeking
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	location	to first	L=Leucine, M=Methionine, N=Asparagine,
ì	corresponding to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
)	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	bequence	\=possible nucleotide insertion)
<u></u>	bequence		OEKEQITISOLSLVDLAGSERTNRTRAEGNRLREAGNINQSLMT
Ì	ŀ	[	LRTCMDVLRENOMYGTNKMVPYRDSKLTHLFKNYFDGEGKVRMI
1	j	]	VCVNPKAEDYEENLOVMRFAEVTOEVEVARPVDKAICGLTPGRR
	l		YRNQPRGP\IGNEPLYTDVVLQSFPPLPSCRILDINDRQTLPRL
Ì		Į.	IBALEKRHNLROMMIDEFNKOSNAFKALLOEFDNAVLSKENHMO
ļ			GKLNEKEKMISGOKLEIERLEKKNKTLEYKIEILEKTTTIYEED
	<b>[</b>		KRNLQQELETQNQKLQRQFSDKRRLEARLQGMVTETTMKWEKEC
1	[	Ĭ	ERRVAAKQLEMONKLWVKDEKLKQLKAIVTEPKTEKPERPSRER
ĺ	}		DREKVTQRSVSPSPVPVSYL
7005	63	876	RNMALYQRWRCLRLQGLQACRLHTAVVSTPPRWLABRLGLFERL
1		1	WAAQVKRLASMAQKEPRTIKISLPGGQKIDAVAWNTTPYQLARQ
	1	1	ISSTLADTAVAAQVNGEPYDLERPLETDSDLRFLTFDSPEGKAV
ļ	1	1	FWHSSTHVLGAAABQFLGAVLCRGPSTEYGFYHDFFLGKERTIR
	1	4	GSELPVLERICQELTAAARPFRRLEASRDQLRQLFKDNPFKLHL
l	1	1	LWRSSG
7006		898	NAFGRHSTAVKMAAAAWLQVLPVILLLLGAHPSPLSFFSAGPAT
7006	22	849	VAAADRSKWHIPIPSGKNYFSFGKILFRNTTIFLKFDGEPCDLS
	1	1	LNITWYLKSADCYNEIYNFKABEVELYLEKLKEKRGLSGKYQTS
Ì	1		SKLFONCSELFKTOTFSGDFMHRLFLLGEKQEAKENGTNLTFIG
]	l		DKTAMHEPLQTWQDAPYIFIVHIGISSSKESSKENSLSNLFTMT
1		Į.	VEVKGPYEYLTLEDYPLMIFFMVMCIVYVLFGVLWLAWSACYWR
1			DLLRIQFWIGAVIFLGMLEKAVFYAGFQ
7007	2	1001	AMTVSGPGTPRPRPATPGASSVEQLRKEGNELFKCGDYGGALAA
j		j	YTQALGLDATPQDQAVLHRNRAACHLKLEDYDKAETEASKAIEK
	ļ.		DGGDVKALYRRSQALEKLGRLDQAVLDLQRCVSLEPKNKVFQEA
			LRNIGGQIQEKVRYMSSTDAKVEQMFQILLDPERKGTEKKQKAS
1	· ·	1	QNLVVLAREDAGABKIFRSNGVQLLQRLLDMGETDLMLAALRTL
•		Ì	VGICSEHQSRTVATLSILGTRRVVSILGVESQAVSLAACHLLQV MFDALKEGVKKGFRGKEGALIVGEWKQVWGLLDVTVMBGMGLSQ
1	,	ĺ	PGQFFGDQTCSCRLPGIRPGDIILL
7008	70	1478	CRSALGHERPPPAHLPAGGRRLQTCPRSCRNLGRPPSGLPPGPR
, ,,,,,	1 "	1	SPPPLAGPGQKMVQKKPABLQGPHRSFKGQNPFELAPSLDQPDH
l	1	1	GDSDFGLQCSARPDMPASQPIDIPDAKKRGKKKKRGRATDSFSG
1	1	1	RPEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH
1	1	1	IRSRVFREVEMLYQCQGHRNVLELIEFFREEDRFYLVFEKMRGG
	1	1	SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGLAHRDLKPE
l	1		NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPRLUTPCGS
ł	1	1	AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG
İ		1	RCGSDCGWDRGRACPACQNMLFESIQEGKYEFPDKDWAHISCAA
l	Į.		KDLISKLLVRDARQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR
			WDSHPLLPPHPCRIHVRPGGLVRTVTVNR
7009	1	626	ARQLENSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG
		1	RVGASEAALFLKKSGLSDIILGKINDLADPEGKGFLDKQGFYVA
1	<b>!</b>	1	LRLVACAQSCHEVTLSNINLSMPPPKFHDTSSPLMVTPPSAEAH
	1	1	WAVRVERKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE
7010	70	E77	SHTRRAVPETILSPLCPLLGGGTAMSGGEQKPERYYVGVDVGT
,010	79	571	GSVRAALVDQSGVLLAFADQPIKNNEPQFNHHEQSSRDIWAACC
]	1	1	VYTKKVVQGIDLNQIRGLGFDATCSLVVLDKQFHPLPVNQEGDS
	1	1	HRNVIMWLDHRAVSQVNRINETKHSVLQYVGG
7011	3	994	RIOTLPHONOSOTOPILKTPPAVLQPIAPQTTFGVQTQPQPQSL
'311	,	1	LOAQISAASITPLLQTQPQPLLQQPQQKAGLLQPPVRIVSQPQP
1	į	1	ARRIDPPSRFSGRNDRGDQVPNRKDDRSRERERERRRSRERSPQ
	1	1	RKRSRERSPRRERSPRRVRRVVPRYTVQFSKFSLDCPSCDMM
	Ī		ELRRRYONLYIPSDFFDAQFTWVDAFPLSRPFQLGNYCNFYVMH
	<del></del>	L	

	_	·	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of amino acid	S=Serine, T=Threonine, V=Valine,
ŀ	residue of amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	sequence	sequence	Codon, /=possible nucleotide deletion,
<del></del>	seducitice		\=possible nucleotide insertion    REVESLEKNMAILDPPDADHLYSAKVMLMASPSMEDLYHKSCAL
1			REVESSERNMATEDPYDADHLYSAKVMEMASPSMEDLYHKSCAL AEDPQELRDGFQHPARLVKFLVGMKGKDEAMAIGGHWSPSLDGP
			DPEKDPSVLIKT\AIRCCKALTG
7012	1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA
1	_	2001	AAAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA
1			VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME
i			TGIABTPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEERR
			NAKARKEKKLPPPPPQAPPEERNESEPEEPSGVEGAAFQSRLPH
			DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQL
			TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL
1			PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLRARDRVGGRV
1			ATPRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP
			LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP
•			VSLGQALBVVIQLQEKHVKDEQIBHWKKIVKTQEELKELLNKMV
			NLKEKIKBLHQQYKBASEVKPPRDITAEFLVKSKHRDLTALCKB
1		,	YDELARTOCKLEEKLOELEANPPSDVYLSSRDRQILDWHFANLE
			FANATPLSTLSLKHWDQDDDFRFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL
1			PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV
i			PWDPSVNLPGHVGSTTASRGELPLFWNLYKAPILLALVAGEAAG
l			IMENISDDVIVGRCLAILKGIFGSSAVPOPKETVVSRWRADPWA
1			RGSYSYVAAGSSGNDYDIMAQPITPGPSIPGAPQPIPRLFFAGB
1 1			HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP
			AQQSPSM
7013	1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA
1 1			AAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA
1			VGERTPRKKEPPRASPPGGLABPPGSAGPQAGPTVVPGSATPME
]		-	TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER NAKAEKEKKLPPPPPQAPPEEENESEPKEPSGVEGAAFQSRLPH
1 1			DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQL
			TFEATLQQLEAPYNSDTVLVHRVHSYLBRHGLINFGIYKRIKPL
1 1			PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV
<b>i</b> i			ATFRKENYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKOKCP
i l			LYRANGQAVPKEKDEMVEQRFNRLLBATSYLSHQLDFNVLNNKP
			VSTCOTEANIOTOEKHAKDEGIEHMKKIAKLOEEFKETTNKWA
ļ			NLKEKIKBLHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE
]			YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHPANLE
			PANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG
j Í			LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTPIYKCDAVLCTL
1 1		•	PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG
		•	IMENISDDVIVGRCLAILKGIFGSSAVPOPKETVVSRWRADPWA
1 1	i		RGSYSYVAAGSSGNDYDLMAQPITFGPSIFGAPQPIPRLFFAGE
[	)	•	HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP
			AQQSPSM
7014	3	3950	DFEVGDKIRILATLEDGWLEGSLKGRIGIFPYRFVKLCPDTRVE
[			ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEABEPD
[			CIISEAPTSPIGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM
}	į		PLATDSPTSDPTEVVNGISSQPQVPFHPNLQKSQYYSTVGGSHP
			HSBQYPDLLPLRARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS
j			SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG
			PQAQGLVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP
			DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR
			PCTPVSTSPHLLVDQNLKPAPPLVVRPSRPAPLPPSAQQRTNAV
]			SPKLLSRHRPTCETLEKEGPGHMGRSLDQTSPCPLVLVRIERME
L <u>.</u> f			RDIJMYSRAQREINLMLEEKQDESSRAETLEDLKFCESNIESLN

	ent containing signal peptide
10 000000000000000000000000000000000000	ysteine, D=Aspartic Acid, E=
10.	F=Phenylalanine, G=Glycine,
	Isoleucine, K=Lysine,
June 19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	thionine, N=Asparagine,
	utamine, R=Arginine,
	eonine, V=Valine,
	zTyrosine, X=Unknown, *=Stop
	ole nucleotide deletion,
	eotide insertion)
MELQQLREMTLLSSC	SSSLVAPSGSVSAENPEQRMLEKRAKVIE
BLLQTERDYIRDLEM	ICIERIMVPMQQAQVPNIDFEGLFGNMQMV
IKVSKQLLAALEISE	DAVGPVFLGHRDELBGTYKIYCQNHDEAIA
LLEIYEKDEKIQKHI	QDSLADLKSLYNEWGCTNYINLGSFLIKP
VQRVMRYPLLLMELI	nstprshpdkvpltnavlavkbinvnine
YKRRKDLVLKYRKGI	DEDSLMEKISKLNIHSIIKKSNRVSSHLKH
LTGFAPOIKDEVFE	TEKNFRMOERLIKSFIRDLSLYLOHIRES
	MERGHROLEOFERVHRYISDOLFTNFKER
	IFTGPHKLVQKRFDKLLDFYNCTERAEKLK
	KALNAQILDELPKFHQYAQGLFTNCVHGY
	kpllsllkvagregnliaipheehsrvlq
OT.OVETTEDRCI.DAT	TKKPPERKTIDRQSARKPLLGLPSYMLQSB
	LFOABRNFNAAQDLDVSLLEGDLVGVIKKK
	TKGFVYSSPLKPYNPRRSHSDASVGSHSS
	QNSGSTLTFNPN\S\MAVSFTSGSCQKQPQ
	Basinpsnsesspsrcpsdpdstsqprsgd
	PRSYRNFRHPEIVGYSVPGRNGQSQDLVKG
	PDGSEAEGNQVYFAVYTFKARNPNELSVSA
	TEWWLAEVNGKKGYVPSNYIRKTEYT
	CARLVQSVLRVWQVGPHVARERVI PFSSLL
	PSGPRLASASRSNGQGSALDHFLGFSQPDS
	EQDVLLVHHPDMPENSRVLRVVLLGAPNAG
	PVSRKVHTTRCQALGVITEKETQVILLDTP
GIISPGKQKRHHLEI	LSLLEDPWKSMESADLVVVLVDVSDKWTRN
QLSPQLERCLTRYSC	QIPSVLVMNKVDCLKQKSVLLELTAALTEG
	SHEGTHCESPAVKDENTQSVGNEQRIGWEH
	VKTLKQYLLTQAQPGPWEYHSAVLTSQTPB
	LPQBVPYNVQQKTAVWEEGPGGELVIQQKL
i k	KCHVISQIAQRAGHDLMDIPLCDVDIRLSV
KLLK	
	EAVAAKRDTGGGSWGTGMDVSGQETDWRST
	RKAGVAHSKSSKDMESHVFLKAKTRDEYLS
	KKSQASVSDPMNALQSLTGGPAAGAAGIGM
PPRGPGQSLGGMGSI	LGAMGQPMSLSGQPPPGTSGMAPHSMAVVS
TATPQTQLQQVA	aaaaaatarsssssrrrysssssssnskQ
FQAQQSAMQQ\QFQ	A/VVQQQQCL/QQQQQQQQHLIKLHHQNQQ
QIQQQQQQLQRIAQI	POTOGOGOGOGOGOGO PATOR PROPERTING P
	OOLOOMHHTOHHQPPPQPQQPPVAQNQPSQ
LPPQSQTQPLVSQA	QALPGQMLYTQPPLKFVRAPMVVQQPPVQP
AQATQVATQQQQVQ	AQMVAPGVQVSQSSLPMLSSPSPGQQVQTP
QSMPPPPQPSPQPG	QPSSQPNSNVSSGPAPSPSSFLPSPSPQPF
\QSPVTARTPQNFS	vpspgplntpvnpssvmspagssqaebqqy
LDKLKQLSKYIEPL	RRMINKIDKNEDRKKDLSKMKSLLDILTDP
SKRCPLKTLQKCBI	ALEKLKNDMAVPTPPPPPPVPPTKQQYLCQP
LLDAVLANIRSPVF	NHSLYRTFVPAMTAIHGPPITAPVVCTRKR
	QGEVARLDPKFLVNLDPSHC\$NNGTVHLIC
	LSVPADYPAQSPLWIDROWQYDANPFLQSV
	HSVTALLNTWAQSVHQACLSAA
7017 1 1785 INLENTCYMNSVI*	THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE P
	ALFMATDFRRQVLSLNLNGCNSLNKKUOHL
T THE THE THE THE THE THE THE THE THE TH	ALFMATDFRRQVLSLNLNGCNSLMKKLQHL RIFFBASRPPWFTPRSOODCSEYLRFLLDR
FAFLAHTORBAYAP	RIFFRASRPPWFTPRSQQDCSEYLRFLLDR
FAFLAHTQRRAYAPI LHEEEKILKVQASH	riffrasrppwftprsqqdcseylrfildr kpseilecsetslqevaskaavltetprts
FAFLAHTQRRAYAPI LHEEEKILKVQASH DGEKTLIEKMFGGK	RIFFBASRPPWFTPRSQQDCSEYLRFLLDR KPSEILBCSETSLQEVASKAAVLTETPRTS LRTHIRCLNCRSTSQKAEAFTDLSLAFWPS
FAFLAHTQRRAYAPI LHEEEKILKVQASH DGEKTLIEKMPGGK YSLEYMSCPDCSQS	RIFFBASRPPWFTPRSQQDCSEYLRFLLDR KPSEILBCSETSLQEVASKAAVLTETPRTS LRTHIRCLNCRSTSQKAEAFTDLSLAFWPS PSIQDGGLMQASVPGPSEEFVVYNPTTAAF
FAFLAHTQRBAYAPI LHEEEKILKVQASH DGEKTLLIRKNFGGK YSLEYMSCPDCSQS ICDSLVNRKTIGSP	RIFFBASRPPWFTPRSQQDCSEYLRFLLDR KPSEILBCSETSLQBVASKAAVLTETPRTS LRTHIRCLNCRSTSQKAEAFTDLSLAFWPS PSIQDGGLMQASVPGPSEEPVVYNPTTAAF PNEFYCSENTSVPNESNKILVNKDVPQKPG
FAFLAHTQRBAYAP LHEEEKILKVQASH DGEKTLIEKHPGGK YSLEYMSCPDCSQS ICDSLVNEKTIGSP GKTTPSVTDLLNYF	RIFFEASRPPWFTPRSQQDCSEYLRFLLDR KPSEILBCSETSLQEVASKAAVLTETPRTS LRTHIRCLNCRSTSQKAEAFTDLSLAFWPS PSIQDGGLMQASVPGPSEEFVVYNPTTAAF

•		. * - *	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, +=Stop
ı	amino acid	eedneuce	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ı	1	j	FSSLSESWSVDVDFTDLSENLAKKLKPSGTDEASCTKLVPYLLS
		Į	SVVVHSGISSESGHYYSYARNITSTDSSYQMYHQSEALALASSQ
1	1		SHLLGRDSPSAVFEQDLENKEMSKEWFLYNDSRVTFTSFQSVQK
1	1	ļ	ITSRFPKDTAYVLLYKKQHSTNGLSGNNPTSGLWINGDPPLQKE
i	ļ		LMDAITKONKLYLQEQELNARARALQAASASCSFRPNGFDDNDP
7020	L	1055	PGSCGPTGGGGGGFNTVGRLVP
7018	484	1066	SLVFRGNTWSGBAGHHCSALPNLAAYHQLFVGTERIRAPEIIFQ
1	Į.		PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQNVFLTGGNTMYP
į.	ì		GMKARMBKELLEMR PFRSSFQVQLASN PVLDAWYGARDWALNHL
1			DDNEVWITRKEYBEKGGEYLKEHCASNIYVPIRLPKQASRSSDA QASSKGSAAGGGGAGEQA
7019	1048	335	APGGFLVTMVFPAPSPPWMLGCCSHEVTAGPPTLCKDMSALVAA
1		,,,,	RMRHIPLAPGSDWRDLPNIEVRLSDGTMARKLRYTHHDRKNGRS
1	!		SSGALRGVCSCVEAGKACDPAARQFNTLIPWCLPHTGNRHNHWA
i	1		GLYGRLEWDGFFSTTVTNPEPMGKQGRVLHPEQHRVVSVRBCAR
Ĭ			SQGFPDTYRLFGNILDKHRQVGNAVPPPLAKAIGLEIKLCMLAK
ŀ			ARESASAKIKEEKAAKD
7020	1	2154	PADSKRKSVLLDKIKNLQVALTSKQQSLETAMSFVARNTFKRVR
ĺ	ĺ		NGPLMRKVAVFFSNTPTRASPQLREAVLKLSDAGITPLFLTRQE
	İ		DRQLINALQINNTAVGHALVLPAGROLTDFLENVLTCHVCLDIC
1		•	NIDPSCGFGSWRPSFRDRRAAGSDVDIDMAFILDSAETTTLFQF
ĺ			NEMKKYIAYLVRQLDMSPDPKASQHFARVAVVQHAPSESVDNAS
			MPPVKVBFSLTDYGSKBKLVDFLSRGMTQLQGTRALGSAIEYTI
1	.		ENVFESAPNPRDLKIVVLMLTGEVPEQQLEEAQRVILQAKCKGY
.,			PFVVI.GIGRKVNIKEVYTFASEPNDVFFKLVDKSTELNEEPLMR
1			FGRLLPSFVSSENAFYLSPDIRKQCDWFQGDQPTKNLVKFGHKQ VNVPNNVTSSPTSNPVTTTKPVTTTKPVTTTTKPVTTTTKPVTI
Ì			INQPSVKPAAAKPAPAKPVAAKPVATKTATVRPPVAVKPATAAK
•		· ·	PVAAKPAAVRPPAAAAKPVATKPEVPRPQAAKPAATKPATTKP
1			MVKMSREVQVFEITENSAKLHWERPEPPGPYPYDLTVTSAHDOS
1			LVLKQNLTVTDRVIGGLLAGQTYHVAVVCYLRSQVRATYHGSFS
1			TKKSQPPPPQPARSASSSTINLMVSTEPLALTETDICKLPKDEG
1			TCRDFILKWYYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCA
			PVLAKPGVISVMGT
7021	2	338	VNAVSFFPNGYAFATGSDDATCRLFDLRADQELLLYSHDNIICG
			ITSVAFSKSGRLLLAGYDDFNCNVWDTLKGDRAGVLAGHDNRVS
			CLGVTDDGMAVATGSWDSFLRIWN
7022	2	856	VYIGSFWSHPLLIPDMRKLFEAEEQDLFRDIQSLPRNAALRKLN
1 1	•		DLIKRARLAKVHAYIISSLKKEMPSVFGKDNKKKBLVNNLAEIY
			GRIEREHQISPGDFPNLKRMQDQLQAQDFSKFQPLKSKLLEVVD
]			DMLAHDIAQLMVLVRQEBSQRPIQMVKGGAFEGTLHGPFGHGYG
			EGAGEGIDDAEWVVARDKPMYDEIFYTLSPVDGKITGANAKKEM
			VRSKLPNSVLGKIWKLADIDKDGMLDDDBFALANHLIKVKLEGH ELPNELPAHLLPPSKRKVAB
7023	2	748	AMVFGGVVPYVPQYRDIRRTQNADGFSTYVCLVLLVANILRILF
''*'		1.70	WFGRRFESPLLWQSAIMILTMLLMLKLCTBVRVANELNARRRSF
			TAADSKDEEVKVAPRRSFLDFDPHHFWQWSSPSDYVQCVLAFTG
]			VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST
			EGMS I KMVLMWTSGDAPKTAYPLLKGAPLOFSVCGLLOVLVDLA
<b>j</b>			ILGOAYAFARHPOKPAPHAVHPTGTKAL
7024	1207	190	RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV
		-50	SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS
	l		QLKPPVLPGTLGGQALHLRSWLLSRQGPABTGGQGQPQGPGLRT
	ļ		RILLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD
}			FHLLDHRGRARCKADFRGOWVLMYFGFTHCPDICPDELEKLVQV
			VRQLEARPGLPPVQPVFITVDPERDDVEAMARYVQDFHPRLLGL
<del></del>			

	<u> </u>		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, P=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ţ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	"	\=possible nucleotide insertion)
	<del>                                     </del>	<del>                                     </del>	TGSTKQVAQASHSYRVYYNAGPKDEDQDYIVDHSIAIYLLNPDG
<b>{</b>		İ	LFTDYYGRSRSAEQISDSVRRHMAAFRSVLS
7025	232	832	ERNSPIGNNENL*K\HSLDCLCFRGDWEGNTQFQTLQDNOBECF
1 /023		1 332	KQVIRTCEKRPTFNQHTVFNLHQRLNTGDKLNRFKKLGKAFISG
1		,	SDHTQHQLIHTSEKFCGDKECGNTFLPDSEVIQYQTVHTVKKTY
ł	ł		
Į.	İ		ECKECGKSFSLRSSLTGHKRIHTGEKPFKCKDCGKAPRFHSQLS
7006			VHKRIHTGEKSYECKECGKAPSCG
7026	328	1146	NPNPSIGDIKDIKKAAKSMLDPAHKSHFHPVTPSLVFLCFIFDG
]			LHQALLSVGVSKRSNTVVGNENEERGTPYASRFKDMPNFIALEK
	į.		SSVLRHCCDLLIGVAAGSSDKICTSSLQVQRRFKAMMASIGRLS
1		]	HGESADLLISCNAESAIGWISSRPWVGELMFTFLPGDFESPLHK
ſ	ſ	}	LRKSS*LPRKHR*QPINAVRMFLDQCMDGSIALRAIVSEIPVFR
	· ·		BKKNNG*KGIGEIF*VWGCTLPPHYWGAVTTNVPKLSNSGKLLG
L	L	<u> </u>	QDEQPHIFG
7027	43	954	GRRLQQQQRPEDARDGAEGGGKRGEAGWEGGYPEIVKENKLPEH
		1	YYQELKIVPEGEWGQFMDALREPLPATLRITGYKSHAKEILHCL
	}	ļ	KNKYFKELEDLEMDGQKVEVPQPLSWYPERLAWHTNLSRKILRK
1	<b>;</b>		SPHLEKFHOFLVSETESGNISRQEAVSMIPPLLLNVRPHHKILD
ļ			MCAAPGSKTTQLIEMLHADMNVPFPEGFVIANDVDNKRCYLLVH
1	į.	•	QAKRLSSPCIMVVNHDASSIPRLQIDVDGRKEILFYDRILCDVP
1		ļ	CSGDGTMRKNIDVWKKWTTLNSLQLHGLQLRIATRGAEQL
7028	189	608	SRPPPEPEPGTMVEKGSDSSSEKGGVPGTPSTQSLGSKNYIRNS
1			KKMQSWYSMLSPTYKORNEDFRKLFSKLPEAERLIVDYSCALOR
l			BILLOGRLYLSENWICFYSNIFRWETTISIOLKEVTCLKKEKTA
			KLIPNAIQ
7029	1343	40	VLKSNTBAKOATGTSSKLRHGTGOEKGREGPRCPSGLAOLRLWG
ļ.			/PCPHAGRETGPRASAPIPGS*GHGWHW*RKDGRGERSEGPSAL
1			SPHSPSLLNMQQAPTHVGPGMGSQRPRSSVVPEQVGVGSQLSRE
1			RWRA+RSLPGAAASERTEMTKERSP/RPCQGYDSSNWFTQPGKK
f.:			TRKRNSRRNTMVSRGGGCLLYPLQSIMPE*QLR*GAHASPPTQG
1			R*GKGGPRSPLTKASGTTHIPTPFFGSIP/RPTRDSGPGTDNS\
1		'	AAPGQKRGHREA*QGPEPV/WGRVTTHLQGPAG*TKPLGS\RNW
l '			VPGPAEGEQGEGAGLEGRP*PLKGCRSTLTFSPQLSIPMVGKKP
			PEGTTASFFF\RSCHSE*RKPPPSCPHAPALSLPHPLPLPPL
			PLPLPGAGT*HSARSGRPGQSETGSLCHNCHHCPPHCPKCSPGG
1			T TO THE THE TANK OF THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE
7030	2	521	FVCFSAPGSGOGGKRRVNMELSAVGERVFAAEALLKRRIRKGRM
	•	J-2-3.	BYLVKNKGWSOKYSTWEPEENILDARLLAAPEEREREMELYGPK
	·		KRGPKPKTFLLKAOAKAKAKTYEPRSDSARGIRIPYPGRSPODL
		,	ASTSRAREGLEN\RVCPRQRAAPAPAAP\PRRGPSGPGPRPG+G
7031	960	<u> </u>	PGLHPPGPGGPSKHGFVPASEQHQHQQHLPRRGPSGPGPRPG
1031	טסע	59	HCSVPGAEWPRKPPAQICPQLTSRPHLSSPRSLSPGCGHSPGPG
}			/CKPS/RHCDELHEGPSRTAALPCGKPQPKHGVEECG/PCPCLA
			PRRLTEPPALTVSPVGRAAPSGAL*PSGRACSACSHRLAPBAAL
			SAAAPRPSLGSGQNASGLPAASLPPQDSSQPHKTVPSPARSVPP
ļ			LGAQARAAPPRLWCPRALVSG*EASPEAVSVAAGPPVPGPTPST
'			SGSTASHSRRGC*SPR*TPAPPRRDHGRSAAFEVLTAAASAQPC
[	i		ASQGGPRPTGAGRTPSPLGLPFSRGPPAASARPFCRHPSL
7032	1393	2104	RRPGRTEPVEPPPVPPPPRASNSKSRCR*RNLHLAPL*QSPLRK
]	İ		SRQIGTSSLPFGRSAGERPRPAATFCLSRGGSSPVFL*PSSSSL
j !			BPNMKRQFGRLHSLFWKSWQKMNSFLLTPKLDTSLMSGWRYRQR
			LPRINTFLKKSLOMASELAPPLPTPAPLASSLPPPPGPPPLLPV
			PLA+LSRSGILVPPNSGFSLSC\PLGDH+GSSGEVRGSCGSPPP
( i	İ		HHCWVLPPPP*LLLPPR
7033	689	815	RSRDCLSSSATSNRARRSKCSGPKRATPLDSGPGP*APPGPSSA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
110	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Ţ.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
ľ	sequence	i -	\=possible nucleotide insertion)
			LMMPSSCPWRTGALGPSPAGSRALGRCTSSVGPGSRWLTRTSSP
1			GCATRTWRTMRMEPRPLRSRMGESAPGIPAELPSAAPSGPSAPS
			AAAPSAPTTPAAAGPNTL*SRRTAEWCWPPSCSCCWGWC*SWSA
		İ	WDWRRPPLOVSPAPSSSCRASCCWCLESIT+SSSTARSRATGAS
	1		SSSTCPTSRSDRGAAWTP\SPMGAPLLPCSVPLISREEALQDPR
			NPSP*GVCSGSSGHAGLALGKPPVACSVP
7034	92	1942	EDTSSMPFRLLIPIGLCALLPOHHGAPGPDGSAPDPAHYRERV
7034	92	1942	
	į.		KAMFYHAYDSYLBNAFPFDELRPLTCDGHDTWGSFSLTLIDALD
	}		TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
1		<u>}</u>	RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMABEAARKLLPA
	<b>{</b>		FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVBFATLSSL
1			TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
l	ł	ł	IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDN
		Ì	YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
İ	]		TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT
1			GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
ł	1	1	FLAETVKYLYLLFDPTNFIHNNGSTBDAVITPYGECILGAGGYI
<b>!</b>	1		FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQ
ì		l .	KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS
1		i	QPFTSKLALLGQVFLDSS+PLDNFFIFIFLRLNYNKLLLAIIKK
		i .	K
7035	92	1942	RDTSSMPFRLLIPLGLLCALLPOHHGAPGPDGSAPDPAHYRERV
			KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
1	ļ .		TLL\TLFYFOILGNVSEFORVVEVLODSVDFDIDVNASVPBTNI
<u> </u>		Ì	RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
I.		ļ	FOTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTPIVRFATLSSL
	Ì	<u> </u>	TGDPVPRDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
1	ŀ	Ì	IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW
	ì	i	YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
	ł		TVWKQFGGLPBFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT
		1	GDPTLLELGRDAVESIEKISKVECGPATIKDLRDHKLDNRMESF
		ľ	FLARTVKYLYLLPDPTNFIHNNGSTFDAVITPYGECILGAGGYI
İ		ļ	FNTEAHPIDPAALHCCORLKEEQWEVEDLMREFYSLKRSRSKFQ
1	Ì		KNTVSSGPWEPPARPGTLPSPENHDQARERKPAKQKVPLLSCPS
			QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
Ĺ			К
7036	442	761	CLAPLESCEQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
1	l .		RNW*KRKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
Ì	L `	L	PPPPPPPPPRRPPRNRRPG
7037	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
1	1		RNW+BRKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
1	1		PPPPPPPPPRRPPRNRRPG
7038	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEETIL
1	1	_	OYNKLLEKSDLHSVLAQKLQARKHDVPNRHEISPGHDGTWNDNQ
			LOEMAQLRIKHQKELTELHKKRGELAQ\RVIDLNNQMQRKDREM
	1		OMNEAKIAECLOTISDLETECLDLETKLCDLERANQTLKDBYDA
}	1		LOITFTALEGKLRKTTEENOELVTRWMAEKAQEANRLNARE*KR
l	1		LOEAASPAAERACRSSKGTSTSRTG
7030-	1		
7039	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL
Ī			QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ
i	1		LQEMAQLRIKHQEKLTELHKKRGKLAQ\RVIDLNNQMQRKDREM
1	1	]	QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
1	1	ļ	LQITFTALEGKLRKTTEENQELVTRWMABKAQEANRLNARB*KR
1	1	}	LQEAASPAAERACRSSKGTSTSRTG
7040	34	789	KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS
1		1	GYESVMRDSEATGSASSAQDSTSENSSSVGGRCRSLKTPKKRSN
	L	<u> </u>	<u></u>

•			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alamine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	ľ	\=possible nucleotide insertion)
	<del> </del>		PGSQRRRLIPALSLDTSSPVRKPPNSTGVRWVDGPLRSSPRGLG
			EPFBIKVYEIDDVERLORRRGGASKEAMCFNAKLKILEHROORI
			AEVRAKYEWLMKELEATKQYLMLDPNKWLSEPDLEQVWELDSLE
			YLEALECVTERLESRVNFCKAHLMMITCFDIT
7041	1	567	SGRVAMGRRRAPAGGSLGRALMRHOTORSRSHRHTDSWLHTSEL
		i	NDGYDWGRLNLOSVTEOSSLDDFLATAELAGTEFVAEKLNIKFV
	1	l	PARARTGLLSPERSORIKKLHKENKOFLCIPRRPNWNONTTPER
			LKQAEKDNFLEWRRQL\VRLEEEQKLILTPFERNLDFWRQLWRV
		j	IERSDIVVQIVDA
7042	7	345	PIHMAAAALRADI\ISPLFPHIQGYLLLSASHG\ATSLHTKGAL
7042	} '	343	PLETVIMYTVIPKSKYVLVKPDTOYPYSENLDEFKRLAENSASN
			DDLLMARVAISDYGDKLTLELREKY
7043	2	2170	ARGMAARDSDSEEDLVSYGTGLKPLBEGERPKKPIPLQDQTVRD
	Į.		EKGRYKRFHGAFSGGFSAGYFNTVGSKEGWTPSTFVSSRQNRAD
	}		KSVLGPRDFMDEEDLSEFGIAPKAIVTTDDFASKTKDRIREKAR
	ł	İ	QLAAATAPIPGATLLDDLITPAKLSVGFELLRKMGWKEGQGVGP
		ŀ	RVKRRPRRQKPDPGVKIYGCALPPGSSEGSEGEDDDYLPDNVTF
			APKDVTPVDFTPKDNVHGLAYKGLDPHQALFGTSGEHFNLFSGG
	ŀ	į ·	SERACDICEIGLNKGRKLGISGQAFGVGALEBEDDDIYATETLS
	Į.		KYDTVLKDBEPGDGLYGWTAPRQYKNQKESEKDLRYVGKILDGF
			SLASKPLSSKKIYPPPELPRDYRPVHYFRPMVAATSENSHLLQV
	İ	Ì	LSESAGKATPDPGTHSKHQLNASKRABLLGETP1QGSATSVLEP
	ł		LSQKDKERIKEMKQATDLKAAQLKARSLAQNAQSSRAQPSPAAA
	1	l .	AGHCSWNMALGGGTATLKASNFKPFAKDPEKQKRYDBFLVHMKQ
			GQKDALERCLDPSMTEWERGRERDEFARAALLYASSHSTLSSRF
	Į.	} .	THAKEEDDSDQVEVPRDQENDVGDKQSAVKMKMFGKLTRDTFEW
			HPDKLLFQ/RLVGLPRVKRDKYSVFNFLTLPETASLPTTQASSE
			KVSQHROPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK
			QQSSPLVNKEEEHAPELSAN
7044	276	734	EVYLTDEFAKGRKVADLYELVQYAGNI IPRLYLLITVGVVYVKS
	}		FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG
		l	EPTDEETTGDISDSMDFVLLNFAEMNKLNVRMQHQGHSRDREKR
	}	ļ	EREROELRILVGTNLVRLSQV
7045	3	513	LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP
			KANOWEKTDIEGTLFVYRRSASPYHGFTTVNRLNMHNLVBPVNK
	1	ŀ	DLEFOLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE
	1		ETRRSQQA/RSGQTESQPGQWI.QRPQAHRHPGDAEQSQG
7046	3	513	LGFKMEALSRAGOEMSLAALKQHDPYITSIADLTGQVALYTFCP
,010			KANOWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK
	1	j	DLEFOLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE
			BTRRSQOA/RSGQTESQPGOWLQRPQAHRHPGDAEQSQG
7047	<del>                                     </del>	Anc.	OMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNILNSKN
7047	103	486	
	1	Ī	IMLIDVRBIWEILEYQXIPESINVPLDEVGEALQMNPRDFKEKY
ma: =	<b> </b>	ļ	NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER
7048	92	627	FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEBERANY
		1	WKDLAMTYKQRAENTQEBLREFQEGSREYEABLETQLQQIETRN
	1		RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA
	1	1	IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLM\QAI
	İ	İ	EKKW
7049	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL
			VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL
	1	1	NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT
	<b>\</b>	(	EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX
	1		ASSLWG
7050	1	I	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL
7050	393	938	ARIGONS IGGERFGLIGGENTANSVHORCSSVGRIFARRCIBUBL

450		15 37 5 5 1	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ĺ	sequence	Dequence	\=possible nucleotide insertion)
<b> </b>	sequence	<del> </del>	VPVPEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL
ł			
i		ł	NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKRERILEEIAKVT
l		]	EGVLDVIVYASAADKMKNRGLRLRGVRBPPRGCHWLGRKLIAWX
1	<u> </u>		ASSLWG
7051	119	816	KKMNLABICDNAKKGREYALLGNYDSSMVYYQGVMQQIQRHCQS
)			VRDPAIKGKWQQVRQELLEEYEQVKSIVGTLESFKIDKPPDPPV
ŀ			SCODEPFRDPAVWPPPVPAEHRAPPQIRR/ROSRSKTSEERNGR
1	1	J	SRSPGTCRPST\PISKSEKPSTSRDKDYRARGRDDKGRKNMQDG
l		]	ASDGEMPKFDGAGYDKDLVEALERDIVSRNPSIHWDDIADLEEA
l	j	1	KKLLRRAGVLPMWM
7052	467	715	SCPGRGKMSKLLNPKEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
7032	10'	(1,5)	
	<del> </del>	l	TYRNSMYHNKHVPKDKVVLDVGSGTGYLSMFAARQGPRR
7053	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDRVRTL
L	<u> </u>		TYRNSMYHNKHVFKDKVVLDVGSGTGILSMFAARQGPRR
7054	1	1036	GTSQRSRETDARRRSAGAEPTARLPWPAALREWPSCPCEPLGPG
ļ			RRCRWDAMBYDEKLARFRQAHLNPFNKQSGPRQHEQGPGEBVPD
l	ł	i	VTPEEALPELPPGEPEFRCPERVMDLGLSEDHFSRPVGLFLASD
Ī		1	VQQLRQAIBECKQVILBLPEQSBKQKDAVVRLIHLRLKLQBLKD
ļ	Į.	ì	PNEDRPNIRVLLEHRFYKEKSKSVKOTCDKCNTIIWGLIOTWYT
Į.			CTGCYYRCHSKCLNLISKPCVSSKVSHOAEYELNICPETGLDSO
•			DYRCAECRAPI/CS/DGVVPSEARQCDYTGQYYCSHCHWNDLAV
į	t	Į.	IPARVVHNWDFEPRKVSRCSMRYLALMVSRPVLRLREIN
7055	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNOGP
/053	, 2	321	
			RYHYLHOMLG/ALCLSRASASVLNLNCSLILLPMCRTLLAYLRG
ļ		i	SQKVPSRRTRLLDKSRTFHITCGATICIFSGVHVAAHLVNALN
i			FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL
			М
7056	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNQGP
	· ·	1	EYHYLHOMLG/ALCLSRASASVLNLNCSLILLPMCRTLLAYLRG
<b>\</b>	į.	}	SQKVPSRRTRRLLDKSRTFHITCGATICIFSGVHVAAHLVNALN
1	1		FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMRVVLFL
	1	1	и
7057	1368	431	GIYLHVNEKIPRPTCIGDRQENDKENINI.ENHRDQELIHASCQA
			SGEVPSQASLRGFFTEDEPGCFGEGENLPEALQNIQDEGTGEQL
١.		ł	SPOERISEKOLGOHLPNPHSGEMSTMWLEEKRETSOKGOPRAPM
1	1	1	AOKI.PTCREOGKTFYRNSQLIFHQRTHTGETYFQCTICKKAPLR
ł		i	SSDFVKHORTHTGEKPCKCDYCGKGFSDFSGLRHHEKIHTGEKP
I		1.	YKCPICEKSPIQRSNFNRHQRVHTGEKPYKCSHCGKSFSWSSSL
1	1	1	
l	}	1	DKHQRSHLGKKPFQ+PVTKLSFPISISQPSHKNTQLHQRKLCLR
	.L	<u> </u>	GYPC
7058	_ 1	469	FSGFGAVPDALGCRMSDLRITEAFLYMDYLCFRALCCKGPPPAR
<b>!</b>		1	PEYDLVCIGLTGSGKTSLLSKLCSESPDNVVSTTGFS1KAVPFQ
1			NAILNVKBLGGADNIRKYWSRYYQGSQGVIFVLDSASSBDDLEA
ì	1	1	ARN*SCTQLLQHPQLCTLPFLILA
7059	1	1178	WPAPPROPAAAAMDALLGTGPRRARGCLGAAGPTSSGRAARTPA
]	]		APWARPSAWLECVCVVTFDLBLGOALELVYPNDFRLTDKBKSSI
1	1		CYLSPPDSHSGCLGDTOFSFRMRQCGGGRSPWHADDRHYNSRAP
	1		1 · · · · · · · · · · · · · · · · · · ·
-		l .	VALQREPAHYFGYVYFRQVKDSSVKRGYFQKSLVLVSRLPFVRL
1		j	FQALLSLIAPEYFDKLAPCLRAVCSEIDQWPAPAPGQTLNLPVM
			GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF
ŀ		1	RCFRPVLTHMQTLWELMLLGEPLLVLAPSPDVSSEMVLALTSCL
ì	1		QPLRFCCDFRPYFTIHDSEFKEFTTRTQAPPNVVLGVTNPFFIK
1		1	TLQHWPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP
7060	90	1670	SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ
	1	1	YRFEHLVTQMKWRLQEGRGEAVYQIGVEDNGLLVGLAEEEMRAS
Į.	B.		

Predicted   Predicted   Predicted on   Incleditide   Contain   Incleditide   Contain   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corre				
modiectide   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Coatsion   Costresponding	ID			
to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence    Percidine, O-Glutamine, Ra-Raparagine, serine, T-Threcoine, V-Valine, amino acid sequence   Vertigophan, V-VyCosine, X-Unknown, *=Stop Codon, /=possible nucleotide deletion, v-possible nucleotide deletion, v-possible nucleotide deletion, v-possible nucleotide insertion)   Internative of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property	NO:	nucleotide		
to first amino acid residue of amino acid residue of amino acid sequence  P-PCOLINE, C-GLULRamine, R-ATJAINE, S-Serine, T-Thresoline, V-Valline, amino acid sequence  P-PCOLINE, V-Valline, V-Valline, amino acid sequence  Codon, /-possible nucleotide deletion, \-\text{-possible nucleotide deletion,} \-\text{-possible nucleotide insertion}  LKTLERRAEKVADLTVIKERREVOTISDMORKLITEVILVEKVEPDN OPELDRAVALGAVUSKESTLIGUNISGELDBORGRARUNLEH LHEIGSGETSSISPELIGENSIGEVAGILHGTVORGYTERGH**  RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVARLFELT** RT*DOGGEVAR		location	corresponding	
to first amino acid residue of amino acid residue of amino acid sequence    Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine, V-Aulaine, V-Aulaine,   Secripe T-Threatonine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V-Aulaine, V		corresponding		L=Leucine, M=Methionine, N=Asparagine,
amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen			amino acid	P=Proline, Q=Glutamine, R=Arginine,
residue of amino acid sequence amino acid sequence con /-possible nucleotide deletion, con /-possible nucleotide deletion, con /-possible nucleotide deletion, con /-possible nucleotide insertion)  IKTLIERNAEKUGADTYJEERRYVYJEMPKYPTEVIVJEKVPDN (COO, /-possible nucleotide insertion)  IKTLIERNAEKUGADTYJEERRYVYJEMPKYTEVIVJEKVPDN (COO, /-possible nucleotide insertion)  IKTLIERNAEKUGADTYJEERRYVYJEMPKYTEVIVJEKVPDN (COO, /-possible nucleotide insertion)  IKTLIERNAEKUGADTYJEERRYVYJEMPKYTEVIVJEKVPDN (COO, /-possible nucleotide insertion)  IKTLIERNAEKUGADTYJEERRYVYJEMPKYTEVIVJEKVPDN (COO, /-possible nucleotide insertion)  IKTLIERNAEKUGADTYJEERRYVYJEMPKYTEVIVJEKVPDN (COO, /-possible nucleotide insertion)  IKTLIERNAEKUGADTYJEERRYVYJEMPKYTEVIVJEKVPDN (COO, /-possible nucleotide)  IKTLIERNAEKUGADTYJEERRYVYJEMPKYTEVIJEKSTAPKKOEGILAV (LERVAET)  IKTLIERNAEKUGADTYJETTYJEKSTAPKKOEGILAV (LERVAET)  IKTLIERNAEKUGADTYJEKSTAPKKOEGILAV (LERVAET)  IKTLIERNAEKUGADTYJEKSTAPKKOEGILAK (LERVAET)  IKTLIERNAEKUGADTYJEKSTAPKKOEGILAK (LERVAET)  IKTLIERNAEKUGADTYJEKSTAPKKOEGILAK (LERVAET)  IKTLIERNAEKUGADTYJEKSTAPKKOEGILAK (LERVAET)  IKTLIERNAEKUGADTYJEKSTAPKAGATA (LERVAET)  IKTLIERNAEKUGADTYJEKSTAPKAGATA (LERVAET)  IKTLIERNAEKUGADTYJEKSTAPKAGATA (LERVAET)  IKTLIERNAEKUGADTYJEKSTAPKAGATA (LERVAET)  IKTLIERNAEKUGADTYJEKSTAPKAGATA (LERVAET)  IKTLIERNAEKUGADTYJEKSTAPKAGATA (LERVAET)  IKTLIERNAEKUGADTYJEKSTAPKAGATA (LERVAET)  IKTLIERNAEKUGADTYJEKSTAPKAGATA (LARVAET)  IKTLIERNAEKUGADTYJEKSTAPKAGATA (LARVAET)  IKTLIERNAEKUGADTYJEKSTAPKAGATA (LARVAET)  IKTLIERNAEKUGADTYJEKSTAPKAGATA (LARVAET)  IKTLIERNAEKUGADTYJEKSTAPKAGATA (LARVAET)  IKTLIERNAEKUGADTYJEKSTAPKAGATA (LARVAET)  IKTLIERNAEKUGADTYJEKSTAPKAGATA (LARVAET)  IKTLIERNAEKUGADTYJEKSTAPKAGATA (LARVAET)  IKTLIERNAEKUGADTYJEKSTAPKAGATA (LARVAET)  IKTLIERNAEKUGADTA (LARVAET)  IKTLIERNAEKUGADTA (LARVAET)  IKTLIERNAKUGADTA (LARVAET)  IKTLIERNAEKUGADTA (LARVAET)  IKTLIERNAEKUGADTA (LARVAET)  IKTLIERNAEKUGADTA (LARVAET)  IKTLIERNAEKUGADTA (LARVAET)  IKTLIERNAEKUGADTA (LARVAET)  IKTLIERNAEKUGADTA (LARVAET)			residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence Codon, /-possible nucleotide deletion, equence Litting sequence   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litting action   Litti				W=Truntophan, Y=Tyrosine, X=Unknown, *=Stop
A-possible nucleotide insertion				Codon /-mossible nucleotide deletion.
LITTLERRAKVQADITVIERRKYDTSDMPKRITEVIJVEKVDOR  OPEDINAVAUGNOSGSTILGVUTGGENINGERARIALFER LIBEIGSGRISSISPEILGFRISKGEVHGINGTVORGUTLARGGRISHLENDER RTPOGGRVURFLEFTV MARIAGUETSSGAPIKKSERGINFTENG VXIKRGGEPGNILGPGNSGADGRISH-GYPALGOVVAYSDGR TABBIGSSSSMITFIDLAGHHKYLATTITELTSCADLILV SANTGINGFTRRHIGIALALAVPFRIVASCIDLACHTVERTVR QLERVILGPGCHKVPHLYTSEDDAVTARAGGRASPAVTFIFTL SANGSSDDLAKVFRHILFDITNISKGERIMGGLIEFTV PROGTOTISR* IDLAGHHKYLATTITELTSCADRITTSPGUDETTV PROGTOTISR* IDLAGHHKYLATTITELTSCADRITTSPGUDETTV PROGTOTISR* IDLAGHHKYLATTITELTSCADRITTSPGUDETTV PROGTOTISR* IDLAGHHKYLATTITELTSCADRITTSPGUDETTV PROGTOTISR* IDLAGHHKYLATTITELTSCADRITTSPGUDETTV PROGTOTISR* IDLAGHHKYLATTITELTSCADRITTSPGUDETTV PROGTOTISR* IDLAGHHKYLATTITELTSCADRITTSPGUDETTV PROGTOTISR* IDLAGHHKYLATPODSITISKSNPRAGGRGI ALAGRISHGELGRICAVRICAGRISHAMALARICAGNIQPEARSE VALUE SANGSPERAPALAVRICAGNICATION REGRESSION PROGTORIST REGRESSADALAVRICAGNICATION REGRESSADALARICAGNIQPEARSE QUEBRIALIZARGGESPERAPALARICAGNIQPEARSE QUEBRIALIZARGGESPERALARICAGNICAGNICAGNICAGNICAGNICAGNICAGNICAGN		1	sequence	\-noccible nucleotide insertion)
OPELDIEVATUGNUSGESTILLOVITGELINGGERAKILLIPENE HISTOGGRVBRLER TILOPINGGERAKILLIPENE HISTOGGRVBRLER TILOPINGGERUGHT TICHQUAYUNG THE TOGGRVBRLER TV MBALKGL*TSSAPLEKSKGOQIA*TING VKIKRQGHERGKIGGORGEGVGRGERH*GPRALGQVVYYSDER TABBICSSSKMITFIDLAGHHKYLHTTITOLISTSCPDCALLIV SANTGIAGTTREHLGIALALKVPFFIVVSKIDLCARTTVRKTUR QLERKYLMQOGHKYMINTSEDDAVTARQQYAGYVTYFITIS SVSGSLDLLKVFLNILLPLTINSKEGERLMQQLTERQVDELTY PROGTVUGGTISK*I TILLATLTPOSPITSKTSHPGGDETI ARBESFIGUPELGVMDFETTIEFPSTARLBYRGGPCIGVNAGPER EGGPRGSBERAALVEGLGIDP ARMESPLGPCLEVMDFETTI EEPETALLBREGCCYGRVAGPERSLARLRISCCCYMQFPARISKE QMLEMLVLEQFLGTLPPBIQAWVRGGRPGSPERAALVEGLQHD FOGLIG  7062 71. 744 AKAGTNIBELINILSTYFCIPKHKLÄSSGRUKVQPAACTQAGER TALYCLTQMSMCLDBATDSFPGNPDSLHRESHRRANDIKKKLLIPLPBIQAW EGGPRGSBERAALVEGLGHD FYGRIKLÄSSGRUKVQPAACTQAGER TALYCLTQMSMCLDBATDSFPGNPDSLHRESHRRANDIKKKLLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCDSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCSMEKLKALLIPLBGBLKDTARFRA TQCERSREPLLOGHTBLGCSMEKLKALLIPLBGBLKDTARFRA TATYCLLTQCGGSGRANG TARGCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	L	sequence		
IMEIGSGRYSISTELIGMSKGEVIGI INGTORGYTLEMGH*+* RT*DOGRVENLEDL*TSSADIRSON(N**ING VXTRROGRENILGFORSGVORAGREN* GPNALGOVYNYSDSR TABELCUSSSRINTYTEILAGHKYLITTI PIALITSYCPDCALLIV SANTGI AGTTREHLGLALALKYPPTIVYSKIDLCARTTVERTUR QLERVILGQPCHKYPMIVTSIDDAVTARQPAGENYPTIFTIS SVSGSSLDILLAVILTNISEDGAVTARQPAGENYPTIFTIS SVSGSSLDILLAVILTNISEDGAVTARQPAGENYPTIFTIS SVSGSSLDILLAVILTNISEDGAVTARQPAGENYPTIFTIS SVSGSSLDILLAVILTNISEDGAVTARQPAGENYPTIFTIS SVSGSSLDILLAVILTNISEDGAVTARQPAGENYPTIFTIS SVSGSSLDILLAVILTNISEDGAVTARQPAGENYPTIFTIS SVSGSSLDILLAVILTNISEDGAVTARQPAGENYPTIFTIS SVSGSSLDILLAVILTNISEDGAVTARQPAGENYPTIFTIS SVSGSSLDILLAVILTNISEDGAVTARQPAGENYPTITTIP PROTIVICIONAL STADILLAVILTNISEDGAVTARQPAGENYPTITTIPETIQAMV RGGROSPERARAVEGLOPH** ARMPSELLEPTYMDETILL EPETRALIZECOOLOPERABKEQMLEMINISEDFLOTHYPETIQAMV RGGROSPERARAVEGLOPH** ARMPSELLEPTYMDETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETICHYPETIC			1	
RT*OGGEVWRLETU*MANLEGL*TSSAPLRKSMCRQU*I TIKG VXXRQGHPGNLGFORSGGUR*GRGRIGH*GRALGOVYNYSDGR TABBICGSSSRNTTPIDLAGHRKYLETT*I TRIJTSYCPDCALLIV SANTGIAGTTREHIGIALALIVPPTTVVSKIDATTVRGTUR QLERVILQQPGCHKVPMLVTSEDDAVTAAQQFAQSPNVTPITTIS SVSGSSLDILKVFINTLIPPLTNSKEQBELMQQUTEFQVDELTYV PEWGTVUGGTISH*I DILAATLIPPLTNSKEQBELMQQUTEFQVDELTYV PEWGTVUGGTISH*I DILAATLIPPLTSPBTYSKTSDBFGGDRGI ALMERISCOCHQERHSHKGQMEMINIAGPJCFTGLPPEQDAV RGQRFGGFBEAAALVBGLOHDP*ARMFGGFCGVXMGPBFA ALABLRISLCOCHQLEPASHSKQCMEMINIAGPJGTATPPETQAWV RGQRFGGFBEAAALVBGLOHDP*ARMFGGFGFCGVXMGPBFACTAGBFT ALACAGNITABLHHILSYPYCTPKHKKASSQGEVQPHACTAGBF TALYCLTQMENKLIDBATDGFFQMPDGLHBESMRNADKKKLEBL YGRYRDGQDBRKICGVDGTQGFCDGLAGPBRAADLVBGLQDD POOLIG  7062 71 744 ALAGGNIGBLHAUSYPYCTPKHKKASSQGEVQPHACTAGBR TALYCLTQMENKLIDBATDGFFQMPDGLHBESMRNADKKKLEBL YGRYRDGQDBRKICGVDGTQGDLALDPASISVLVIAMKFRAA TQCEFSRREFLDGMTBLGCURREKLGALDFRLGGKINGDAKKL YGRYRDGQDBRKICGVDGTQDLALDPASISVLVIAMKFRAA TQCEFSRREFLDGMTBLGCURREKLGALDFRLGGKINGDAKFD FYDFFFTARMFGGGGLD-MAGAYWKCUGFGFKRLIAMFTD MBHB  7063 2 562 LRTYPDDLGGRFFAMKTGGRF*PELPPDMSLEQAEDKKAFER LTSYLHCLQPATGRRIFMLLUVSVCTPATGAMNHLIDPETGKVFF FTSLMMHFFFTTSCCTLIGLFPAGATHRVANPGGFRFKRLIAMFT KYMGCDDTKLLIKPPHVQ*QSSLLVWGIKKTAFFRTSDTAKS HKGFGLRCDAK KYMGCDSSCRGGAAAAGRRGGRGVGKAFRSASSAS KRRTGCWTCPPESGTAAARTSGARAVSAAVAAGG SSRAGRMLBFFGRRGPPACAAAAGRRGRGVGRAVSAVAAAGG SSRAGRMLBFFGRRGPPACAAAAGRRGRGVGRAVSAVAAAGG SSRAGRMLBFFGRRGPPACAAAAGRRGVGSAVAAAGG SSRAGRMLBFFGRRGPPACAAAAGRRGVGSAVAAAGG SSRAGRMLBFFGRRGPPACAAAAGRRGVGRAVBSAVAAAGG SSRAGRMLBFFGRRGPAPAATMIRRRLSGLRAPALAGRRRGFGFBAAP PLLTFJGGRGSGSGABAAASAAGGRGVGFRKAMBGRRTFTGG SSRAGRMBFFGRRGPAPAATMIRRRLSGLRAPALGGRANDASAAAGGRGVGFRKAMBGRRTFTGG SSRAGRMBFFGRRGPAPAATMIRRRLSGLRAPALGGRANDASAAAGGRGVGFRKAMBGRRTFTGG PGGGFGBAABAGGGGARGGGARGAGGAGAGGGAGGGAGGGAGGGA	į	<u>}</u>	ł	
VXIKRQGHPGNILGPGNBEGVGRAGERI "GRNALGQVNYISDSR TARBEICSSSSIMTYTINLAGHIKLIHTI 1961.ISYCPDCALLIV SANTGIAGTTREHIGIALALKYPFITVYSKIDLCAKTTVERTUR QLERVIKQPG-HKVPFITVTHENGEGREMQGLTEFQVDEIYTV QUERVIKQPG-HKVPMINTSEDDAVTAAQPAGSPNYTTFTIS. SVSGSSLDILKVFLNITAPELINSKERGELMQGLTEFQVDEIYTV PEWGTVUGGTLSR* IDLLAKTPTQPSD* IYSKTSWPGGODGF* ALARLREIGCQNIQPRABHSKQMLEMJULGPFLGTUPPDFPTTLAWP RGQRFGSPERAAALVEGLGUP* ARMPSELGPFLYDWDEFTTLE EPETAALRERGCCONLOPERAHSKRQMLEMJULGOFLGTLPPBTQAWV RGQRFGSPERAAALVEGLGUP* ARMPSELGPFLYDWDEFTTL EPETAALRERGCCONLOPERAHSKRQMLEMJULGOFLGTLPPBTQAWV RGQRFGSPERAAALVEGLGUP* ARMPSELGPFLYDWDEFTLL* EPETAALRERGCCONLOPERAHSKRQMLEMJULGOFLGTLPPBTQAWV RGQRFGSPERAAALVEGLGUP* ARMPSELGPFLYDWDETTLL* EPETAALRERGCCONLOPERAHSKRQMLEMJULGOFLGTLPPBTQAWVRGQRFGSPERAAALVEGLGUP* ARAGTNIKLGCONLOPERAHSKRQMLEMJULGOFLGTLPPBTQAWVRGQRFGSPERAAALVEGLGUP* ARAGTNIKLGTLAGTERKALLTVEGLGER* TATYCLTQNBRKLLEGAFDGATSKRALTVEGLGER* TATYCLTQNBRKLLEGAFDGATSKRALTVEGLGER* TATYCLTQNBRKLLGAFDGATSKRALTVEGGR* TATYCLTQNBRKLLGAFDGATSKRALTVEGGR* TATYCLTQNBRKLLGAFDGATSKRALTVEGGR* TATYCLTQNBRKLLGAFDGATSKRALTVEGGR* TATYCLTQNBRKLLGAFDGATSKRALTVEGGR* TATYCLTQNBRKLLGAFDGATSKRALTVEGGR* TATYCLTQNBRKLLGAFDGATSKRALTVEGGR* TATYCLTQNBRKLLGAFDGATSKRALTVEGGR* TATYCLTQNBRKLLGAFDGATSKRALTVEGGR* TATYCLTQNBRKLLGAFDGATSKRALTVEGGR* TATYCLTQNBRKLLGAFDGATSKRALTVEGGR* TATYCLTQNBRKLLGAFDGATSKRALTVEGGR* TATYCLTQNBRKLLGAFDGATSKRALTVEGGR* TATYCLTQNBRKLLTVUSCCTATAANALTARTLAGGATAAAGATAKATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAGATAAAAGATAAAGATAAAGATAAAAGATAAAGATAAAGATAAAGATAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAAA				IHEIQSGRTSSISFEILGFMSKGEVHGINGTQWGQTLRMGW**
TABBICESSISMITEIDLAGHHKULATTI YRGINSYCPDCALLIU SANTOLIGITHERIGIALALAKYPPTUVSKILDETYPTIS SYNESSIDLIKVPILITISPITISKEQBEIMQOLTEROVDELTYU QLERVIKQPGCHKVPMLYTSEDDAVTANQORAGSPNYTPTIS SYSESSIDLIKVPILITIPITISKEQBEIMQOLTEROVDELTYU PRUTVUGGTISR* IDLIANTLYTYPSPTYSKTSWPEGGDPGI  7061 364 710 ARMSSTIGDPCCTPWIDETTILEBETTARLARRGPCYQXVAGRED ALARLRELCOMLOPENHSKEQMIRMSHUNSEGPTGTURPRUTBEIT REGOREOGSBERAAALVEGLOHDP*ARWSGGPCCTGVAGRED ALARLRELCOMLOPENTLE EPETARLARRECOMIQPENTIL EPETTARLARROFCYQXVAGGREGSPERAALVEGLOHD POOLIS  7062 71 744 ARAGYMIRDELHHISYPYCIPRIKKKSSQKDKVRQPHACTOAGER TAIYULTQURSHLIDEATDGFPGOTDFDGLHEESMENAVDKKKLERL YGRYROPQDEMKLGVUGQPCDDLSLDPASISYLVIJANKFRAA TQCEPSREFILOMTELICCHCMEKLGALDPASISYLVIJANKFRAA TQCEPSREFILOMTELICCHCMEKLGALDPASISYLVIJANKFRAA TQCEPSREFILOMTELICCHCMEKLGALDPASISYLVIJANKFRAA TQCEPSREFILOMTELICCHCMEKLGALDPASISYLVIJANKFRAA TQCEPSREFILOMTELICCHCMEKLGALDPASISYLVIJANKFRAA TQCEPSREFILOMTELICCHCMEKLGALDPASISYLVIJANKFRAA TQCEPSREFILOMTELICCHCMEKLGALDPASISYLVIJANKFRAA TQCEPSREFILOMTELICCHCMEKLGALDPASISYLVIJANKFRAA TQCEPSREFILOMTELICCHCMEKLGALDPASISYLVIJANKFRAA TQCEPSREFILOMTELICCHCMEKLGALDPASISYLVIJANKFRAA TQCEPSREFILOMTELICCHCMEKLGALDPASISYLVIJANKFRAA TQCEPSREFILOMTELICCHCMEKLGALDPASISYLVIJANKFRAA TQCEPSREFILOMTELICCHCMEKLGALDPASISYLVIJANKFRAA TQCEPSREFILOMTELICCHCMEKLGALDPASISYLVIJANKFRAA EXTMEDITERORGEGROUPSCORGERFRAINLILOMSCARAMLLDPASIS TEXTHICLQPATGREMARLLIVANSCARATARALLIVANSCARATARALLIVANSCARATARALLIVANSCARATARA EXTMEDITERORGEGROUPSCARAAAGALGRERGVSAAVAAAGC SSRAGNULETPGREGGPDAAAAGALGGERAPSGRAAPASAAS TRATGCHTCTPSSCAGAAAGSERAASAASAAGGRQKORGNINAADPELS TATHISAARGGRGAABAASAAAGARGRQKORGNINAADPELS TATHISAARGGRGAABAASAAAGARGRQKORGNINAADPELS TATHISAARGGRGAABAASAAAGARGRQKORGNINAADPELS TATHISAARGGRGAAGAAAGARGRQKORGPRKAMBGRRTTFOG PCGCFFFFARARGAAAGAAAGARGRQKORGPRKAMBGRATID OOTITULSQCGSSAULTHUTTURGSAADBETHD OOTITULSQCGSSAULTHUTTURGSAADBETHD OOTITULSQCGSSAULTHUTTURGSAADBETHD OOTITULSQCGSSAULTHUTTURGSAADBETHD TRATGRICKSSGCFTANGGTTRIPFTILQAHDSVVARATHWEN NOMMILTDAHGGOVVAVQGSMANNAMVAROAHERGAAGAACAAGA TRATGRATHENIKUTTURGGGG	i	}	į	
SANTGIAGTTREHLGIALALKVPFFTUVSKIDICAKTTVEKTVR OLERVIKOPCHKVPMLVTBEDDAVTAROQESNVTPTFTLS SVSGESLOLLKVEIAHTLEPLTISEKSQESIMQLUTEFQUVBEITVT PRYGTVUGGTLSF*IDLIATLPTOPSPTYSKTYBVBGGDBGI  7061 364 710 AMPSPIGDEPCLPVMDBETTLEBEFSTARLEFRGFCYQEVAGPRE ALARLERLCCOMLQPEAISKEQMLEMILVLEQFIGTLPFRQBVY RQGRGSGSBERAALVBEIQLDB*AMPSPIGTPCLPVMDBETTL EPPETARLEREGCYQBVAGPREALARLERLCCOMLQPEAISKE QMLEMILVLEQFIGTLPFBIQAWVGORPGSPEEAAALVBEIQLD PGOLLG  7062 71 744 AKAGYNLEBLHMLSYPYCIPKHRLKSSQKDKVVQFMACTQAGER TALYCLTQNBWRLDBRATGSPFQNPDSLHRESMRNAVDKKLERL YGRYKOPQDBNKLGYDGIQGCODLSLOPASISHVI JAMFPAA TQCESSREELELDMYBELGCDSNBKLKALLPRISGSLKOTAKFED FYOFYTFTANNPQGGJDL*MAGAVKKLVISGRFRFLYLMNTFL MERH  7063 2 562 LKYVPDLGGRRFFAMFTSQHR*PELPPDMNSLEQAEDLKAFERD HKYPLISELDM MERH 7064 300 884 EDTGSSPSTTRICTGH*PAPPTASPPBRGTCPPASSAS SRRTGGWCPAPATGAARARGAVRAVALVLSGRFRFLYLMNTFL HKYPLICAGPATGRMENLTUVSVCTARGAMNALIDPSTQKVSF FTSLNNHPFPTISCTILLGPRAGITHKVVAPSILTARGRTVLA HYMNSCDDTGKLILKPRPHVQ*QSSLIVMSLKLAFERI SIDTAKS RKGFLIREIDM  7064 300 884 EDTGSSPSTTRICSTCTGH*PAPPTASPPPRGTCPPASSAS SRRTGGWCPPTGRGRPAAAANLARRESGSPSPKSAAP PLLTPLCAGGAAGGSRANS TRYGGWCPPARTGAAAAACRAGGRGAAPAAAPAAPACC SSRAGRWLETTGRRGSPPGAAAAAACRAGGAVRSAVAARGC SSRAGRWLETTGRRGSPCAAAAACRAGGRAAAPAAPAPABPENGTAVPAA CRCPAARTGAPAAATWLIKRISCSLAPALGHSGPSPFSAAPA PLLTPLCAGGAAGGSRANS  7065 1 555 AYTTHSARGSGRAAAAAAAAAAAAAACGCWCPPKKAMBGRRTTPGG RSQSBFKAPPPOKRSBAAPAAMAHSPVAVQVPGMONNTADPEBL PTKLBRIGGSFGEVFKGIDNTOOVOVALILDEABADBIEDI OQEITVLSQCDSSYVTKYTGSYLRGSKLMIIMFYLGGGSALDLL RAGPFDERQ  7067 152 973 KBITHATEIGSPPRFHIPPFFOHOAPRALFYKFPDGAQQAM CVEVEVGSGGCLEBETPDF  7068 222 816 DTMKKVLLGPLACAGARPFSBHLAKNMLKDPPAACHERITINTPFVET HSPPCKAPP HSPPCKAPP  FSPCKRIPT GSSPRFFHIMPEFFOHOAPRAFREARREFHINTPF FSVVPLVAWKLPSKCILGABMIGLOCPTGAMPLEPINDFSDLTAGG UNGSWCKLGRANNANKTVICHTERETILQAHDSPVRAMTWSHT HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAPP HSPPCKAP	ĺ	[		
QLERTLACPECHINSERGELMQLUTPEOVER TYPE SVSGESLOLLKAYELMILEPUTNSERGELMQLUTPEOVER TYPE SVSGESLOLLKAYELMILEPUTNSERGELMQLUTPEOVER TYPE PRYGTUVGGTLGR* IDLLATLPTOPS PIYSKTSWPKGGDPGI ALMERSPEGPPGT PARTER PERTALLER PROFEVERAGERE ALMERICACOMIQ PENARES PROFEVERAGERE ALMERICACOMIQ PENARES PROFEVERAGERE ALMERICACOMIQ PENARES PROPER PROPERTY ARE PROFESSED ALMERICACOMIQ PENARES PROPER PROPERTY ARE PROPERLY ARE PROPERLY AND PROCESSED ALMERICACOMIQ PENARES PROPER PROPERTY AND PROCESSED ALMERICACOMIQ PENARES PROPERTY AND PROCESSED ALMERICACOMIQ PENARES PROPERTY AND PROCESSED ALMERICACOMIC PENARES PROPERTY AND PROCESSED ALMERICACIÓN PRODUCTOR PRODUCTOR PRODUCTOR PRODUCTOR PRODUCTOR PRODUCTOR PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND PROPERTY AND	l	1		
SUSGESLDILKVEINTLEPPENTSKERQELIMQQLITEPQUBETTY PERGUTUVGETISR* DILLARLPOPESTISKSMERKEGDEGI  7061 364 710 ARMPSPLGPPCLPVMDPETTLEEPETARLRPRGPCYQEVAGPER ALARLREICCOMLQPEAHSREMMLIMQPLGTLEPETQAW RGQRGSGSBERAALVEGLQIDD* ARMPSPLGPPCLPVMDPETTL EPPETARLRPRGPCYQEVAGPERALARLREICCOMLQPEAHSRE QMLDHILLEQDFGTLPPEIQAWVRGGRGSPERAALVEGLQID PGOLIG  7062 71 744 ARAGTRILERLHULSYPYCIPKHKLKSGKKVRQFWACTQAGER TALYCLYQMENRILDRATUSPPODPSLHRSSHRNAVDKKKLERL YGRYKDPQDENKLGYDGIQQPCDDLSLDPASISVLYIAMFFRAA TQCBSGRREFLDOMTELGLOSHSKKALLERLEGGSLKDTAKFKD FYOFTTTAKNPGQKGLDL*MAGAYWKLVLSGFFKFLILWNTFL MESH  7063 2 562 LRTVPDLDGGRFFRAMRTGQRR*DELDPDMSLEQAEDLKAFECR FYSHTHCLQPATGERMLLVVSVCTATGAMWKLULDETQKVSF FTSLMNHBFFTISCITLIGLFFRAGHKRVVANPSILARCKTVLA EYMMSCDDTGKLILKGREHUQ*GSSLVWARSVLANGC SSRAGKMLETPGRREGDPACAAAAGRLAGGAPA*AADFCACSSRAGK KRSFLIRLDM  7064 300 884 RDTGSDSSTERLGSTCCTGH*DRYPLASPHDFRGTCPASSAS SRRTGCTCPPESCHAQARRSRRASASRWGARGAVVSAVAARC SSRAGKMLETPGRREGDPACAAAAGRLAGGAPA*AADFCACSSRAGK CRCPAARTGAPAAAWKLRRLSGLAAPALGRREFGPSPKSAAP PLLTPLGAGAGGSRANS CRCPAARTGAPAAAWKLRRLSGLAAPALGRREFGPSPKSAAP PLLTPLGAGAGGSRANS CRCPAARTGAPAAAWKLRRLSGLAAPALGRREFGPSPKSAAP PLLTPLGAGAGGSRANS CRCPAARTGAPAAARWLRRGGRAPA*AADFLAGGAVWYGMUNNTADPELL PTKLBRIGKGSFGEVFKGIDNRTQQVVAIKIIDLEBAEDBIRDI OOBTITULSQCDSSYVTKYTGSYLKUSKLWIIMSTLGGGSALDLL CRCPAARTGAPAABGRUNDQTVAVYSLLRDVPLADGGDMD VGWEUGGGGGLEERTPP  7066 356 676 GGQGGFFRAMBPCGHAPAGALRSNVRAATMOICDT VOKHELSMANNPTCANNNDQTVAVYSLLRDVPLADGGDMD VGWEUGGGGGLEERTPP  7067 152 973 RENITWATEIGSPFFFHIPPFOHQAPROLFYKRPDFAQQOAMQ CLTPDCKRMRRAVNNPTCANNNDQTVAVYSLLRDVPLADGGDMD VGWEUGGGGGLEERTPP  7068 222 816 DTMEXVLLLFLALGSAKPFFSSHILAKMMLKDMEDDDD DDDDDDDDDDDDDDDSDLSLPFTREBRSHIPPFHLPFPMCPFGQCYSRV VHCDLGJUSVPTN UFFTREBRSHIPPFFHLPFPMCPFGQCYSRV VHCDLGJUSVPTN UFFTREBRSHIPPFFHLPFMCPFGCQCYSRV VHCDLGJUSVPTN UFFTREBRSHIPPFFHLPFFHLARGFILDDDDD DDDDDDDDDDDDBDSLSPTTRESSERSGQASENDDDDDDDDDDDDDDDDDDSSLSPTTRESSERSGQASENDBTLAXQ GLILNNNKLTK HPKAPLTYKKRCHUSHSKLINGLIFFFH	} ·	<b>}</b>		SANTGIAGTTREHLGLALALKVPFFIVVSKIDLCAKTTVERTVR
SUSGESLDILKVEINTLEPPENTSKERQELIMQQLITEPQUBETTY PERGUTUVGETISR* DILLARLPOPESTISKSMERKEGDEGI  7061 364 710 ARMPSPLGPPCLPVMDPETTLEEPETARLRPRGPCYQEVAGPER ALARLREICCOMLQPEAHSREMMLIMQPLGTLEPETQAW RGQRGSGSBERAALVEGLQIDD* ARMPSPLGPPCLPVMDPETTL EPPETARLRPRGPCYQEVAGPERALARLREICCOMLQPEAHSRE QMLDHILLEQDFGTLPPEIQAWVRGGRGSPERAALVEGLQID PGOLIG  7062 71 744 ARAGTRILERLHULSYPYCIPKHKLKSGKKVRQFWACTQAGER TALYCLYQMENRILDRATUSPPODPSLHRSSHRNAVDKKKLERL YGRYKDPQDENKLGYDGIQQPCDDLSLDPASISVLYIAMFFRAA TQCBSGRREFLDOMTELGLOSHSKKALLERLEGGSLKDTAKFKD FYOFTTTAKNPGQKGLDL*MAGAYWKLVLSGFFKFLILWNTFL MESH  7063 2 562 LRTVPDLDGGRFFRAMRTGQRR*DELDPDMSLEQAEDLKAFECR FYSHTHCLQPATGERMLLVVSVCTATGAMWKLULDETQKVSF FTSLMNHBFFTISCITLIGLFFRAGHKRVVANPSILARCKTVLA EYMMSCDDTGKLILKGREHUQ*GSSLVWARSVLANGC SSRAGKMLETPGRREGDPACAAAAGRLAGGAPA*AADFCACSSRAGK KRSFLIRLDM  7064 300 884 RDTGSDSSTERLGSTCCTGH*DRYPLASPHDFRGTCPASSAS SRRTGCTCPPESCHAQARRSRRASASRWGARGAVVSAVAARC SSRAGKMLETPGRREGDPACAAAAGRLAGGAPA*AADFCACSSRAGK CRCPAARTGAPAAAWKLRRLSGLAAPALGRREFGPSPKSAAP PLLTPLGAGAGGSRANS CRCPAARTGAPAAAWKLRRLSGLAAPALGRREFGPSPKSAAP PLLTPLGAGAGGSRANS CRCPAARTGAPAAAWKLRRLSGLAAPALGRREFGPSPKSAAP PLLTPLGAGAGGSRANS CRCPAARTGAPAAARWLRRGGRAPA*AADFLAGGAVWYGMUNNTADPELL PTKLBRIGKGSFGEVFKGIDNRTQQVVAIKIIDLEBAEDBIRDI OOBTITULSQCDSSYVTKYTGSYLKUSKLWIIMSTLGGGSALDLL CRCPAARTGAPAABGRUNDQTVAVYSLLRDVPLADGGDMD VGWEUGGGGGLEERTPP  7066 356 676 GGQGGFFRAMBPCGHAPAGALRSNVRAATMOICDT VOKHELSMANNPTCANNNDQTVAVYSLLRDVPLADGGDMD VGWEUGGGGGLEERTPP  7067 152 973 RENITWATEIGSPFFFHIPPFOHQAPROLFYKRPDFAQQOAMQ CLTPDCKRMRRAVNNPTCANNNDQTVAVYSLLRDVPLADGGDMD VGWEUGGGGGLEERTPP  7068 222 816 DTMEXVLLLFLALGSAKPFFSSHILAKMMLKDMEDDDD DDDDDDDDDDDDDDDSDLSLPFTREBRSHIPPFHLPFPMCPFGQCYSRV VHCDLGJUSVPTN UFFTREBRSHIPPFFHLPFPMCPFGQCYSRV VHCDLGJUSVPTN UFFTREBRSHIPPFFHLPFMCPFGCQCYSRV VHCDLGJUSVPTN UFFTREBRSHIPPFFHLPFFHLARGFILDDDDD DDDDDDDDDDDDBDSLSPTTRESSERSGQASENDDDDDDDDDDDDDDDDDDSSLSPTTRESSERSGQASENDBTLAXQ GLILNNNKLTK HPKAPLTYKKRCHUSHSKLINGLIFFFH	}			QLERVLKQPGCHKVPMLVTSEDDAVTAAQQFAQSPNVTPIFTLS
7061 364 710 ARRESPICAPPCLEVMOPETTLERPETARLREFIGETQUEVAGERE ALARIERICCONLOPENSISEROMINEM ALROPLATILPER LOAW ROGRESPERABALVEGIQHD + ARMES PLEPPCLEVMOPETTL EPERTARLREFIGE CYQEVAGERER ALARIERIC COMLOPENSISE QUIREMULVE PLOAVING FROSPERABALVEGIQHD PGOLIG  7062 71 744 ARAGYNILERLHWILSYFYCI PKHKIKSSQKDKVRQPHACTQAGER TAIYCLTQNEWRILDEATOSP PONDOSIHRESMRANVDKKKLERLI YGRYKDPQDENKIGYDGXQQPCDDLSLDPASI SUVLVIAWKPRAA TQCESSREFILDAMTELGCOSMELIKABLIFILEGEIKDTAKERD PYOPTFTEANKPGQKGLDL*NAGAYWKUVLSGREKFI,TUMNTFL MEHH  7063 2 562 LETVPDLDGRIFFRAMETGOR* PELPPDMISLEQAEDLKAFERE LTYYITICLQPATGRWEMILITUSVCTATGAMWHILDETQKVSF FTSIANHPFTISC TILIGLPPAGIHKRVVAPS I LARCRTVLA EYMMSCDDTGKLLKERPHVQ* QSSLI VMIKIAFLERISDTAKS HKSFLIRIDM  7064 300 684 RDTGSDPSSTERILSTCCIGH*PAEPTASPHPSRTCPPASSAS SERTIGGWTCPPESGHADARSRRAASSASRWARGAVRSAVARGC SSRAGRWILETPGRRGPPACAAAAGRLRGRAP*AAPPDASVPAR CRCPAARTGAPAAATWILRRISGLRAPALGRRFSPSPKSAAD PLITPLGRAGAGSKRAN CRCPAARTGAPAAATWILRRISGLRAPALGRRFSPSPKSAAD PLITPLGRAGAGGSRANS CRGPAARTGAPAAATWILRRISGLRAPALGRRFSPSPKSAAD PLITPLGRAGAGGSRANS AGGRGKGPPKKAWEGRFTTPGG RSQSEFKAPPPOKRSSRAAFASMAHSPVAVQVVGMONNIADPBEL PTKLERIGKGSPGEVFKGIDMRTQOVVATKI IDLERARDEBLI PTKLERIGKGSPGEVFKGIDMRTQOVVATKI IDLERARDEBLI PTKLERIGKGSPGEVFKGIDMRTQOVVATKI IDLERARDEBLI PTKLERIGKGSPGEVFKGIDMRTQOVVATKI IDLERARDEBLI QUITVLGSCGSALDIL RAGPPDERQ CLTPCKKMRRAVMRT IDVMSVILKVENTSTKKCGGSALDIL RAGPFDERQ CLTPCKKMRRAVMRT IDVMSVILKVENTSTKKCCYVVVW NORMSLEVANDAVTVASSESSETTILLAGLTNIPTST ILQAHDSPURANTWISH NDAMMITADHGGYVKWQDSMMNVKMPQAHKKAI KRARFHINIT PFVVPI TWKWLPSKCILGABMIGLOPICLENDEMDATUTI TITPFFVFT HSPPCRAPP  7068 222 816 DTMKEVILLIFLALCSAKPFFSSHIALKNAMLKDEDDDDD DDDDDDDDDDDDDDDNINSLEPTERPRSHIPPFDLFMCPFGQCYSKU VHCGDLGTSLY GLINNNKLTKRINGLQNNKKKEIKKROPKGUTSLY GLINNNKLTKRINGLQNNKKEIKKROPKGUTSLY GLINNNKLTKRINGLQNNKKEIKREIKENDLGFSCLUSSLENDLEFSLALAGARTHANDILGNNKKEIKREIKERSPEPTPF FSPVPT HSPPCTRADLQNNKKEIKREIKERSPEPTPFVFT HSPPCTRADLQNNKKEIKREIKSPEPTPFVFT HSPPCTRADLQNNKKEIKREIKERSPEPTPFWFT HSPPCTRADLQNNKKEIKREIKERSPEPTPFWFT HSPPCTRADLQNNKKEIKREIKERSPEPTPFWFT HENDENDERGESGGGGERDBTL	)		}	SVSGESLDLLKVFLNILPPLTNSKEQEBLMQQLTEFQVDEIYTV
7061 364 710 ARRESPICAPPCLEVMOPETTLERPETARLREFIGETQUEVAGERE ALARIERICCONLOPENSISEROMINEM ALROPLATILPER LOAW ROGRESPERABALVEGIQHD + ARMES PLEPPCLEVMOPETTL EPERTARLREFIGE CYQEVAGERER ALARIERIC COMLOPENSISE QUIREMULVE PLOAVING FROSPERABALVEGIQHD PGOLIG  7062 71 744 ARAGYNILERLHWILSYFYCI PKHKIKSSQKDKVRQPHACTQAGER TAIYCLTQNEWRILDEATOSP PONDOSIHRESMRANVDKKKLERLI YGRYKDPQDENKIGYDGXQQPCDDLSLDPASI SUVLVIAWKPRAA TQCESSREFILDAMTELGCOSMELIKABLIFILEGEIKDTAKERD PYOPTFTEANKPGQKGLDL*NAGAYWKUVLSGREKFI,TUMNTFL MEHH  7063 2 562 LETVPDLDGRIFFRAMETGOR* PELPPDMISLEQAEDLKAFERE LTYYITICLQPATGRWEMILITUSVCTATGAMWHILDETQKVSF FTSIANHPFTISC TILIGLPPAGIHKRVVAPS I LARCRTVLA EYMMSCDDTGKLLKERPHVQ* QSSLI VMIKIAFLERISDTAKS HKSFLIRIDM  7064 300 684 RDTGSDPSSTERILSTCCIGH*PAEPTASPHPSRTCPPASSAS SERTIGGWTCPPESGHADARSRRAASSASRWARGAVRSAVARGC SSRAGRWILETPGRRGPPACAAAAGRLRGRAP*AAPPDASVPAR CRCPAARTGAPAAATWILRRISGLRAPALGRRFSPSPKSAAD PLITPLGRAGAGSKRAN CRCPAARTGAPAAATWILRRISGLRAPALGRRFSPSPKSAAD PLITPLGRAGAGGSRANS CRGPAARTGAPAAATWILRRISGLRAPALGRRFSPSPKSAAD PLITPLGRAGAGGSRANS AGGRGKGPPKKAWEGRFTTPGG RSQSEFKAPPPOKRSSRAAFASMAHSPVAVQVVGMONNIADPBEL PTKLERIGKGSPGEVFKGIDMRTQOVVATKI IDLERARDEBLI PTKLERIGKGSPGEVFKGIDMRTQOVVATKI IDLERARDEBLI PTKLERIGKGSPGEVFKGIDMRTQOVVATKI IDLERARDEBLI PTKLERIGKGSPGEVFKGIDMRTQOVVATKI IDLERARDEBLI QUITVLGSCGSALDIL RAGPPDERQ CLTPCKKMRRAVMRT IDVMSVILKVENTSTKKCGGSALDIL RAGPFDERQ CLTPCKKMRRAVMRT IDVMSVILKVENTSTKKCCYVVVW NORMSLEVANDAVTVASSESSETTILLAGLTNIPTST ILQAHDSPURANTWISH NDAMMITADHGGYVKWQDSMMNVKMPQAHKKAI KRARFHINIT PFVVPI TWKWLPSKCILGABMIGLOPICLENDEMDATUTI TITPFFVFT HSPPCRAPP  7068 222 816 DTMKEVILLIFLALCSAKPFFSSHIALKNAMLKDEDDDDD DDDDDDDDDDDDDDDNINSLEPTERPRSHIPPFDLFMCPFGQCYSKU VHCGDLGTSLY GLINNNKLTKRINGLQNNKKKEIKKROPKGUTSLY GLINNNKLTKRINGLQNNKKEIKKROPKGUTSLY GLINNNKLTKRINGLQNNKKEIKREIKENDLGFSCLUSSLENDLEFSLALAGARTHANDILGNNKKEIKREIKERSPEPTPF FSPVPT HSPPCTRADLQNNKKEIKREIKERSPEPTPFVFT HSPPCTRADLQNNKKEIKREIKSPEPTPFVFT HSPPCTRADLQNNKKEIKREIKERSPEPTPFWFT HSPPCTRADLQNNKKEIKREIKERSPEPTPFWFT HSPPCTRADLQNNKKEIKREIKERSPEPTPFWFT HENDENDERGESGGGGERDBTL		i	1	PKYGTVYGGTLSR*IDLLATLPTQPSPIYSKTSWPKGGDPGI
ALARLIEBIC CONLOPEAISIRE OMBIANUL REPUTEL PPET OF RORPES PERAPAL VERGUL PHE * ARMES PLOPPCL PYMOPETT L EPPETARLIR PROGUCE OF THE PET OF ARMES PLOPPCL PYMOPETT L EPPETARLIR PROGUCE OF THE PET OF ARMES PLOPPCL PYMOPETT L EPPETARLIR PROGUCE OF THE PET OF ARMES PROPER PALAL VERGUL PROGULS  7062 71 744 ARACINI SERLIBULS Y PCI PERKIKAS SORDKYROPHACTO AGER TALY CLTUREN RUBENTUS PPONDED LARBES MINAUVAK KLIRLI YOR YKUPODEN KLIG VERGUL PARACINA VINAU LISOR PROPERTO SERVICI AND TO CERSIR REPLACIONI PROGULT AND THE MARKER A TOCES SERVE PLOOM THE CONTROL PARACINA VINAU LISOR PREPLYMENT PL MESSIR  7063 2 562 LETYPOLIP GREF PRAMETOCOR * PEL PDOMIS LEGARD LARFER R LTRY HICLOPATGRIBEM VINAU LISOR PREPLYMENT PL MESSIR RYMSCODTO SERVIC PROGULT AND THE ARCEST LAR EYMINGCODT SELLI VINAU LISOR PROGULT AND THE ARCHIVAL EXPRISED TO SELLI VINAU LISOR PROGULT AND THE ARCHIVAL EXPRISED TO SELLI VINAU LISOR PROGULT AND THE ARCHIVAL EXPRISED TO SELLI VINAU LISOR PROGULT AND THE ARCHIVAL EXPRESSODE SERVE PROGULT AND THE AGENT AND THE ARCHIVAL EXPRESSODE SERVE PROGULT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGENT AND THE AGEN	7067	364	710	ADMOSDICEDOCLOUMDPETTLEEPETARLEFEGECYOEVAGPRE
RIGGREGSPERAALLVEGUCHDP *ARMSPIEGPCLEYMDPETTL EEPETARLEPRGECYCGVAGPREALARLELCCONLOPERHEISER QHEBHUYLEGFLGTLPPBIQAWVRGQRPGSPERAALVEGLQHD PGOLLG  7062 71. 744 AKAGYNLERCHWLSTYPCTPKHKLKSSQKDKVRQPMACTQAGER TATYCLTGNENRILDEATDSPFONPDSIHRESMRAAVDKKKLERL YGRYKDPQDENKIGWDGJQPCDDLSIDASISUNLTAMFRAA TQCSPSRKSPLDGMTELGCDSMEKLKALLERLSQKLKOTAKFROA TQCSPSRKSPLDGMTELGCDSMEKLKALLERLSQKLKOTAKFROA TQCSPSRKSPLDGMTELGCDSMEKLKALLERLSQKLKOTAKFROA TQCSPSRKSPLDGMTELGCDSMEKLKALLERLSQKLKOTAKFROA TQCSPSRKSPLDGMTELGCDSMEKLKALLERLSQKLKOTAKFROA TQCSPSRKSPLDGMTELGCDSMEKLKALLERLSQKLKOTAKFROA TYPETAKNPGQKGLDL*NAGAYWKLVLGSERFYLYLWNTYL MEHH TYPETAKNPGQKGLDL*NAGAYWKLVLGSERFYLYLWNTYL MEHH TYPETAKNPGQKGLDL*NAGAYWKLVLGSERFYLYLWNTYL MEHH TYPETAKNPGQKGLDL*NAGAYWKLVLGSERFYLYLWNTYL MEHH TYPETAKNPGQKGLDL*NAGAYWKLVLGSERLSQKLKOTAKFRO LATYTHCLQPATGWREWHLLTVSVCTATGAWWKLDETGKKVSF FTSLMSHPSPTSCTCTGH*PSLSPHSRSTCTPASSAS SKRIGGWTCPPSGSHAGARGAKSRASASKWAGAWGAVASAVARGC SSRAGRWLETPGRRGCPACAAAAGLRGGPA*AAPPTASVPAR CRCPAARTGAPAAATWLRRELSGLRAPALGRAFASPASPASPASPASPAP PLLTPLGAGRAGGSRANS SRRIGGWTCPPSGSHAGARGARAAGARGAWGAGVASAVAARGC SSRAGRWLETPGRRGCPACAAAAGLRGGPA*AAPPTASVPAR CRCPAARTGAPAAATWLRRELSGLRAPALGRAFASPASPASPGSPKKAAB PLLTPLGAGRAGGSRANS ATTHEARRSGRGAARAAAGARGRGKGPDRKAWEGRRTTPGG SSSSEFRAPPOKRSSBAAPASMAHSPVAVQVVGMGNNTADPBELL PTILBRIGGGSPGVFKGGLDNRTQVVALKI IDLSBARDBIRDI QOEITVLSQCDSSYVIKYTGSYLKGSKLWILGGGSALDIL RAGPPIDERO TOGG 356 676 GGGCEBRETPB TOGGREFFERDERORDFADASLCSHATMGCCDT VRQHELSTLWNGLTTRIPTGCGGSALDIL RAGPTUBCY UVCUGLGGSGCLEBRTPP PGRAPPYUVVGLSSCETTLNNGLTTRIPTTI LQGADPGLDMD VGVEVGGSGGCLEBRTPP PSVPTVWWKLPSKCILGABHHGLQPILGMSHATMSH NDMMLTADHGGVVKWQSNMNNVMPQAIKRAIRRAPHINTP PSVVPTVWKLPSKCILGABHHGLQPILGMENTDDDDD DDDDDDDDDDLSDNSLEPTERPSHIPPDLFFENCPFGQCYSKV VHCCDLGITSVPTHIPPTOTMLLQNNKKEILKRMPKLKDENGLTSLY GLILNNNKLTKIHVKALTTYKKRRLYLSHNQLGE IPINLIPKSL AERLIBENKVKRQKNTONNTKKRLKRRLYLSHNQLGE IPINLIPKSL AERLIBENKVKRQKNTONNTKKRLKRRLYLSHNQLGE IPINLIPKSL AERLIBENKVKRQKNTONNTKKRLKRRLYLSHNQLGE IPINLIPKSL AERLIBENKVKRQKNTONTONNTKSETSFSGOVSSSSIMPLITPEW	1,007	204	/10	NI ADI DRI CCONT. OPRAHSKPOMI EMI VI BOFI GTLPPRIOAWV
EEPETARLRFRGCYQRVAGGREGSPERAALARLRELCCQNILQPEAHSKE QMLEMLVILEQFLGTLPPEIQAWRGQRFGSPERAAALVEGLQHD PGOLLG  7062 71 744 AKAGINLERLHWLSYFYCIPEHKLKSSQKDKVRQPMACTQAGBR TAYCLIQNERRLDEATDGFFQNPDSLHRESMRNAVDKKKLERL YGRYKDPQDBKKIGVDQIQQFCDDLSLDPASISYLVIJANFFRAA TQCESPSRKSFLDGMTELGCDSMEKLKALLPELSGELKRUTAKFRA TQCESPSRKSFLDGMTELGCDSMEKLKALLPELSGELKRUTAKFRA TQCESPSRKSFLDGMTELGCDSMEKLKALLPELSGELKRUTAKFRA TQCESPSRKSFLDGMTELGCDSMEKLKALLPELSGELKRUTAKFRA TQCESPSRKSFLDGMTELGCDSMEKLKALLPELSGELKRUTAKFRA TQCESPSRKSFLDGMTELGCDSMEKLKALLPELSGELKRUTAKFRA TQCESPSRKSFLDGMTENGGCSMEKLKALLPELSGELKRUTAKFRA TYPDLEGRRFRAMFRGGRF*PELPPDMNSLEQAEDLKAFERR LTRYTHCLQPATGRRFRLAUVSVCTATGARNMLIDPETQKVGF FTSLNNHPFFTISCTTLIGLPPAGIHKRVAPGEILAARGETVLA EYMBSCDDTGKLILKFRPRVQ*QSSLIVWKIKTAFLRISDTAKS HKGFLLRIDM RDGSSPSSTKRLCSTCCTGH*PAEPIASPHPSGTCFPASSAS SRRTGCWTCPPSGGHAQARSRRASASKGARGAVRSAVAARGC SSRAGRWELTPGRRRGPPACAAAAGLRGPAP*AAPPTASVPAR CRCPAARTGAPAAATWLRRRLSGLARPALGRRSAVAAARGC SSRAGRWELTPGRRRGPPACAAAAGLRAGPAPAPPTASVPAR CRCPAARTGAPAAATWLRRRLSGLARPALGRRSBGPSPKSAAP PLLTPLGAGRAGGSRANS PLLTPLGAGRAGGSRANS ATTHISARRSGRGAAARAAAAAAGLRGPAPAPPTASVPAR CRCPAARTGAPAAAATWLRRRLSGELARPALGRRSBGFSPSPKSAAP PLLTPLGAGRAGGSFRANS TTHLIFLAGGSSFGLYTYTYGSYLKGSKWITMBVLGGGSALDLL RAGPFDEFQ QOEITVLSQCSSYLTYTYGSYLKGSKWITMBVLGGGSALDLL RAGPFDEFQ 7066 356 676 GFGQEGEGWARRGGHPLDPADHFRAPASLRSNVRAATPMOICUTT YNQRHSLFNAMRFJGAVNNMDQTVMVPSLLRDVPLADPGLDND VGVEVGSSGGCLEBKTPP UPPLYMTKJFSKCIJABMHGLCQFLKFREFTFAPAGRATA NDMMTATBIGGSPTLWFSTINNGKLTFTFKREFTTENTSTTTSCKCVPVVWK NDMMTATBIGGSPTLWNGLTFTFKREFTTENTSTTSCKCVPVVWK NDMMTATBIGGSTVKVRQSMMNNVKMFQAHKKATRRARFTHNDF FSVPPTVMVKLFSKCIJABMHGLCQFLGMFHIPINTTFFFFFH HSPPCMAPF  7068 222 816 DTMKEVULLLFLALCSAKPFFSPSHTALKNMMLKOMEDTDDDDD DDDDDDDDDDDDDDDRDRNSLFPTRBRSHFPFFFDLFMCFGCQCYSRV VHCSDLGLTSVPTNTPFOTRALLCNMLKCMEDTDDDDD DDDDDDDDDDDRNSLFPTRBRSHFPFFFDLFMCFGCQCYSRV VHCSDLGLTSVPTNTPFOTRALLKNMLKCHKERKFLKNDFKGLTSLY GLILNNKLTKLTBAAFHTTKKLRRLLSESFSGOVSSSLMPHTPFW	1	İ		DOODDCCDERAALVEGLOUDD+ARMDSDLCDPCT.PVMDPKTTL
OMLEMINIEQFIGTLPPEIQAWVRGQRPGSPERAAAI.VEGIQHD PGOLLS 7062 71 744 AKAGIMIERIHWISYFYCIPKHKLKSSQKDKVRQPMACTQAGER TALYCLITQMEMRIDEATDSPFQNPDSILRESHMAVDKKLERL YGRYKDPQDBKKIGUDGIQQFCDDLSDPASISUUTJAKFRAA TQCBPSRKEFIDGMTELGCDSMEKLKALLPRLEGGELDKAKRD FYDFTFTPARMPGQKGIDL*MAGAYWKIVLSGRKDTAKRD FYDFTTPTARMPGQKGIDL*MAGAYWKIVLSGRKDTAKRD FYDFTTPARMPGQKGIDL*MAGAYWKIVLSGRKDTAKRD FYDFTTPARMPGQKGIDL*MAGAYWKIVLSGRKDLKAFERR LTTYHCLQPATGERMILITUSYCTAGAMNWILIDPETQKVSF FTSIMMHPFFTISCITLIGLPPAGIHKRVVAPSILAARCRTVLA BYMMSCDDTGKLILKPRPHVQ*QSBLIVWGIKTAFIRISDTAKS HKSFLIRIDM  7064 300 884 RDTGSDPSSTTRLCSTCCTGH*PAPPIASPTRGTCPPASSAS SRRTGCWTCPPESCHAQARSRRASASRWGARGARVASARGC SRRAGWILETPGRRRGPPACAAAGCILGGPAP*APPTASVPAR CRCPAARTGAPAAATWLRRILSGLRAPALGRRRSPGPSPKRAAP PLITPILAGAGAGGSGRAWS  7065 1 555 ATTTHSARRSGRGAAABAAAAGGRQKGFDRKAWEGRRTTPGG RSGSEPKAPPPQKRSGAABAAAAGRLKGPAP*APPTASVPAR CRCPAARTGAPAAATWLRRILSGLRAPALGRRRSPGPSPKRAAP PLITPILAGAGAGGSGRAWS  7066 1 556 676 PGPQRGPWBAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT YNQKHSLEMAMMRYIGAVNRMOYTVAVPSLLRDVPLADFGLDND VGEVVGSGGCLERERTPP  7067 152 973 KENITMATEIGSPRFFHMPRFOHQAPRQLFYKRPDFAQQOAMQ QLTFDCKNMRKAVRKYIDVNPSVLKYLENNIQRDQRDWRATQ PDAGYYNDLVPPICAMNNNVKMPQAHEBALREAFFHNIP FSVVPIVMKLPSKCILGABMHGLQOFLANHTHNIPFFVET HSPPCMAPP 10768 222 816 DTMKEYVILLIFLALCSAKPFFSPSHLALKNMMLKOMEDTDDDDD DDDDDDDDDDDDDRDNSLFFPTREPRSHFPPFDLPPMCPFGQQYSRV VHCSDLGLTSVPTNIPFOTEMLOLQNIKKEIKENDEKGITSLY GLILINNKLTKHTRAFFITHKKIRGHLGEIPINLIPFFYLH FSVVPIVMKLPSKCILGABMHGLQOFLANHTHNIPFFYLESLY GLILINNKLTKHTRAFFITHKERSFTTSCKLKESFSGQVSSSLMPITPPEP	ł			REPORTANT REPOSONOFIZACIONAL PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PRINCIPALICA PR
PGGLLG  7062  71  744  AKACTNLERLHWLSYFPCIPKHKLKSSGKOKVROPMACTOAGER TAIYCLTQNENRILDEATDSPFONPDSLHRESMRNAVDKKKLERL YGRYKDPQDBMKIGVDGIQQPCDDLSLDPASISVLVITAMKFPRAA TQGESSRKFILDGMFBLGCHENKLKALLFRLSDGLKDTAKFKO PYOPTFTPAKNPGQKGLDL*MAGAYWKLVLSGRFKFLYLWNTFL MENH  7063  2  562  LRTVPDLPGRRFRAMRTGQRR*PELPPDMNSLEQAEDLKAFERR LTSYLHCLQPATGEWRHLLIVUSVCTATGAMMLIDPETQKVSF FTSINNHNPFFTISCTILIGLPPAGIHKRVVAPGILAARGRTVILA RYMMSCDDTGKLILKPRPHVQ*QSSLIVWGLKIAFLRISDTAKS HKGFLIRLDM  7064  300  884  RDTGSDPSSTRRLCSTCCTGH*PAEPYASPHPSRGTCPPASSAS SRRTGCWTCPPESGHAQARRSRRASASRKGRAGVASAVARGC SRRAGRUEFTPGRREGPPACAAARGRAVRSAVARGC SRRAGRUEFTPGRREGPPACAAARGLKGPAP*AAPPTASVPAR CRCPAARTGAPAAATWLRRRLSGLRAPALGRRRSPGPSPKSAAP PLLTPLGAGRAGGSRANS  7065  1  555  ATTHEARRGGGGAAARAAASAAGGRQKGFPKKAWEGRRTTPGG RSGSEKAPPPOKRSRAAFAANHPVAUQVGKQNNILAPPBEL FTKLERIGKGSFGEVPKGIDNRTOQVVALKI IDLEBRADBELDI COEITVLSQCDSSVTTYTGSYLRGSKLWI IMEYLCGGSALDLL RAGPFDEFQ  7066  356  676  FGPGRGGFWAAREGGHPLDPADHFRAPASLRSNVRAATMGICDT YNQKHSLRAAMMRFIGAVNMNDQTVMVPSLLRDVPLADFGLDND VGVEVGSGGCLEBERTPP KBNITMATBIGSPPRFFHMPRFOHQAPRQLFYKRFDFAQQQAMQ QLTFDCKNNRKAVNRKTIDVNPSV LKYLENRINQRDQRDMRATQ PDAGYYNDLVPPIGMANPMADTYFKYSTNTKKKCVPVVVWR TPBGRRLVTGASSGEFTLWNGLTFNPFTILQAHDS PVRAMTWSH NDMMLTADHGGTVKYNQSSMANNVRHFOHRHEATRRARFIHIND FSVVPTYUMKLFSKCIGABMHIGCFFLGNFHHIPNTFFFFH HSPPCNAPF  7068  222  816  DIMKEYVLLLFLALCSAKPFFSPSHTALKNMMLKOMEDTDDDDD DDDDDDDDDDDDNDRINSLFPTREPRSHFPPFDLPPMCPFGQCYSRV VHCSDLGLTSVPTNTPFDTTRLOLQNIKKKEIKRNDFKGLTSLY GLILINNKLTKHTPKAFITTKKLRRLLERILLSRNQLESIFSLY GLILINNKLTKHTPKAFITTTKKLRRLLERILLSRNQLESIFSLY GLILINNKLTKHTPKAFITTTKKLRRLLERILLSRNQLESIFLALQ AELRIHENKVKRIQKDTFKKK  FFDHRRYFFVNRGGSGSGCMEPPDSEBEBESQOAENRBETLAKQ  THORTYTONSTITSSETSTSTGSLCKESFSGOQAENRBETLAKQ  THORTYTONSTITSSETSTSTGSLCKESFSGOQAENRBETLAKQ  TIKNKTGTDNSTSTSSTTSTGSLCKESFSGOQAENRBETLAKQ  TIKNKTGTDNSTSTSSTTSTGSLCKESFSGOQAENRBETLAKQ  TIKNKTGTDNSTSTSSTSTSTGSLCKESFSGOQAENRBETLAKQ	ł	1	1	EELETHETEE COLCIONAL COLCORDA STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD STATES COLORD
7062   71	1	1	1	
TALYCLTQBERKLDRATDSPPONPOLIHRESHRINADDKKKLERL YGRYKDPQDBNKLGVDGYQDCDLLDPASISVLV1AMKPRAA TQCEPSRKEFILGMTELGCDSMEKLKALLPRLEQGILKDTAKFKD PYOPTFTPAKNPGQKGLDL*MAGAYWKLVLSGRFKFLYLWNTFL MENH  7063 2 562 LRTVPDLPGRRFRAMRTGQRR*PELPDMNSLEQAEDLKAFERR LTSYLHCLQPATGRRRMILLVUSVCTATGAWNHLLDPETQKVSF FTSLMHPPFTISCTTLIGLSPRGHKRVUAPSILARCCRTVLA EYMMSCDDTGKLILKPRPHVQ*QSSLIVMILKIAPIRISDTAKS HKOFLLRLDM  7064 300 884 EDTGSDPSTTRLCSTCTIGH*PAEPTASPHPSRGTCPPASSAS SRRTGCWTCPPESGHAQARRSRRASASRWAGAGAVBSAVAARGC SSRAGRWLETPGRRGSPPACAAAGRLRGPAP*AAPPTASVPAR CRCPARTGAPPAATWLRRRISGLRAPALGRRKSPGPSPKRAAD PLLTPLGAGRAGGSRANS  7065 1 555 ATTHEARRSGRGAAABAAASAAGGRQKGFDRKAWBGRRTTPGG RSGSEPKAPPPQKRSHAAFAAMAISPVAVQVPGWQNNIADPEEL FTKLREIGGSFGVVFKGIDMRTQOVVAIKIIDLEBARBSIBDI QOEITVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLGGSSALDIL RAGPFDEFQ 7066 356 676 PGPQRGFWRAREGGHELDPADHPRAPASLERNVRAATMWQICDT YNQKHSLFNAMMRPIGAVHMNDQTVMVPSILLRDVPLADFGLDND VGVEVGSGGCLEERTPP VGVEVGGSGGLEERTPP 7067 152 973 KBNITMATBIGSPPRFFHIPPFFOHQAPROLFYKRPDFAQQAMQ CLFTEDGKRWRKAVMRKTIDVMPSVIKYLRARINGORDGRMMRATQ PDAGYYNDLVPPIGMLNNPMNAVTTKEVRTSTMKVKCPVFVVRW TPBGRELVTGASSGFTLWNGLITNFFSTILADHISPKVAMTHMSP MOMMHLTADHGGYVKWQSNNNNVMFPQAHKBAIRRRRFTHN1P FSVVPIVMVKLPSKCILGABMHGLCQFLGNFLHPINTIFFFVFT HSPFCMAPF FSVVPIVMVKLPSKCILGABMHGLCQFLGNFLHPINTIFFFVFT HSPFCMAPF GLILINNKLITKHPKAPLITTKKLRILYLGHLEVMPGGCYSRV VHCSDLGLISVPTNIFFDTRNLDLQNNKLRIKKIKENKENDFKGLTSLY GLILINNKLITKHPKRAFLITKKLRILYLSHNQLSETFINKLTSLY GLILINNKLITKHPKRAFLITKKLRILYLSHNQLSETFINKLTLAK AELRIHENKVKKIQKDTFKKK 7069 1147 1765 FRDHRKYFYUNGGGGSGWFPDGEREESESQAQBNRDETLAKQ TLKNKKTOTNSTSTESSETSTGSLCKESFSGQVSSSSLMPLITPFW	1		Í	PGQLLG
YGRYKOPODRIKIGYOGIQOFCDLSLIDPASISVLVIANFERAR TQCBFSRREFLORMTELGCDSMEKLKALLFRLEGGILKDTAKFKD FYOFTFTPAKNPGQKGIJDL*MAGAYWKIVISLGGFKKLTIMNTYL MRHH  7063 2 562 LRTVPDLPGRRFRAMRTSQRR*PELPPDMNSLEQAEDLKAFERR LTSYLHCLQPATGRRRMLLIVUSVCTATGAMNHLIDPETQKVSF FTSLMNHPFTTSCTTLIGLFPAGIHKRVVAPSI LARCRIVIA RYMNSCDDTGKLILKPRPHVQ*QSSLIVMGLKIAFIRISDTAKS HKOFFLERIDM  7064 300 684 EDTGSDPSSTRELGSTCCTGH*PAEPTASPHFSRGTCPFASSAS SRRTGCWTCPPESGHAQARRSRRASASRWGARGAVRSAVAARGC SSRAGRWLETPGRRRGPPACAAAAGRLRGPA*AAPPTASVPAR CRCPAARTGAPAAATWLRRRISGLRAPALGRRRSPGPSPKSAAP PLLTPLGAGRAGGSRANS  7065 1 555 ATTHEARRSGRAAARAASAAGGRQKGPDRKAWEGRRTTPGG RSGSEPKAPPPQKRSRAAFASMARSPVAVQVPGMQNNTADPEEL FTKLERIGKSPFGVFKGIDNRTQOVVALKIIDLBERKBEISDD QCEITVLSQCDSSVVTKYTGSYLKGSKIMIIMEYLCGGSALDLL RAGPFDEFQ  7066 356 676 PGPQRGPWRRAEGGHPLDPADHPBAPASLESNVRAATMMQICDT YNQKHSLENAMMRPIGAVNNMDQTVMVPSLLRDVPLADFGLDND VGVEVGGSGGCLERETPP GPQKGPWRRAEGGHPLDPADHPBAPASLERNVRAATMMQICDT YNQKHSLENAMMRPIGAVNNMDQTVMVPSLLRDVPLADFGLDND VGVEVGGSGGCLERETPP DAGYYNDLVPPIGHLNNPMAVTTKFVRTSTKKVKCFVFVVW TPBCRRLVTGASSGFTLMNGLTFNFFTILQAHDS PVRAMTWSH NDNMMLTADHGGVVKYMQSNNNNVMPQAHKBAIREARFIHNIP FSVVPIVMVKLPSKCILGABMHGI.QOFLGNFLHPINTIFFFVFT HSPPCNAPP  7068 222 816 DTMKEVYLLIFIALCSAKPFFSPSHIALKNMMLKOMEDTDDDDD DDDDDDDDDDDDDRDNSLFPTREPRSHFFPFDLPPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFTURNLDLINNKLKEIKENDFKGLTSLY VHCSDLGLTSVPTNIPFTURNLDLINNKLKEIKENDFKGLTSLY VHCSDLGLTSVPTNIPFTURNLDLINNKLEKEIKENDFKGLTSLY VHCSDLGLTSVPTNIPFTURNLDLINNKLEKEIKENDFKGLTSLY VHCSDLGLTSVPTNIPFTURNLDLINNKLEKEIKENDFKGLTSLY VHCSDLGLTSVPTNIPFTURNLDLINNKLEKEIKENDFKGLTSLY VHCSDLGLTSVPTNIPFTURNLDLINNKLERKEIKENDFKGLTSLY VHCSDLGLTSVPTNIPFTURNLDLINNKLESETPLANLPKSL ABLRIEMVKKIQKDTFKKK  7069 1147 1765 FREHRRYFYVNEQGSGSQWEFPDGEKEESESQQSSSSSLMPLTFFW	7062	71	744	AKAGTNLRRLHWLSYFFCIPKHKLKSSQKDKVRQFMACTQAGER
TQCBGSRRBFLIGMTBLIGCISMBEKLKALLFRLEGGLINTTAKFKD PYQFTFTPAKNPGQKGLDL*MAGAYWKLVLSGRPKPLYLWNTFL MEBH  7063 2 562 LRTVPDLBGRRFRAWRTGGRR*PELPPDMISLEQAEDLKAPERR LTEYHCLQPATGRWRMLLTUVSVCTATGAMWMLIDPETQKVGF FTSLMNHPFFTISCITLIGLFPAGHHKRVVAPSIIAARCRTVLA BYMMSCDDTGKLILKPRPHVQ*QSSLIVWGLKIAFLRISDTAKS HKGFLIRLDW  7064 300 884 RDTGSDFSSTRRLCSTCCTGH*PAEPTASPHPSRGTCPPASSAS SRRTGCMTCPPESGHAQARRSRRABASRWGARGAVRSAVAARG SRRGWRLETPGRRRGPPACAAARARGRLGGPP*AAPPTASPVPAR CRCPAARTGAPAAATWLRRLSGLRAPALGRRRSPGPSPKSAAP PLLTPLGAGRAGGSRANS  7065 1 555 ATTTHSARRSGRGAARAAASAAGGRQKGPDRKAWBGRRTTPGG RQSEPKAPPPQKRSBAAFASAAHSPVAVQVPGMQNNIADPEEL FTKLBRLGKGSFGEVFKGIDNRTQOVVAIKLIDLEBARDBIRDI OOEITVLSQCOSSYVTKYGSYLKGSKLWIIMSYLGGGSALDLL RAGPFDEPQ  7066 356 676 PGPQRGFWRRREGGHFLDPADHPRAPASLRSNVRAATWMQICDT YNQKHSLFNAMNRFIGAVANMNDQTVMVPSLLRUVPLADFGLDND VGVEVGGSGGCLEBRTPP  7067 152 973 KENITWATBIGSSPRFFHMPRFGHQAPRQLFYKRPDFAQQQAMQ QLTEDGKRMKAVNRRTIDMPSVIKYLENRIWQRDQRMRATQ PDAGYYNDLVPPIGMLNNIMNNAVTTKFVRTSTINKVKCPVFVVWW TPBGRBLVTGASSGBFTLWNGLTTNFFTILQAHDSPVRAMTWSH NDMMMLTADHGGVVKVWQSNMNNVKMPQAHKRAIRRARFIHNIP FSVVPIVMVKLPSKCILGABMHGLCQFLGNFLHPINTIFFFVFT HSPFTWAPF 17068 222 816 DTMKEYVILLIFLALCSAKPFFSSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDDDDRDSLPPTRSPRSHPPPFDLFFROCPGCQCYSRV VHCSDLGLTSVPTNIFDTTRMLDQNNKIKEIKRNDFKGLTSLY GLILINNNKLTKIRPKAFLITKKLRRIYLSHNQLSEIPIALPKSL AELRIBENKVKKIOKDTPKKK PRDHRXYFYVNEQSGSGWEFPDGEBEBESKQAQENRBTLAKQ TLKNKGTDTDSNTSTESSETTSGLCKESFSGOVSSSSLMBLTFPW	1	i	1	TAIYCLTQNEWRLDEATDSFFQNPDSLHRESMRNAVDKKKLBRL
PYOPTTPAKNPGQKGLDL*MAGAYWKLVLSGRPKPLYLWNTPL MEHH  TO63  2 562 LRTVPDLPGRRFRAWRTGQRR*PELPPDMNSLEQAEDLKAFERR LTRYHEIQPAGGRWEMLLTUVSVCTATGAMWLDDBTQKVGF FTSLMNHPFFTISCITLIGLPPAGHKRVVAPGILARCRTVLA EYMMSCDDTGKLILKRPRPLV-QSSLLVMGLKIAFLRISDTAKS HKGPLIRIDM  TO64  300 884 RDTGSDPSSTRRLCSTCCTGH*PAEPIASPHPSRGTCPPASSAS SRRTGCMTCPPESGHAQARSKRASASKWGARGAVRSAVAARGC SSRAGRWLETPGRRRGPPACAAAAGRLRGPAP*AAPPTASVPAR CRCPAARTGAPAAATWLRRLSGLRAPALGRRSSPSPSKSAAP PLLTPLLAGGRAGGSRANS  TO65 1 555 ATTHSARRSGRGAAABAASAAGGRQKSPDRKAWBGRRTTPGG RSQSEPKAPPPQKRSBAAFSAMAHSPVAVQVPGMQNNTADPBEL FTKLBRIGKGSFGSVFKGIDNRTQOVVAIKIIDLEBABDBIRDI QOEITVLSQCDSSYVTKYTGSYLKGSKLWIIMBYLGGGSALDLL RAGPFDERQ  TO66 356 676 GFQPGGFWRAREGGHFLDFADHPRAPASLRSNVRAATMMQICDT YNQRHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADFGLDND VGVEVGSGGCLEBERTPP  TO67 152 973 KBNITMATBIGSPFRFHMPRFOHQAPRGLFYKRPDFAQQQAMQ QLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWGRDGRDMRAIQ PDAGYYNDLVPPIGMLNNFMNAVTTKFVSTSTINKVKCEVFVVWR TPBGRRLVTGASGSFETLMNGLTFNFFTILGADGSPCRAMTWSH NIDMMLTADHGGYVKYWQSNMNNVKMPQAHKBAIRBAFHNIP FSVVPIVMVKLPSKCTLGABMHGLCQFLGMFLHPINTIFFFVFT HSPFCMAPP  TO68 222 816 DTMKEVYLLLFLALCSAKPFFSPSHIALKNMLKDMEDTDDDDD DDDDDDDDDDDDDDNSLSFTRRPRSHFPPFDLFPRCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDQNNKIKEIKKBDKKGLSLY GLILINNKLTKHBVAFLITTKKLRRLYLSHNQLSETPLNIPKSL AELHIBNKVKKIQKDTPKKK  FRDHRKYFYVNRQSGBSQWEFPDGBEBEBKGQAQENRBETLAKQ TKRKTGTDSNXTSSESETTGSLCKSFSGQVSSSSLMELTPFW	l .			YGRYKDPQDENKIGVDGIQQPCDDLSLDPASISVLVIAWKFRAA
MEHH	l	1		
To63   2   TRTVPDLPGRRFRAMRTGQRR*PELPPDMNSLEQAEDLKAPERR   LTTYPHICLQPATGRWMILLTUSUCTATGAWMILDPETQKVSF   FTSLMNHIPFTFTISCTTHIGHPAGIHKRVUAPSITAARCRTVLA   EYMMSCDDTGKLILKPRPHVQ*QSSLIVMGLKTAFLRISDTAKS   HKGFLIRIDM   RDTGSDPSSTRRIGSTCCTGH*PABPTASPHPSRGTCFPASSAS   SRRTGCWTCPPESGHAQARRSRRASASRWGARGAVRSAVAARGC   SSRAGRWLETPGRRRGPPACAAAAGRIRGEAP*AAPFTASVPAR   CRCPAARTGAPAATMURISGLRAPALGRRRSPGPSPKSAAP   PLLTPLGAGRAGGSRANS   PLLTPLGAGRAGGSRANS   PLLTPLGAGRAGGSRANS   PLLTPLGAGRAGGSRANS   PLLTPLGAGRAGGSRANS   PRITTHSARRSGRGAAABAAASAAGGRQKGPDRKAWBGRRTTPGG   RSQSEPKAPPPQKRSRAAFASMAHSPVAVQVPGMQNNTADPBEL   FTKLBRIGKSFGEVFKGIDNRTQQVVAIKIIDLEBAKDBIRDI   QOEITVLSQCDSSYVTKYYGSYLKGSKLWIIMBYLGGGSALDLL   RAGPFDERQ   PGPGGFWRREGGHPLDPADHPRAPASLRSNVRAATMMQICDT   YNQKHSLFNAMNRPIGAVNNMDQTVMVPSLLRDVPLADPGLDND   VGVEVGSGGCLBERTPP   KENITMATEIGSPPRFHMPRFOHQAPROLFYKRPDFAQQAMQ   QLTFDGKRMRRAVMRKTIDYMPSVLKTLENKURDQRDMRATIQ   PDAGYYNDLVPIGSGGFTPHPWRFFOHQAPROLFYKRPDFAQQAMQ   QLTFDGKRMRRAVMRKTIDYMPSVLKTLENKURDQRDMRATIQ   PDAGYYNDLVPIGSGGFTPHWDRTFUTAFTTILQHDSPVRAMTHSH   NDMWHLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIP   FSVPIVMVKLPSKCILGABHHGLQFIGNFLHFINTTIFFFFT   HSPPCMAPF   HSPPCMAPF   HSPPCMAPF   HSPPCMAPF   GLILNNKLTKIHPKAFLITTKKIRRLYLSHNQLSEIPLNLPKSL   AELKHHNKVKKIQKOPFFKKK   FRDHRKYFYVNEQSGESQMEFPPDGEKEEESQAQENRDBTLAKQ   TUKKKTTDNNTSTSSTSTSTGSLCKESFSGQVSSSLMPLITFFW   TUKKKTTDNNTSTSSTSTSTGSLCKESFSGQVSSSLMPLITFFW   TUKKKTTDNNTSTSSTSTSTGSLCKESFSGQVSSSLMPLITFFW   TUKKKTTDNNTSTSSTSTSTGSLCKESFSGQVSSSLMPLITFFW   TUKKKTTDNNTSTSSTSTSTGSLCKESFSGQVSSSLMPLITFFW   TUKKKTTDNNTSTSSTSTSTGSLCKESFSGQVSSSLMPLITFFW   TUKKKTTONNTSTSSTSTSTGSLCKESFSGQVSSSLMPLITFFW   TUKKKTTDNNTSTSSTSTSTGSLCKESFSGQVSSSLMPLITFFW   TUKKKTTDNNTSTSSTSTSTGSLCKESFSGQVSSSLMPLITFFW   TUKKKTTDNNTSTSSTSTSTGSLCKESFSGQVSSSLMPLITFFW   TUKKKTTDNNTSTSSTSTSTGSLCKESFSGQVSSSSLMPLITFFW   TUKKKTTDNNTSTSSTSTSTGSLCKESFSGQVSSSSLMPLITFFW   TUKKKTTDNNTSTSSTSTSTGSLCKESFSGQVSSSSLMPLITFFW   TUKKKTTDNNTSTSSTSTSTGSLCKESFSGQVSSSSLMPLITFFW   TUKKKTTDNNTSTSSTSTSTGSLCKESFSGQVSSSSLMPLITFFW   TUKKKTTDNTSTGSLTAMA   TUKKK	l	}	İ	FYOFTFTPAKNPGQKGLDL*MAGAYWKLVLSGRFKFLYLWNTFL
LTEYIHCLQPATGRWRMLLIVUSVCTATGAWMLIDPETQKVSF FTSLMNHPFFTISCITLIGLFPRAGHKRVVAPSILARCRIVLA BYMMSCDDTGKLLLKPRPHVQ*QSSLIVWSLKTAFLRISDTAKS HKGPLLRLDM  7064 300 884 RDTGSDPSSTRRLCSTCCTGH*PAEPIASPHPSGTCPPASSAS SRRTGCWTCPPESCHAQARRSRRASASRWARGAVRSAVARGC SSRAGKWLETPGRRRGPPACAAAAGRLRGPAP*AAPPTASVPAR CRCPAARTGAPAAATWLRRRLSGLRAPALGRRSPGPSPKSAAP PLLTPLCAGRAGGSRANS  7065 1 555 ATTHSARRSGRGAAAAAASAAGGRQKGPDRKAWBGRRTTPGG RSQSEPKAPPPQKRSRAAFASMAHSPVAVQVPGMQNNITADPEEL FTKLBRIGKGSFGEVFKGLDIKTQOVALKI IDLEBARDBIEDI QOEITVLSQCDSSYVTKYYGSYLKGSKLWI IMBYLGGGSALDLL RAGPFDEFQ  7066 356 676 EGPQRGWRAREGGHPLDPADHPRAPASLERNVRAATMMQICDT YNQKHSLFNAMNR PIGAVNNMDQTVMVPSLLRDVPLADPGLDND VGVEVGSGGGCLEERTPP  7067 152 973 KENITWATEIGSPPRFFHMPRFOHQAPROLFY KRPDEAQQAMQ QLTFDGRRMRRAVNRKT ID YNDSVI KYLENRI WQRDQRDMRAIQ PDAGYYMDLVPPIGMINAPMNAVTTEFVRTSTRKVKCPVFVVRW TPBGRRLVTGASSCEPTLWNGLTFNPETILQAHDSPVRAMTWSH NDWMLTADHGGVVKYNGSNMNNVKMFQAHKRAIRRARFHINIP FSVVPIVMVKLPSKCILGABMHGLCOFLGNPLHPINTTFFFVFT HSPPCMAPF  7068 222 816 DTMKEYVILLFLALCSAKPFFSPSHLALKNMMLKOMEDTDDDD DDDDDDDDDDDDDDNSLFPTREPRSHFPPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHFPPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHFPPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHFPPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHFPPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHFPPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHFPPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHFPPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHFPPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHFPPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHFPPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRLSHCHRINGLSEIPINLPKSL AELHIHMKVKKIQKDTFKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFPDGBEBEBESQAQENRBETLAKQ THROKTGTDSNSTESSETSTGGLCKSSFSGQUSSSSSMPLITFW	1 .	i		WEHH
LTEYLHCLQPATGRWRMLLIVUSVCTATGAWNMLIDPETCKVSF FTSLMNHPFFTISCITLIGLPPAGIHKRVVAPSILARCRIVLA BYMMSCDOTGKLILKPRPHVQ*QSSLIVWGLKIAFIRISDTAKS HKGFLIRLDM  7064 300 884 RDTGSDPSSTRRLCSTCCTGH*PABPIASPHPSRGTCFPASSAS SRRIGCHTCPPESGHADARSSRRASASRWARGAVRSAVARRGC SSRAGRWLETPGRRRGPPACAAAAGRLRGPAP*AAPPTASVPAR CRCPAARTGAPAAATWLRRRLSGLRAPALGRRSPGPSPKSAAP PLLTPLGAGRAGGSRANS  7065 1 555 ATTTHSARRSGRGAAAAAAAAAAAGCRQKGPDRKAWBGRRTTPGG RSQSEPKAPPPQKRSEAAFASMAHSPVAVQVPGWONNIADPEL FTKLBERIGKGSFGEVFKGLDNRTQOVALKIIDLEBABDBIEDI OOGLITVLSQCDSSYVTKYTGSYLKGSKLWIIMBYLGGGSALDLL RAGPFDEFQ  7066 356 676 PGPQRGPWRAREGGHPLDPADHPRAPASLESNVRAATMMQICDT YNQKHSLFNAMNRFIGAVNIMDQTVMVPSLLRDVPLADPGLDND VGVEVGSGGCLEBERTPP  7067 152 973 KENITWATEIGSPPRFFHPPRTOHQAPROLFYKRPDFAQQAMQ QLTFDGKRMKRAVRKTIDYNPSVIKYLENRIWQRDDMRAIQ PDAGYYNDLVPPIGMINNPMNAVITAFVRTSTKKVKCPVFVVRW TPBGRRLVTGASSGEPTLWNGLTFNPETILQAHDSPVRAMTWSH NDMMLTADHGGYVKYNGSNMNNVKNFQAHKBAIRRARFHINIP FSVVPIVWKLPSKCILGABMHGLCOFLGNPLHPINTIFFFVFT HSPPCMAPF  7068 222 816 DTMKEYVILLFIALCSAKPFFSPSHLTALKNMMLKOMEDTDDDD DDDDDDDDDDBDDNSLFPTREPRSHPPPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHPPPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHPPPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHPPFPDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHPPFPDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHPPFPDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHPPFPDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRRSHPPFPDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTRRKLRRLYLSHNQLSEIPINLPKSL AELHIHENKVKKIQKDTFKKK  7069 1147 1765 FRDHRKYFKIQKDTFKKK	7063	2	562	LRTVPDLPGRRFRAMRTGQRR*PELPPDMNSLEQAEDLKAFERR
FTSLMNHPFFTISCITLIGLPPAGHKRVAPBILARCRIVLA EYMMSCDDTGKLLIKPRPHVQ*QSSLIVMGIKIAFIRISDTAKS HKGFLIKIDM  7064 300 884 RDTGSDPSSTRRLCSTCCTGH*PAPPIASPHPSRGTCPPASSAS SRRTGCMTCPPESGHAQARRSRRABASRMGARGAVRSAVAARGC SSRAGRWLETPGRRGPPACAAAAGRLRGPAP*AAPPTASVPAR CRCPARTGAPAAATWLRRRLSGLRAPALGRRRSPGPSPKSAAP PLLTPLGAGRAGGSRANS  7065 1 555 ATTTHSARRSGRGAAARAASAAGGRQKGPDRKAWEGRRTTPGG RSQSEPKAPPPQKRSRAAFASMAHSPVAVQVPGMQNNIADPEEL FTKLBRIGKGSFGEVFKGLDNRTQQVVALKI IDLEEARDBIRDI QQEITVLSQCDSSYVTKYYGSYLKGSKLWI IMBYLGGGSALDLL RAGPFDEFQ 7066 356 676 FGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQI CDT YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND VGVEVGGSGGCLERRTPP  7067 152 973 KENITWATEIGSPRFFHMPRFOHQAPROLFYKRPDFAQQQAMQ QLTFDGKRMRAVWRKT LDYNPSVI KYLRNRI MQRDQRDMRAIQ PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW TPBGRRLVTGASSGRFTLNNGLTFNFET ILQAHDSPVARMTWSH NDMMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNI P FSVVPIVMVKLPSKCILGABMGLACFILGNFLHPINTIFFFVFT HSPPCMAPP  7068 222 816 DTMKEYVLLFLALCSAKPFFSFSHALKNMMLKDMEDIDDDDD DDDDDDDDDDDDDDNSLFPTREPRSHFPPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNI PFDTRMLDLQNKLKEI KENDFKGLTSLY GLILNNNKLTK IHPKAFLTTKKLRRI YLSHNQLSEI PINLPKSL AELRI HENKVKKI QKDTFKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFPDGRKEEEKSQAQENRDETLAKQ TIKKNTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTFFW	,,,,,	-		LTRYIHCLOPATGRWRMLLIVVSVCTATGAWNWLIDPETQKVSF
### SYMMSCDDTGKLILKPRPHVQ*QSSLIVMGI.KIAFIRISDTAKS HKGFLIRIDM  7064 300 884 RDTGSDPSSTRRLCSTCCTGH*PARPTASPHPSRGTCPPASSAS SRRTGCMTCPPESGHAQARRSRRASASRWGARGAVRSAVAARGC SSRAGRMLETFGRRGPPACAAAAGRIRGPAP*AAPPTASVPAR CRCPAARTGAPAAATWLRRRLSGLRAPALGRRRSPGPSPKSAAP PLLTPLCAGRAGGSRANS  7065 1 555 ATTTHSARRSGRGAAAAAASAAGGRQKGPDRKAWEGRRTTPGG RSQSEPRAPPPQKRSEAAFASMHSPVAVQVPGMONNIADPELL PTKLERIGKGSFGEVFKGIDNRTQQVVAIKI IDLEBRANBIRDI QORITVLSQCDSSYVTKYTGSYLKGSKLWIIMBYLCGGSALDLL RAGPFDEFQ  7066 356 676 PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT YNQKHSLFNAMMRFICAVNMMDQTVMVPSLLRDVPLADPGLDND VGVEVGGSGGCLBERTPP  7067 152 973 KENITMATBIGSPPRFFHHPRFOHQAPROLFYKRPDFAQQAMQ QLTFDGKRMRRAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIQ PDAGYYNDLVPPIGMLNNPMNAVITKFVRTSTINKVKCPVFVVRW TPBGRRLVTGASSGBFTLWNGLTFNFFTILQAHDSPVRAMTWSH NDMMMLTADHGGYVKXWQSMNNVKMPQAHKBAIRBARFIHNIP FSVVPIVWKLPSKCILGABMHGLQOFLGNFHPINTIFFFVFT HSPPCWAPP  7068 222 816 DTMKEYVILLELALCSAKPFFSSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDDLNSLFPTREPSHFPFDLPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFFTTMLOLQNNKIKEIKENDPKGLTSLY GLILNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHERKVKKIQKOTFKKK  FRDHRRYFYVNEQSBESQWEFPDGEBEBERSQAQENRDBTLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW	1		1	FTSLWNHPFFTISCITLIGLFFAGIHKRVVAPSIIAARCRTVLA
HKGFLLRLDM	ł	1		
TOG4   300   884   RDTGSDPSTRRLCSTCCTGH*PAEPTASPHPSRGTCPPASAS   SRRTGCTTCPPESGHAQARGRARGAVRSAVAARGC   SSRAGRWLETPPESGHAQARGRARGAVRSAVAARGC   SSRAGRWLETPGRRRGPPA*AAPPTASVPAR   CRCPAARTGAPAATMIRRILGGLRAPALGRRSPEPSKSAAP   PLLTPLGAGRAGGSRANS   PLLTPLGAGRAGGSRANS   PLLTPLGAGRAGGSRANS   PLTTHSARRSGGGAAARAASAAGGRQKGFDRKAWBGRTTTPGG   RSGSEPKAPPQKRSHAAPPAWQVPGMQNNIADPBEL   PTKLERIGKGSPGEVFKGIDNRTQOVVAIKIIDLEBEAKDBIEDI   QOEITVLSQCDSSYVTKYYGSYLKGSKLWIIMBYLGGGSALDLL   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFQ   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFG   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF   RAGPFDEFFF	1	1	1	
SRRTGCWTCPPESGHAQARRSRRASASRWGARGAVRSAVAARGC SSRAGRWILBTPGRRRGPPACAAAAGRILRGPAP*AAPPTASVPAR CRCPAAPTGAPAAATWIRRILSGLRAPALGRRRSPGPSPKSAAP PLITPLGAGRAGGSRANS  7065 1 555 ATTTHSARRSGRGAAEAASAAGGRQKGPDRKAWBGRRTTPGG RSQSEPKAPPPOKRSKAAFASMAHSPVAVQVVGMQNNIADPEEL FTKLBRIGGSPGEVPKGIDNRTQQVVAIKIIDLEBAKDBIEDI QOEITVLSQCDSSYVTKYYGSYLKGSKLWIIMBYLGGGSALDLL RAGPFDEFQ  7066 356 676 FGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT YNQKHSLENNAMRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND VGVEVGGSGGLEERTPP  7067 152 973 KENITMATEIGSPFRFFHMPRFOHQAPROLFYKRPDFAQQAMQ QLTFDGKRMRKAVNRKTIDYNPSVIKYLENKIWQRDQRDMRAIQ PDAGYYNDLVPPIGMLNNPMRAVTTKEVRTSTNKVKCPVFVVRW TPBGRRLVTGASSGEFTLWNGLTFNFETILQAHDSPVRAMTWSH NDMMILTADHGGYVKYWQSNMINVKMPQAHKKAIRBARFIHNIP FSVVPIVMVKLPSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT HSPFCWAPP DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDNSLFPTREPRSHFPFFDLFPMCPFGCQCYSRV VHCSDLGITSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILINNKLTKIHPKAFLITTKKIRRLYLSHNQLSEIPINLPKSL ABELRIHEMKVKKUQKDTPKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFPDGBKKEEBESQAQENRDBTLAKQ TLKQKTGTDSNSTESSETSTGSLCKESFSGOVSSSLMPLITFFW	L	200		
SSRAGRWLETPGRRRGPPACAAAAGRLRGPAP*AAPPTASVPAR CRCPAARTGAPAAATWLRRRLSGLRAPALGRRRSPGPSPKSAAP PLLTPLGAGRAGGSRANS  1 555 ATTTHSARRSGRGAAARAASAAGGRQKGPDRKAWEGRRTTPGG RSQSEPKAPPPQKRSEAAFASMAHSPVAVQVPGMQNNIADPELL PTKLERIGKGSPGEVFKGIDNRTQQVVALKIIDLEBAKDBIRDI QOETTVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLGGGSALDLL RAGPFDEFQ PGPQRGPWBAREGGHPLDPADHPRAPASLRSNVRAATMQICDT YNQKHSLENAMNRPIGAVNNMDQTVMVPSLLRDVPLADPGLDND VGVEVGGSGGCLERTPP  7067 152 973 KENITMATEIGSPPRFFHMPRFOHQAPROLFYKRPDFAQQOAMQ QLTPDGKRMKAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIQ PDAGYYNDLUPPIGMLNNPMNAVTTKFVETSTNXVKCPVFVVRW TPBGRRLVTGASSGEFTLWNGLTFNFETILQAHDSPVRAMTWSH NDMWMLTADHGGYVKYWQSNMNNVKMPQAHKEAIRBARFIHNIP FSVVPIVWVKLPSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT HSPPCWAPP  7068 222 816 DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTKIHPKAFITTKKLRRLYLSHNQLSEIPLNLPKSL AELRHENKVKKIQKDTPKKK  7069 1147 1765 FRDHRYFYVNEQSGESQWEFPDGEEBEBESQAQENRDETLAKQ TLKDKTGTDSNSTSSSETSTGSLCKESFSGQVSSSSLMPLIPFW	7064	300	004	CODTCOTTCDDFCCUACAPRSPRASASRWGARGAVRSAVAARGC
CRCPARTGAPAAATWLRRRLSGLRAPALGRRRSPGPSPKSAAP PLLTPLGAGGRAGGSRANS  1 555 ATTTHSARRSGRGAAABAASAAGGRQKGPDRKAWBGRRTTPGG RSQSEPKAPPQKRSBAAFASMAHSPVAVQVBGMQNNTADPBEL PTKLBRIGKGSPGBVFKGIDNRTQQVVAIKIIDLEBAKDBIEDI QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMBYLGGGSALDLL RAGPFDBFQ  7066 356 676 PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMQICDT YNQKHSLENAMMRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND VGVEVGGSGGCLBERTPP  7067 152 973 KENITMATBIGSPPRFFHMPRFOHQAPROLFYKRPDFAQQAMQ QLTPDGKRMRKAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIQ PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW TPBGRRLVTGASSGFFTLWNGLTFNFFTILQAHDSPVRAMTWSH NDMWLTADHGGYVKYWQSNMNNVKMFQAHKBAIRBARFIHNIP FSVVPIVMVKLFSKCILGABMHGLCQFLGNFLHPINTIFFFVFT HSPFCWAPP  7068 222 816 DTMKEYVILLFLALGSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDNDSLFPTREPRSHFFPPDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKBNDFKGLTSLY GLILNNNKLTKIHPKAFLTTKKIRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTFKKK PRDFRKYFYVNEQSGGSQWEFFDGBKBEBKSQAQENRDBTLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW				SKRIGENIEPESCHDIERDACANAACDI.DCDADAAADDPACVDAD
PILTPLGAGRAGGSRANS  1 555 ATTTHSARRSGRGAARAASAAGGRQKGFDRKAWEGRRTTPGG RSQSEPKAPPPQKRSEAAFASMAHSPVAVQVPGMQNNIADPEEL FTKLBRIGKGSPGEVFKGIDNRTQQVVAIKIIDLEBABDBIRDI QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMBYLGGGSALDLL RAGPFDEFQ  7066 356 676 PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND VGVEVGGSGGCLBERTPP  7067 152 973 KENITMATEIGSPPRFFHMPRFOHQAPROLFYKRPDFAQQOAMQ QLTFDGKRMRRAVNRKTIDYNPSVIKYLERRIWQRDQRDMRAIQ PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW TPBGRRLVTGASSGBFTLWNGLTTNFETILQAHDSPVRAMTWSH NDMMHLTADHGGYVKWQSNMNNVKMPQAHKEAIRBARFIHNIP FSVVPPIVMVKLPSXCILGABMHGLQQFLGNFLHPINTIFFFVFT HSPFCMAPP TO68 222 816 DTMKRYVLLLFLALCSAKPFFSPSHLALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDDDDDDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFTTRKLDLQNNKIKBIKENDFKGLTSLY GLILNNNKLTKIHPKAFLITTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQNTFKKK TO69 1147 1765 FRDHRRYPYVNEQSGESQWEFPDGBEBEBESQAQENRDBTLAKQ TILKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW	1			SSKAJANIE POKRAJPPALAMAGKIRGPAP MAP PALAMAG
7065 1 555 ATTTHSARRSGRGAARAASAAGGRQKGFDRKAWEGRRTTPGG RSQSEPKAPPPQKRSBAAFASMAHSPVAVQVPGMQNNTADPBEL FTKLERIGKGS FGBVFKGIDNRTQQVVALKIIDLEBAKDBIRDI QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLCGGSALDLL RAGPFDEFQ  7066 356 676 PGPQRGPWRAREGGHFLDPADHPRAPASLRSNVRAATMMQICDT YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND VGVVBVGGSGGCLBERTTP  7067 152 973 KENITMATBIGSPFFFFHMPRFQHQAPRQLFYKRPDFAQQAMQ QLTFDGKRMKAVNRKTIDYNPSVIKYLBRRIWQRDQRDMRAIQ PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW TPBGRRLVTGASSGBFTLWNGLTFNFETILQAHDSPVRAMTWSH NDMWMLTADHGGYVKWQSNMNNVKMFQAHKEAIRBARFIHNIP FSVVPIVMVKLPSKCILGABMHGLCQFLGNFLHPINTIFFFVFT HSPFCMAPP  7068 222 816 DTMKBYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDRDNSLFPTREPRSHFPFFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTKIHPKAFLITTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKKQNTFKKK  7069 1147 1765 FRDHRKYPKVRQSGRSQWEFFPDGEBEBEBGQAQENRBETLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW			Ì	
RSQSEPKAPPPQKRSBAAFASMAHSPVAVQVPGMQNNIADPBEL FTKLERIGKGS FGBVFKGIDNRTQQVVAIKIIDLEBARDBIRDI QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLGGGSALDIL RAGPFDEFQ  7066 356 676 PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND VGVEVGGSGGCLBERTPP  7067 152 973 KENITMATBIGSPPFFFHMPRFQHQAPRQLFYKRPDFAQQQAMQ QLTFDGKRMRKAVNRKTIDYNPSVIKYLERRIWQRDQRDMRAIQ PDAGYYNDLUPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW TPBGRRLVTGASSGBFTLWNGLTFNFETILQAHDSPVRAMTWSH NDMWMLTADHGGYVKYMQSNMNNVKMFQAHKEAIRBARFIHNIP FSVVPIVMVKLPSKCILGABMHGLCQFLGNFLHPINTIFFFVFT HSPFCMAPP  7068 222 816 DTMKBYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDRDNSLFPTREPRSHFPFFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTTHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL ABERIHENKVKKIQKDTFKKK  7069 1147 1765 FRDHRKYFVNEQSGESQWEFFDGEEBEEKSQAQENRBETLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW	i	1	l	
FTKLERIGKGSPGEVPKGIDNRTQQVVAIKIIDLEBARDBIRDI QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMBYLGGGSALDLL RAGPFDEFQ PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMQICDT YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND VGVEVGGSGGCLBERTPP  7067 152 973 KENITMATBIGSPPRFFHMPRFQHQAPRQLFYKRPDFAQQAMQ QLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIQ PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW TPBGRRLVTGASSGFTLWNGLTFNFBTILQAHDSPVRAMTWSH NDMWHLTADHGGYVKYWQSNMNNVKMFQAHKBAIRBARFIHNIP FSVVPIVMVKLPSKCILGABMHGLQFLGNFLHPINTIFFFVFT HSPPCWAPF  7068 222 816 DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDDNSLFPTRBPRSHFPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKBIKENDFKGLTSLY GLILNNNKLTKIHPKAPLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTFKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFPDGBKBEBESGQAQENRDBTLAKQ TILKDKTGTDSNSTESSETSTGSLCKESFSGVVSSSSLMPLTPFW	7065	1	555	ATTTHSARRSGRGAAARAAASAAGGRQKGPDKKAWBGRRTTPGG
OQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMBYLGGGSALDLL RAGPFDEFQ  7066 356 676 PGPQRGPWRAREGGHFLDPADHPRAPASLRSNVRAATMMQICDT YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADFGLDND VGVEVGSGGCLBERTPP  7067 152 973 KENITMATEIGSPPRFFHMPRFOHQAPRQLFYKRPDFAQQAMQ QLTPDGKRMRKAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIQ PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW TPBGRRLVTGASSGBFTLWNGLTFNFETILQAHDSPVRAMTWSH NDMWMLTADHGGYVKYWQSNMNNVKMPQAHKBAIREARFIHNIP FSVVPIVMVKLPSKCILGABMHGLCQFLGNFLHPINTIFFFVFT HSPPCMAPF  7068 222 816 DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDDNSLFPTREPRSHPFPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTKIHPKAPLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTFKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFPDGKKEEERSQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW	1		1	RSQSEPKAPPPQKRSBAAFASMAHSPVAVQVPGMQNNIADPBEL
RAGPFDEFQ  7066 356 676 PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT YNQKHSLFNAMMFIGAVNMMDQTVMVPSLLRDVPLADPGLDND VGVEVGGSGGLBERTPP  7067 152 973 KENITMATEIGSPPRFFHMPRFOHQAPROLFYKRPDFAQQAMQ QLTFDGKRMRRAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIQ PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW TPBGRRLVTGASSGBFTLWNGLTFNFETILQAHDSPVRAMTWSH NDMMHLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIP FSVVPIVMVKLFSKCILGABMHGLQFLGNFLHPINTIFFFVFT HSPPCWAPF  7068 222 816 DTMKEYVLLLFLALCSAKPFFSPSHLALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDDDNSLFPTREPRSHFFFFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTFKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFFDGEKEBERSQAQENRDETLAKQ	1			PTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDLEEAKDEIKDI
7066 356 676 PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND VGVVVVGGSGGCLERRTPP  7067 152 973 KENITMATEIGSPFRFFHMPRFQHQAPRQLFYKRPDFAQQQAMQ QLTFDGKRMRKAVNRKTIDYNPSVIKYLERRIWQRDQRDMRAIQ PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW TPBGRRLVTGASSGBFTLWNGLTFNFETILQAHDSPVRAMTWSH NDMMMLTADHGGYVKYWQSNMNNVKMPQAHKEAIREARFIHNIP FSVVPIVMVKLPSKCILGABMHGLCQFLGNFLHPINTIFFFVFT HSPPCMAPP  7068 222 816 DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDRDNSLFPTREPRSHFPFFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNKLTTHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKLQKDTFKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFFDGEKEBERSQAQENRDETLAKQ TILKDKTGTDSNSTESSETSTGSLCKESFSGOVSSSSLMPLTPFW	1		1	QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMKYLGGGSALDLL
YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND VGVEVGGSGGLBERTPP  7067 152 973 KENITMATEIGSPPRFFHMPRFQHQAPRQLFYKRPDFAQQQAMQ QLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIQ PDAGYYNDLUPPIGMLINPMNAVTTKFVRTSTNKVKCPVFVVRW TPBGRRLVTGASSGBFTLWNGLTFNFETILQAHDSPVRAMTWSH NDMWHLTADHGGYVKYWQSNMNNVKMFQAHKRAIRBARFIHNIP FSVVPIVMVKLPSKCILGABMHGLCQFLGNFLHPINTIPFFVFT HSPPCWAPP  7068 222 816 DTMKBYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDNSLFPTREPRSHFPFFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTTHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL ABLRIHENKVKKUQNTPKKK 7069 1147 1765 FRDHRRYFYVNEQSGESQWEFFDGEBEBEBGQAQBNRDETLAKQ TILKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW	1		}	
YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND VGVEVGGSGGLBERTPP  7067 152 973 KENITMATEIGSPPRFFHMPRFQHQAPRQLFYKRPDFAQQQAMQ QLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIQ PDAGYYNDLUPPIGMLINPMNAVTTKFVRTSTNKVKCPVFVVRW TPBGRRLVTGASSGBFTLWNGLTFNFETILQAHDSPVRAMTWSH NDMWHLTADHGGYVKYWQSNMNNVKMFQAHKRAIRBARFIHNIP FSVVPIVMVKLPSKCILGABMHGLCQFLGNFLHPINTIPFFVFT HSPPCWAPP  7068 222 816 DTMKBYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDNSLFPTREPRSHFPFFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTTHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL ABLRIHENKVKKUQNTPKKK 7069 1147 1765 FRDHRRYFYVNEQSGESQWEFFDGEBEBEBGQAQBNRDETLAKQ TILKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW	7066	356	676	
VGVEVGGSGGLEERTPP  7067 152 973 KENITMATEIGSPPRFFHMPRFOHQAPROLFYKRPDFAQQOAMQ QLTFDGKRMRRAVNRKTIDYNPSVIKYLERRIWQRODRDMRAIQ PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW TPBGRRLVTGASSGBFTLWNGLTFNFETILQAHDSPVRAMTWSH NDMWHLTADHGGYVKYWQSNMNNVKMFQAHKBAIRBARFIHNIP FSVVPIVMVKLPSKCILGABMHGLCOFLGNFLHPINTIPFFVFT HSPFCWAPF  7068 222 816 DTMKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDDRNSLFPTREPRSHFPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTKINPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTFKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFPDGRKEEBESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGVSSSSLMPLTPFW	'"		1	
7067 152 973 KENITMATEIGSPPRFFHMPRFOHQAPROLFYKRPDFAQQAMQ QLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIQ PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW TPEGRRLVTGASSGEFTLWNGLTFNFETILQAHDSPVRAMTWSH NDMWMLTADHGGYVKYWQSNMNNVKMFQAHKBAIREARFIHNIP FSVVPIVMVKLPSKCILGABMHGI.CQFLGNFLHPINTIPFFVFT HSPPCWAPP  7068 222 816 DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDDNSLFPTREPRSHFPFFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTKIHPKAPLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTFKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFFDGEKEEBESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGVVSSSSLMPLTPFW	ļ	1	1	VGVEVGGSGGCLEERTPP
QLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIQ PDAGYYNDLVPPIGMLNNPMNAVTTKFVERTSTNKVKCPUFVVRW TPEGRELVTGASSGEFTLWNGLTFNFETILQAHDSPVRAMTWSH NDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIP FSVVPIVMVKLPSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT HSPFCWAPF  7068 222 816 DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDDDNSLFPTREPRSHFPFFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTKIHPKAPLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTFKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFFDGEKEEEESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGVVSSSSLMPLTPFW	7000	+	077	
PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW TPEGRRLVTGASSGEFTLWNGLTFNFETILQAHDSPVRAMTWSH NDMWHLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIP FSVVPIVMVKLPSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT HSPPCWAPP  7068 222 816 DTMKEYVLLLFLALCSAKPFFSPSHLALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDDDDDDDDDDDDD	1 '06'	152	1 7/3	OLTEDCKEMERAVNEKTIDYNPSVIKYLENRIWORDORDMRAIO
TPEGRRLVTGASSGBFTLWNGLTFNFETILQAHDSPVRAMTWSH NDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIP FSVVPIVMVKLFSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT HSPFCMAPF  7068 222 816 DTMKEYVILLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDBDNSLFPTREPRSHFPFFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTTMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTFKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFPDGEKEEBESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW	1 .	1	1	DUNCAANDL'ADDICINL'NIDWINAALERIDAGAMKAKADAGAMKAKADAGAMAADA
NDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIP FSVVPIVMVKLPSKCILGABMHGLCQFLGNFLHPINTIFFFVFT HSPPCWAPP  7068 222 816 DTMKBYVLLLFLALCSAKPFFSPSHLALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDRDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRHEHKVKKIQKDTFKKK  7069 1147 1765 FRDHRYFYVNEQSGRSQWEFPDGRKEEBESQAQENRDBTLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW	'	1.		
FSVVPIVMVKLPSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT HSPFCWAPP  7068 222 816 DTMKEYVILLFLALCSAKPFFSPSHLALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDNSLSFPTREPRSHFPFFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTFKKK  7069 1147 1765 FRDHRYFYVNEQSGESQWEFPDGEKEEEESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGVVSSSSLMPLTPFW	Į	}	1	
HSPFCWAPF  7068 222 816 DTMKEYVILLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDDDSDNSLFPTREPRSHFPFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTN1PFDTRMLDLQNNK1KEIKENDFKGLTSLY GLILNNKLTKHPKAPLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTFKKK  7069 1147 1765 FRDHRYFYVNEQSGESQWEFPDGEKEEEESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGVVSSSSLMPLTPFW	l	ì	1	
7068 222 816 DTMKEYVILLEFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDDDDDDDDDDDDDDDDDDDD	i	5		
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD		1	j	HSPFCWAPP
DDDDDDDDDDDDDDDDDDDDDDDDDLFPPREPRSHFFFFDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTKIHPKAPLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTFKKK  7069 1147 1765 FRDHRRYFYVNEQSGESQWEFFDGEKEEEKSQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGVSSSSLMPLTPFW	7068	222	816	
GLILNNNKLTKIHPKAPLTTKKLRRLYLSHNQLSEIPLNLPKSL ABLRIHENKVKKIQKDTPKKK  7069 1147 1765 FRDHRRYFYVNBQSGBSQWEFPDGEKEEBESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW	1	1		
GLILNNNKLTKIHPKAPLTTKKLRRLYLSHNQLSEIPLNLPKSL ABLRIHENKVKKIQKDTPKKK  7069 1147 1765 FRDHRRYFYVNBQSGBSQWEFPDGKKEEBESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW	1		1	
AELRIHENKVKKIQKDTPKKK  7069 1147 1765 FRDHRRYFYVNBQSGRSQWEFPDGEKEEBESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW	Į	1	1	
7069 1147 1765 FRDHRRYFYVNBQSGRSQWEFPDGEKEEBESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW	1	i	ł	
TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW	70.00	9417	1765	
TLLQSNVPVLQPPLEMPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	7069	114/	1/65	
TILIQSNVPVLQPPDPILMIKFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	1			THE TOTAL TO DE LE EMBEDDE SUCCESSOR SE LE LES LES LES LES LES LES LES LES L
	L	<u> </u>		TOPGOMA KATMAKARAKAKAKARAKARAKAKAKAKAKAKAKAKAKAKAKA

	··		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Í	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
į.	sequence	bequence	\=possible nucleotide insertion)
		<del> </del>	EKTKKGRKDKAKKSKTKMPSLVKKWQSIQRELDEEDNSSSSKED
1			RVSTAQKRIEEWKQQQLVSGMABRNANFEA
7070	1	547	DGTMEDSEAVQRATALIEORLAQEBENEKLRGDAROKLPMDLLV
			LEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLI
1			ELRKKRKOKKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGK
i			MKVIBKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNG
ł	l	1	ATVDFQ
7071	2	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
1	1		VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY
l	i	ļ	FQDPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV
1	<u> </u>	Ì	PESSLPPASMPYADHYSTFSPRDRMMSSPYQPPPPQPYGPVPPV
	1	<b> </b>	PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQT
1	l		SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCREQ
2010			IRRKPDQWAQYHTQKAPLVSSTLPVATQSPTPPSTLNRGEGS
7072	2	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
		ł	VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY
		ĺ	PQDPRTQIPPRVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV PRSSIPPASMPYADHYSTFSPRDRMNSSPYQPPPPOPYGPVPPV
ŀ			PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQT
i	{	{	SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCERQ
	1	[	IRRKPDQWAQYHTQKAPLVSSTLPVATQSPTPPSTLNRGEGS
7073	50	504	LAHGSFGVSDFPAPAAAPAHTLTSFSGSLSPQFRKPLGRAPAMP
			LVRYRKVVILGYRCVGKTSLAHQFVEGEFSEGYDPTVENTYSKI
	ĺ		VTLGKDEFHLHLVDTAGQDEYSILPYSFIIGVHGYVLVYSVTSL
-	ļ	ŀ	HSFQVIESLYQKLHEGHGK
7074	263	1003	VCPVLCSTRQEPGHSSLVTYFGKPTRRKEFLLGHCIAAGKMNIS
			VDLETNYAELVLDVCRVTLGENSRKKMKDCKLRKKQNERVSRAM
	ļ		CALLNSGGGVIKAEIENEDYSYTKDGIGLDLENSFSNILLFVPE
Ì.			YLDFMONGNYFLIFVKSWSLNTSGLRITTLSSNLYKRDITSAKV
	ļ		MNATAALEFLKDMKKTRGRLYLRPELLAKRPRVDIQEENNMKAL
7075			AGVFFDRTELDRKEKLTFTESTHVEI
7075	598	1005	NYINFFFRKEYPPHVQKVEINFVRLSRLQGVERIMKKTBBSBSQ
ĺ			VKPKIKKVQQKRHCSTYQPTPPLSPASKKCLTHLEDLQRNCRQ
	· ·		AITLNESTGPLLRTSIHONSGGOKSONTGLTTKKFYGNNVEKVP IDII
7076	279	1049	LQSESSNAAEGNEQRHEDEQRSKRGGWSKGRKRKKPLRDSNAPK
'''	613	1027	SPLTGYVRFMNERREOLRAKRPEVPFPEITRMLGNEWSKLPPER
1			KORYLDBADRDKERYMKELEQYQKTEAYKVFSRKTODROKGKSH
			RODAARQATHDHEKETEVKERSVFDIPIFTEEFLNHSKAREABL
			RQLRKSNMEFEERNAALQKHVESMRTAVEKLEVDVIQERSRNTV
			LOOHLETLROVLTSSPASMPLPEXGETPTVDTIDSYM
7077	3	1119	SSMGSNSEINGLALRKTDKYGFLGGSQYSGSLKSSIPVDVARQR
			BLKWLDMFSNWDKWLSRRFQKVKLRCRKGIPSSLRAKAWQYLSN
			SKELLEONPRKFEELERAPGDPKWLDVIEKDLHROFPFHEMFAA
			RGGHGQQDLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPARQ
			AFWCLVQICDKYLPGYYSAGLKAIQLDGBIFFALLRRASPLAHR
			HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI
			IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQBDF
			LVHEVTNLPVTRALIERENAAQLKKWRETRGELQYRPSRRLHGS
			RAIHEERRRQQPPLGPSSS
7078	483	767	FQGQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG
			VYVFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE
			SLPELY
7079	2	376	SVVBPKRPKBPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ
L	L		MQARKKRRGIIEKRRRDRINSSLSELRRLVPTAFEKQGSSKLEK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence	\=possible nucleotide insertion)
	Redrieuce	L	
			AEVLOMTVDHLKMLHATGGTGTHALLFQASFIQQIP
7080	200	595	VQLPLEAPCLSLLSCRDHSGGNRDLSRRHRDCRVYGSPQDGIPY
ŀ		ł	LTHPLCHQDVVSVGRLQIRALATPGHTQGHLVYLLDGEPYKGPS
1		ŀ	CLFSGDLLFLSGCGEFPRKREELGEEGETEVRAATVPWRALKP .
7081	213	506	AVTEREMILNSLSLCYHNKLILAPMVRVGTLPMRLLALDYGADI
		ł	VYCEELIDLKMIQCKRVVNKVLSTVDFVAPDDRVVFRTCEREQN
l			RVVFOMGTS
7082	3	1137	APSRNTMLMAWCRGPVLLCLRQGLGTNSFLHGLGQRPFEGARSL
7002	,	1137	CCRSSPRDLRDGEREHEAAQRKAPGAESCPSLPLSISDIGTGCL
l	1	Į.	SSLENLRLPTLRESSPRELEDSSGDQGRCGPTHQGSEDPSMLS
1	i	1	
]	1	}	QAQSATEVEERHVSPSCSTSRERPFQAGBLILAETGEGETKFKK
i	1		LFRLNNFGLINSNWGAVPFGKIVGKPPGQILRSSFGKQYMLRRP
1	} '		ALEDYVVLMKRGTAITFPKDINMILSMMDINPGDTVLBAGSGSG
İ			GMSLFLSKAVGSQGRVISFEVRKDHHDLAKKNYKHWRDSWKLSH
ł		ł	VEEWPDNVDF1HKDISGATEDIKSLTFDAVALDMLNPHVTLPVF
1	ł	<b>i</b> .	YPHLKHGGVCPVYVVNITQVIELLD
7083	115	541	RSNAVQLTRMEYAMKSLSLLYPKSLSRHVSVRTSVVTQQLL6BP
			SPKAPRARPCRVSTADRSVRKGIMAYSLEDLLLKVRDTLMLADK
	i	ſ	PPPLVLBEDGTTVETEBYFQALAGDTVFMVLQKGQKWQPPSEQG
ł		Į.	TRHPLSLSHK
7084	<del>  3</del>	522	NSVSVSSQSRFLASVPGTGVQRSAAADMAASTAAGKQRIPKVAK
/004	,	322	VKNKAPAEVQITAEQLLREAKERELELLPPPPQQKITDEEELND
			YKLRKRKTFEDNIRKNRTVISNWIKYAQWEESLKEIQRARSIYE
1	}		
	<u></u>	<u> </u>	RALDVDYRNITLWLKYAEMEMKNRQVNHARNIWDRAITTL
7085	243	1499	RQLARLRRRGWRSPFGGAPMAHITINQYLQQVYEAIDSRDGASC
1			ABLVSFKHPHVANPRLQMASPEBKCQQVLBPPYDBMFAAHLRCT
			YAVGNHDFIEAYKCQTVIVQSFLRAFQAHKEENWALPVMYAVAL
l		1	DLRVFANNADQQLVKKGKSKVGDMLEKAAELLMSCFRVCASDTR
1		1	AGIEDSKKWGMLFLVNQLFKIYFKINKLHLCKPLIRAIDSSNLK
l	1		DDYSTAQRVTYKYYVGRKAMFDSDFKQAREYLSFAFEHCHRSSQ
		1	KNKRMILIYLLPVKMLLGHMPTVELLKKYHLMQFAEVTRAVSEG
l		ì	NLLLLHRALAKHEAFFIRCGIFLILEKLKIITYRNI.FKKVYLLL
i			KTHQLSLDAFLVALKFMQVEDVDIDEVQCILANLIYMGHVKGYI
Į.		i e	SHOHOKLVVSKONPFPPLSTGC
7005	356	525	ILAARMGKONSKLRPEVMODLLESTDFTEHBIQEWYKGFLRDCP
7086	256	525	SGHLSMEEPKKI YGNPFPYGDASKFAEHVFRTFDANGDGTIDFR
}	]	1	
	1	<u> </u>	EF
7087	166	723	LSGSSAGKVAAPCVPPSNHELVPITTENAPKNVVDKGEGASRGG
1	1	1	NTRKSLEDNGSTRVTPSVQPHLQPIRNMSVSRTMEDSCELDLVY
1		1	VTERIIAVSFPSTANBENPRSNLREVAQMLKSKHGGNYLLFNLS
1		1	ERRPDITKLHAKVLEFGWPDLHTPALEKICSICKAMDTWLNAHP
1		I	HRCRVLHNKG
7088	104	759	GTSAASPSSLLEMAGEITETGELYSSYVGLVYMFNLIVGTGALT
		1	MPKAFATAGWLVSLVLLVFLGFMSFMTTTFVIEAMAAANAQLHW
1		1	KRMRNLKEBEDDDSSTASDSDVLIRDNYERABKRPILSVQRRGS
]	}	1	PNPPEITDRVEMGOMASMFFNKVGVNLFYFCIIVYLYGDLAIYA
1			AAVPFSLMQVTCSATGNDSCGVEADTKYNDTDRCWGPLRRVD
L		<del> </del>	
7089	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
Ī		i	HYTLPPGTMPSASDWIGIPKVEAACVRDYHTFVWSSVPESTTDG
Į.			SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE
		1	PRPMDELVTLEKADGGSDILLVVPKATVLQNQLDESQQERNDLM
1		1	QLKLQLEGQVTBLRSRVQBLERALATARQEHTELMEQYKGISRS
1		1	HGEITEBRDILSROOGDHVARILBLEDDIOTISEKVLTKEVELD
1	1	1	RLRDTVKALTREQEKLLGQLKEVQADKEQSEAELQVAQQENHHL
1		1	NLDLKEAKSWOREQSAQAQRLKDKVAQMKDTLGQAQQRVABLEP
<u></u>	<del></del>	L	THE WITH THE PROPERTY OF THE PROPERTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE

WO 01/53312

CCBO	[ N 37   1 . N		្នាំ ។ មករាមក្នុងក្រុមប្រជាជាក្នុងស្រី នៅក្នុងស្រី
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l .	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIAELHRSR
1	Į.	ĺ	LEVAEVNGKLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILK
ļ	ļ	l .	LSABILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKREB
1	1	ĺ	TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
i	ļ		EDATTEDEBAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETO
			ASILLIGLE
7090	33	1775	t control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont
,030	33	1//5	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
i	J		HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTIDG
	1	}	SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRR
1	i		PRPMDRLVTLBEADGGSDILLVVPKATVLQNQLDESQQERNDLM
			QLKLQLEGQVTBLRSRVQBLRRALATARQEHTELMEQYKGISRS
1	1		HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD
Ī			RLRDTVKALTREQEKLLGQLKEVQADKEQSEAKLQVAQQENHHL
<b>!</b> .	!		NLDLKBAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVABLEP
	,		LKEQLEGAQELAASSQQKATLLGEBLASAAAARDRTIAELHRSR
l	1		LEVAEVNGKLAELGLHLKEEKCOMSKERAGLLQSVEAEKDKILK
1	ł		LSAEILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKREL
•			TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
ļ			EDATTEDERAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETQ
	1		ASLLLGLE
7091	186	1076	EGMLTREHRCGRSEEQELEPWPSPKKARSGRWLRNGFKRKMEEP
	[		EEPADSGQSLVPVYIYSPEYVSMCDSLAKIPKRASMVHSLIKAY
			ALHKQMRIVKPKVASMEEMATFHTDAYLQHLQKVSQEGDDDHPD
		,	SIEYGLGYDCPATEGIFDYAAAIGGATITAAQCLIDGMCKVAIN
	·		WSGGWHHAKKDEASGFCYLNDAVLGILRLRRKFERILYVDLDLH
	ł		HGDGVEDAFSFTSKVMTVSLHKFSPGFFPGTGDVSDVGLGKGRY
	j.		YSVNVPIQDGIQDEKYYQICERYEPPAPNPGL
7092	522	809	KQGINEDQEBSQKPRLGEGCEPISKRQMKKLIKQKQWBEQRELR
	]	, 555	KQKRKEKRKKKLERQCQMEPNSDGHDRKRVRRDVVHSTLRLII
			DCSFDXLM
7093	454	655	I
1033	454	. 655	NFGVSGVBLAQQASMVRMSFVIAACQLVLGLIMTSLTESSIQNS
7094			ECPQLCVCBIRPWFTPQSTYREA
7094	2	508	FVRSMHWGVGFASSRPCVVDLSWNQSISFFGWWAGSEBPFSFYG
	l i		DIIAFPLQDYGGIMAGLGSDPWWKKTLYLTGGALLAAAAYLLHR
			LLVIRKQQBIDSKDAIILHQFARPNNGVPSLSPFCLKMETYLRM
			ADLPYQNYFGGKLSAQGKMPWIEYNHEKVSGTEFII
7095	1	411	IASSLPKMASLLQSDRVLYLVQGEKKVRAPLSQLYFCRYCSELR
			SLECVSHEVDSHYCPSCLENMPSARAKLKKNRCANCFDCPGCMH
	· ·		TLSTRATSISTQLPDDPAKTTMKKAYYLACGFCRWTSRDVGMAD
			KSVGR
7096	224	2067	BTRSLAVQBKPSQAGRRRSSRISPAGALFLTRFLLOBLLLNNFC
	l		SAMSPAPDAAPASISLFDLSADAPVFOGLSLVSHAPGEALAR
			APRISCSGSGERESPERKLLOGPMDISEKLFCSTCDOTFONHOE
			QREHYKLDWHRFNLKQRLKDKPLLSALDFEKOSTGDLSSISGS
			EDSDSASEEDLQTLDRERATPEKLSRPPGFYPHRVLFQNAOGOF
			LYAYRCVLGPHQDPPRRABLILLQNLQSKGPRDCVVLMAAAGHFA
			GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN
			LRRYNEATLYKDVRDLLAGPSWAKALBEAGTILLRAPRSGRSLF
i			FGGKGAPLQRGDPRLWDIPLATRRPTFQBLQRVLHKLTTLHVYE
			EDPREAVRLHSPQTHWKTVREERKKPTEEEIRKICRDEKEALGQ
			NEESPKQGSGSEGEDGFQVELELVELTVGTLDLCESEVLPKRRR
			RKRNKKEKSRDQEAGAHRTLLQQTQEBEPSTQSSQAVAAPLGPL
			LDBAKAPGQPBLWNALLAACRAGDVGVLKLQLAPSPADPRVLSL
			LSAPLGSGGFTLLHAAAAAGRGSVVRLLLEAGADPTVQCQDH
7097	256	1228	IRTKSAATWEAWPQCGREGSRIITEPCEANAGSRQELQTERISS
			FLAAQGDQAFHSGLETNNSNSELPLRVGLKVAQGSPLMGGQVSA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	-	\=possible nucleotide insertion)
<b></b>			SNSFSRLHCRNANEDWMSALCPRLWDVPLHHLSIPGSHDTMTYC
			LNKKSPISHEESRLLQLLNKALPCITRPVVLKWSVTQALDVTEQ
}	<u> </u>	,	LDAGVRYLDLRIAHMLEGSEKNLHFVHMVYTTALVEDTLTEISB
Ì	ŀ		WLERHPREVVILACENFEGLSEDLHEYLVACIKNIFGDMLCPRG
	]	)	BVPTLRQLWSRGQQVIVSYEDESSLERHHELWPGVPYWWGNRVK
ļ	l	l	TRALIRYLETMKSCGR
7098	82	956	SSFLKRCRKVLGCWGIPSBQSLFSTLBEPRDKEIDNYCVMRLQT
1		[	EARSGFWAPNRFPVNICRMTAVDGDRGGSSRETCRCHFHPSLEA
]		]	LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLPSKPLLG
[		İ	LGSSVIYPLWNLLLLWPRVLAVALFSALFPSYVALHFLGLWLVL
Ì		}	LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVABGRTRGR
[	f	ł	AIIHPAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPVGCGCPP
			LGLALRLVYYHWLHPSCCWKPDPDQVD
7099	992	210	LFRLAPGFLRSLARQGYHQIWAFPFLPSGATATWPAASRSRSLA ARSLPRSPARPGPNDALLGEHDFRGOGVRAORFRFSEBPGPGAD
•		1	
ł	l		GAVLEVHVPQIGAGVSLPGILAAKCGAEVILSDSSELPHCLEVC ROSCOMNNLPHLQVVGLTWGHISWDLLALPPQDIILASDVPFEP
	1	1	KDYEDILATIYYLMHKNPKVOLWSTYOVRSADWSLEALLYKWDM
{		l	KCVHI PLESFDADKEDIAESTLPGRHTVEMLVI SFAKDSL
7100	205	671	ANGGFWEAAPGSEVSLPLWVPTASHSKTTALGIGSAPPPHLSVL
1,100	205	8/1	FLFSPPPQLGDPLEAFPVFKKYDRNGLNVSIECKRVSGLBPATV
ł	ł		DWAYDLTKINMQIMYEQSEWGWKDREKREEMIDDRAWYLIAWEN
ļ	ļ	ĺ	SSVPVAFSHFRFDVERGDEVLYW
7101	2	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD
	_		VRILLVGEPRVGKTSLIMSLVSERFPEEVPPRAEEITIPADVTP
		1	ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDK
ļ. ·			VTSRWIPLINERTDKDSRLPLILGGNKSDLVRYSR
7102	2	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD
1	,	]	VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAKEITIPADVTP
	!	i	ERVPTHIVDYSBAEQSDEQLHQBISQANVICIVYAVNNKHSIDK
			VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR
7103	119	438	GSQSSVAVNIRSCTDEESMDLMNGQASSVNIAATASEKSSSES
	ļ	ļ·	LSDKGSELKKSPDAVVVDVLKVTPBEYAGQITLMDVPVPKAIQP
			DELSSCGWNKKERYSSAP
7104	1670	795	RLWEHRSVSAGASGWGLSSPGCLLLHPSLPEBERVDILINNAGV
i			MRCPHWITEDGFEMQFGVNHLGEAWAGAAPWVQAILPRRPPKVL
1	}	<b>{</b>	GF*V*VKSDLFIILNPGHFLLTNLLLDKLKASAPSRIINLSSLA
1			HVAGHIDFDDLNWQTRKYNTKAAYCQS\KLAIVLFTKBLSRRLQ
1	{	f	GSGVTVNALHPGVARTELGRHTGIHGSTFLQHHN\WAHLLAAWS KSPRSWPAPAOHNTLAVARELA\VISGKYFDGLKOKAPAPEAED
l		1	RSPRSWPAPAQHNTLAVARBLA\VISGRIFDGURQRAPAPEARD  BBVARRLWAESARLVGLRAPSVRBQPLPR
7105	765	143	GOMCRRPSPKSTSCLSMTCDLP/RGLQDPQCLALFRVAVDKHQA
,,,,,,,	/05	143	LLKAAMSGQGVDRHLFALYIVSRFLHLQSPFLTQVHSEQWQLST
}	}	1	\
1			SQTPVQQMHLFDVHNYPDYVSSCGGFGPADDHGYGVSYIFMGDG MITFHISSKKSSTKTDSHRLGQHIEDALLDVASLFQAGQHFKRR
1		<b>j</b>	FRGSGKENSRHRCGFLSRQTGASKASMTSTDF
7106	14	1064	GLOAGHPHPRSASRIPEADTH\YSKLQRAFDSIVNKDHKRMFGT
1 130	}	1007	YFRVGFFGSKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGQCF
]	1	1	GAEFVEVIKOSTPVDKTKLDPNKAYIQITFVEPYFDEYEMKDRV
1	j	1	TYFEKNENLEREMYTTPETLEGRPRGELHEOYRRNTVLTTMHAF
j	1	İ	PYIKTRISVIOKEEFVLTPIEVAIEDMKKKTLQLAVAINQEPPD
Ì	}	i	AKMLQMVLQGSVGATVNQGPLEVAQVPLAEIPADPKLYRHHNKL
[		l	RLCPKEFIMRCGEAVEKNKRLITADQREYQQBLKKNYNKLKBNL
Í		[	RPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCRTQLSQGS
7107	1145	591	*I *WLQTGKKK
		<u> </u>	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, P=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /-possible nucleotide deletion,.
	sequence		\=possible nucleotide insertion)
7108	1	942	VKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLNSSTFYLAF
1			FLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLCMQMGIIMVLK
1		j	QTWNNFMELGYPLIQNWWTRRKVRQEHGPBRKISFPQWEKDYNI,
ł			QPMNAYGLFDEYLEMILQFGFTTIFVAAFPLAPLLALLNNIIEI
1			RLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITNAFVI
1	1	ł	AITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYVNASLSVFRIS
1	1	}	DFENRSEPESDGSEFSGTPLKYCRYRDYRDPPHSLVPYGYTLQF
L			WHVLAW
7109	964	102	WDQRKRNSLVPGPAHGPAQEEPWEKKESLGAAQEALSIQLQPKE
1	ł		TQPFPKSEQVYLHFLSVVTEDGPEPKDKGSLPQPPITEVESQVF
Į.			SBKLATDTSTFRATSEGTLELQQRNPKAERLRWSPAQEESFRQM
1	i		VVIHKBIPTGKKDHECSECGKTFIYNSHLVVHQRVHSGBKPYKC
1			SDCGKTFKQSSNLGQHQRIHTGEKPFECNBCGKAFRWGAHLVQH
i	j		QRIHSGEKPYECNECGKAFSQSSYLSQHRRIHSGEKPFICKECG
L			KAYGWCSELIRHRRVHARKEPSH
7110	96	697	RLDNFSGFLVEVTKEERHIVKPLYDRYRLVKQMLTRASITPVLG
1			SPSTKRRGQMLQPI1EGETAHFFEEIKEEBEDGVNLSSRLGDML
i			KTAVQVQSSLKNSESDVERNQEKLALDLRLSSSRAASMPRLLEQ
l	i		LWKARAEKKKLRKTLREFERAFYQQNGRNAQKEDRVPVLEEYRR
<u> </u>			YKKIKAKLRLLEVLISKQDSSKSI
7111	2	414	GSGLYRGPTPGGQCIWKPNSMPPDHERNFGFTQFALELNELTAE
l		•	LKRSLPSTDTRLRPDQRYLEEGNIQAAKAQKRRIEQLQRDRRKV
			MEENNIVHQARFFRRQTDSSGKEWWVTNNTYWRLRAEPGYGNMD
<u> </u>			GAVLW
7112	103	495	PRCFPVADRGRLIGGLPDVVTIMEGKTLNLTCTVFGNPDPEVIW
}			FKNDQDIQLSEHFSVKVBQAKYVSMTIKGVTSEDSGKYSINIKN
L			KYGGEKIDVTVSVYKHGEKIPDMAPPQQAKPKLIPASASAAGQ
7113	1	824	KCLRQAWHKAPSSLAFTRWCSREERAEGGGNLHRSITRDPKPPG
1	}		LRPSQRPMDDKKKKRSPKPCLAQPAQAPGTLRRVPVPTSHSGSL
	l i		ALGLPHLPSPKQRAKFKRVGKEKCRPVLAGGGSGSAGTPLQHSF
			LTEVTDVYEMEGGLLNLLNDFHSGRLQAFGKECSFEQLEHVREM
(	·		QEKLARLHFSLDVCGEEEDDEEERDGVTEGLPEEQKKTMADRNL
ļ			DQLLSNLGSCLGALVPGGMRGGEGTYSQSHSWALGEKVGVHGSK
<del></del>			SSGPLNLPRR
7114	3	1492	VWEVDBQIDHYKESQDKFLWQAAFIGKETLKDBSGQECKICRKI
			IYLNTDFVSVKQRLPKYYSWERCSKHHLNFLGQNRSYVRKKDDG
	l		CKAYWKVCLHYNLHKAQPAERFFDFNQRGKALHQKQALRKSQRS
<b>j</b> .	İ		QTGEKLYKCTECGKVFIQKANLVVHQRTHTGEKPYECCECAKAF
	ļ		SQKSTLIAHQRTHTGEKPYECSECCKTFIQKSTLIKHQRTHTGE
			KPFVCDKCPKAPKSSYHLIRHEKTHIRQAFYKGIKCTTSSLIYQ
<u> </u>			RIHTSEKPQCSEHGKASDEKPSPTKHWRTHTKENIYECSKCGKS
]			PRGKSHLSVHQRIHTGEKPYECSICGKTFSGKSHLSVHHRTHTG
			EKPYBCRRCGKAFGEKSTLIVHQRMHTGEKPYKCNBCGKAFSEK
			SPLIKHORIHTGERPYECTDCKKAFSRKSTLIKHORIHTGEKPY
	1		KCSECGKAFSVKSTLIVHHRTHTGEKPYECRDCGKAFSGKSTLI
7000			KHQRSHTGDKNL
7115	1	947	NAAHGYNWGLWCMYIIPPQDWLDRGDESAPIRTPAMIGCSFVVD
			REYFGDIGLLDPGMEVYGGENVKLGMRVWQCGGSMEVLPCSRVA
	Ì		HIERTRKPYNNDIDYYAKRNALRAABVWMDDFKSHVYMAWNIPM
	[		SNPGVDFGDVSERLALRQRLKCRSFKWYLENVYPEMRVYNNTLT
	1		YGEVRNSKASAYCLDQGAEDGDRAILYPCHGMSSQLVRYSADGL
	į		LQLGPLGSTAPLPDSKCLVDDGTGRMPTLKKCEDVARPTQRLWD
		•	PTQSGPIVSRATGRCLEVEMSKDANFGLRLVVQRCSGQKWMIRN
			WIKHARH
7116	866	95	RVRMRRNAEVIEEKLSMKSWAKFRPGEPWKGYPNIDPETDPYVT
			PGSVINNLSINTVREVDHLRDRNSGSSSSLNTTLPSTSAWSSIR

SEQ	Predicted	Predicted end	Amine agid goment contains
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
{	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ASNYNVPLSSTAQSTSARNSDSKLTWSPGSVTNTSLAHELWKVP
1			LPPKNITAPSRPPPGLTGQKPPLSTWDNSPLRIGGGWGNSDARY
[			TPGSSWGESSSGRITNWLVLKNLTPQIDGSTLRTLCMQHGPLIT
			FHLNLPHGNALVRYSSKEEVVKAQKSLHISDLFLLTL
7117	695	1261	LLISTPGGCHPPPSSIRFTYTGAWGKALPAPHMPCAPGALPQGA
ł			FVSQAARAI PLLQPSQAAQAEGLSQPARACGALCSLPWPLRNWG
į	j.	ļ	SPILRLPGGLRTPTNDRKTRTRSAMACWARAQWDTLGPLKLSHR
l .			GKVCLRHPRPTGVRGGPGAAGRQGGMGTRRRGTFTSGARDPGGL
		<u> </u>	RVKHRCQPTGHLP
7118	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVERISLLQPQVE
I			BSVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR
J			LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCOTGGVIAEI
1	!		LRGVRLHPHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD
1			NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT
			YCRLAQFIGNRRBLNRDKLEKLERLTMDGAKAKAILDASRSSMG
	i		MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT
1			RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF
			SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKBAMVOAB
1			EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE
<b>]</b>			EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL
			MSSDLEETAGSTSIPKRKKSTPKEBTVNDPBBAGHRSGSKKKRK
		1	FSKEEPVSSGPEEAAGKSSSKKKKKFHKASOED
			LOWDEL ADDOLUMENTO DO SELECTION OF D
7119	49	1863	PHCEPNPGAGAMVLLHVLFBHAVGYALLALKEVEEISLLQPQVE
7119	49	1863	PHCEPNPGAGAMVILHVLFBHAVGYALLALKEVEETSLLQPQVE ESVLNLGKFHSTVRLVAFCPFASSQVALKNANAVSBGVVHEDLR
7119	49	1863	PHCEPNPGAGAMVLLHVLFBHAVGYALLALKEVEEISLLQPQVE ESVLNLGKPHSIVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEBLGYNCQTGGVIAEI
7119	49	1863	PHCEPNPGAGAMVLLHVLFBHAVGYALLALKEVEEISLLQPQVE ESVLNLGKPHSIVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEKLGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQIGLGHSYSRAKVKFNVNRVD
7119	49	1863	PHCEPNPGAGAMVLLHVLFBHAVGYALLALKEVEEISLLQPQVE ESVLNLGKPHSIVRLVAFCPPASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEKLGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQIGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVRBWYGYHPPELVKIINDNAT
7119	49	1863	PHCEPNPGAGAMVILHVLFEHAVGYALLALKEVEETSLLQPQVE ESVINIGKPHSIVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEEKIGYNCQYTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLERLTMDGAKAKAILDASRSSMG
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSLLQPQVE ESVLNLGKPHSIVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKTGAAIQEBIGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTPSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRREINEDKLEKLERLIMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSILQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEKIGYNCQTGGVIAEI LRGVRLHFHILVKGLIDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRREINEDKLEKLERLTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEBLGYNCQTGGVIABI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEBLTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAAKNKGRISRYLANKCSIASRIDCP
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEBIGYNCQTGGVIAEI LRGVRLHFFHNLVKGLTDLSACKAQLGLGHEYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEBLTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLITNLAXYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGBKLREQVKERLSFYETGEIPRKNLDVMKHAMVQAE
7119	49	1863	PHCEPNPGAGAMVILHVLFEHAVGYALLALKEVEETSLLQPQVE ESVINIGKPHSIVRLVAPCPPASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEKIGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEBLTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLITNLAKYPASTVQIIGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAAKKRIISRYLANKCSIASRIDCP SBVPTSVFGEKLREQVEERLSFVETGEIPRKNLDVMKRAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKTGAAIQEETGYNCGTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVFNVRVD NMIQSISLLDQLDKDINTPSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRREINEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALTGBAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFYGRAAAKNKGRISKYLANKCSIASRIDCF SEVPTSVFGBKLREQVKERLSFYETGRIPKNLDVMKHAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPRECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKKSFSKEEL
	49	1863	PHCEPNPGAGAMVILHVLFEHAVGYALLALKEVEETSLLQPQVE ESVINIGKPHSIVRLVAPCPPASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEKIGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEBLTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLITNLAKYPASTVQIIGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAAKKRIISRYLANKCSIASRIDCP SBVPTSVFGEKLREQVEERLSFVETGEIPRKNLDVMKRAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE
7119	1991	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSILQPQVE ESVLNLGKPHSIVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEBIGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTPSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGHTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGBKLREQVKERLSFYETGEIPRKNLDVMKHAMVQAE EAAAEITRKLEKQEKKRLKKEKKKLAALALASSENSSSTPRECE EMSRKPKKKKQKPQBVPQBNGMEDPSISFSKPKKKKFFSKEEL MSSDLRETAGSTSIPKRKKSTPKEBTVNDPERAGHRSGSKKKRK
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSILQPQVE ESVLNLGKPHSIVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEKIGYNCQTGGVIAEI LRGVRLHFHIJVKGLTDLSACKAQLGLGHSYSRAKVKPNVNRVD NMIIQSISLLDQLDKDINTPSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRREINEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAAKNKGRISRYLANKCSIASRIDCP SEVPTSVFGEKLREQVKERLSFYETGEIPRKNLDVMKKAMVQAE EAAAEITRKLEKQEKKRLKKEKKKLAALALASSENSSTPEECE EMASKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKKFSKEEL MSSDLRETAGSTSIPKRKKSTPKEBTVNDPERAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSILQPQVE ESVLNLGKFHSTVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKTGAALQEKIGYNCQTGGVTAET LRGVRLHFHILVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMITQSISLLDQLDKDINTFSMRVRBWYGYHPPELVKIINDNAT YCKLAQFTGRRREINEDKLEKLEELTMDGAKAKATLDASRSSMG MDISAIDLINTESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTPTGRAAAKNKGRISRYLANKCSTASRIDCP SEVPTSVFGEKLREQVEERLSFYETGETPRKNLDVMKRAMVQAE EAAAETTRKLKQEKKRLKKEKKKKKALAALALASSENSSSTPRECE EMSBRPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKFSKEEL MSSDLRETAGSTSIPKRKKSTPKEBTVNDPERAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFTEPQTANLSVVFKDS
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSLLQPQVE ESVLNLGKPHSIVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEBIGYNCOTGGVIABI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVFNYNRVD NMIQSISLLDQLDKDINTPSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRRBLNEDKLEKLEBLTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLITNLAXYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAANKGRISKYLANKCSIASRIDCF SEVPTSVFGBKLREQVKERLSFYETGRIPKNLDVMKHAMVQAE BAAABITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPRECE EMSBKPKKKKKQKPQBVPQENGMEDPSISFSKPKKKKFFSKEEL MSSDLRETAGSTSIPKRKKSTPKEBTVNDPERAGHRSGSKKKRK FSKBEPVSSGPERAAGKSSSKKKKKFHKASQED QLGTRCLRGDKVTNAMQDFLVTNLEPRFTEPQTANLSVVFKDS NSTTPLIPVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RABAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLKSYSS
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSILQPQVE ESVLNLGKPHSIVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEBIGYNCOTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIQSISLLDQLDKDINTPSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFYGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGBKLREQVKERLSFYETGEIPRKNLDVMKEMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKQKPQBVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLRETAGSTSIPKRKKSTPKEBTVNDPERAGHRSGSKKKRK FSKEPVSSGPEEAAGKSSKKKKKPHKASQED QLGTRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RARAMMRSSIERGKWVFFONCHLAPSWMPALKRLIEHINPDKVH RDFRLWLTSLPSNKPPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY
			PHCEPNPGAGAMVILHVLFEHAVGYALLALKEVEETSLLQPQVE ESVINIGKPHSIVRLVAPCPPASSQVALKRANAVSEGVVHEDLR LLLETHLPSKKKKULGVGDPKIGAAIQEKIGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKI INDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVSISBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLINILAKYPASTVQIIGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAAKNKGRISRYLANKCSIASRIDCP SEVPTSVFGEKLRGQVEERLSFYETGEIPRKNLDVMKHAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPRECE PMSRKPKKKKQEPQEVPQENGMEDPSISFSKPKKKKFFKEEL MSSDLBETAGSTSIPKRKKSTPKEETVNDPERAGHRSGSKKKKK FSKEEPVSSGPEEAAGKSSSKKKKFPKASOED QLGTRCLRGDKVTNAMQDFLVINLEPRFIEPQTANLSVVFKDS NSTTPLIPVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RABAMMRSSIERGKWVFFONCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLESNKFPVSILQNSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEPKSLLSLCLPHGNALBRRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD
			PHCEPNPGAGAMVILHVLFEHAVGYALLAILREVEETSLLQPQVE ESVINIGKPHSIVRLVAPCPPASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKULLGVGDPKIGAAIQEKIGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLERLTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLITNLAKYPASTVQIIGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAAKNKGRISRYLANKCSIASRIDCP SBVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKHAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPRECE EMSBKPKKKKKQEPQBVPQENGMEDPSISFSKPKKKKSPSKEBL MSSDLRETAGSTSIPKKKSTPKEBTVNDPERAGHRSGSKKKKK FSKEEPVSSGPEEAGKSSSKKKKFHKASQED QLGTRRCLRGDKVTNAMQDPLVTNLBPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGGGP RABAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANILKSTSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALBRRKFGPLGFNIPY BFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGBINYGGRVTD DWDRRCIMNILEDPYNFDVLSPEHSYSASGIYHQIPPTYDLEGY
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSLLQPQVE ESVLNLGKPHSIVRLVAPCPPASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKULLGVGDPKIGAAIQEKIGYNCQTGGVIAEI LRGVRLHFHNLVKGLIDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEBLTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLITNLAXYPASTVQIIGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAAKNKRIISRYLANKCSIASRIDCP SEVPTSVFGGKLREQVEERLSFYETGEIPRKNLDVMKHAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPRECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSPSKEBL MSDLRETAGSTSIPKRKKSTFKEBTVNDPERAGHRSGSKKKRK FSKEPVSSGPEEAGKSSSKKKKKKKKHKAQED QLGTRRCLRGDKVTNANQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVISPGTDPAADLYKFAEBMKFSKKLSAISLGQGQGP RAKAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIBPPRGVBANLLKSYSS LGEDFLNSCHKVMEPKSLLLSLCLPHGNALBRRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGBINYGGRVTD DWDRRCINNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPBIFGLHDNANITFAQNETFALLGTIIQLQPK
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSLLQPQVE ESVLNLGKPHSIVRLVAPCPPASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAALQERIGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIQSISLLDQLDKDINTPSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRREINEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLITNLAKYPASTVQIIGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAAKNKRIISRYLANKCSIASRIDCP SEVPTSVFGEKLREQVEERLSFYETGRIPKNILDVMKHAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSRKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKFSKEEL MSSDLRETAGSTSIPKRKKSTPKEBTVNDPERAGHRSGSKKKRK FSKEPVSSGPEAAGKSSKKKKKFHKASQED QLGTRCLRGDKVTNAMQDFLYTNLEPRFIEQTANLSVVFKDS NSTTPLIFVISPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RAHAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMBPKSLLLSLCLFHGNALBRRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPETFGLHDNANITFAQMETFALLGTIIQLQPK SSSAGSQGREBIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSILQPQVE ESVLNLGKPHSIVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEBIGYNCGTGGVIABI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVFNYNRVD NMIQSISLLDQLDKDINTPSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEBLTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLITNLAXYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFYGRAAAKNKGRISKYLANKCSIASRIDCF SEVPTSVFGBKLREQVKERLSFYETGRIPKNLDVMKHAMVQAE BAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPRECE EMSBKPKKKKQKPQBVPQENGMEDPSISFSKPKKKKSPSKEEL MSSDLRETAGSTSIPKRKKSTPKEBTVNDPERAGHRSGSKKKRK FSKEPVSSGPERAAGKSSSKKKKKFHKASQED QLGTRCCLRGDKVTNAMQDFLVTNLEPRFTEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RARAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKPPVSILQNGSKMTIEPPRGVRANLKSYSS LGEDFLNSCHKVMEPKSLLLSLCLFHGNALBRRKFGPLGFNIPY BFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRCIMNILEDFYMPLVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGRBBIVEDVTQNILLKVPBPINLQWWARKYPVLYERS MNTVLVQEVIRYNRLLQVITQTLQDLKALKGLVVMSSQLEIMA
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSILQPQVE ESVLNLGKPHSIVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEBIGYNCGTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIQSISLLDQLDKDINTPSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVSISBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGBKLREQVKERLSFYETGRIPRKNLDVMKHAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKQKPQBVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLRETAGSTSIPKRKKSTPKEBTVNDPERAGHRSGSKKKRK FSKEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RABAMMRSSIERGKWVFFONCHLAPSWMPALKRLIEHINPDKVH RDFRLWLTSLPSNKPPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEPKSLLLSLCLPHGNALBRRKFGPLGFNIPY BFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNFDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPBIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGRBBIVEDVTQNILLKVPBPINLQWVMAKYPVLYEBS MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSLLQPQVE ESVLNIGKFHSIVRLVAPCPPASSQVALKRANAVSEGVVHEDLR LLLETHLPSKKKKULGVGDPKIGAAIQEKLGYNCGYGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVRRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKI INDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVSISBYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLINILAXYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAAKNKGRISRYLANKCSIASRIDCP SEVPTSVFGEKLREQVEERLSFYETGRIPRKNLDVMKHAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKQEPQEVPQENGMEDPSISFSKPKKKKGPSKEEL MSSDLETAGSTSIPKRKKSTPKEETVNDDERAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKPHKASQED QLGTRCLRGDKVTNAMQDFLVINLEPRFIEPQTANLSVVFKDS NSTTPLIPVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RABAMMRSSIERGKWVFFONCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLLPSNKFPVSILQNSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEPKSLLLSLCLPHGNALBRRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPILDMPETFGLHDNANITFAQNETFALLGTIQLQPK SSSAGSQGREBIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLKALKGLVMSSQLBLMA ASLYNNTYPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKWMFE
			PHCEPNPGAGAMVILHVLFEHAVGYALLALKEVEETSLLQPQVE ESVINIGKPHSIVRLVAPCPPASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKULGVGDPKIGAAIQEKIGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVRRVD NMIIQSISLLDQLDKDINTFSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLERLTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVSISBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHASILTNLAKYPASTVQIIGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAAKNKGRISRYLANKCSISRIDCP SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKRAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPRECE EMSEKPKKKKKQEQEVPQENGMEDPSISFSKPKKKKSPSKEEL MSSDLRETAGSTSIPKRKKSTPKESTVNDPERAGIRSGSKKKKK FSKEEPVSSGPEEAGKSSSKKKKFHKASQED QLGTRRCLRGDKVTNAMQDPLVTNLBPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGGGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQMSKMTIEPPRGVBANLLKSTSS LGEDFLNSCHKVMEPKSLLLSLCLFHGNALBRRKFGPLGFNIPY BFTUGDLRICISQLKMFLDEYDDIPYKVLKYTAGBINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIQLQPK SSSAGSQGREBIVEDVTQNILLKVPBPINLQWVMAKYPVLYEBS MNTVLVQEVIHYNRLLQVITQTLQDLKAALGLVMSQLEIMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFNISGFFFPQAPITGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYHGLFLEGARWDPBAFQLAESQPKELYTEM
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSLLQPQVE ESVLNLGKPHSIVRLVAPCPPASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKULGVGDPKIGAAIQERIGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTPSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEBLTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLITNLAXYPASTVQIIGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAAKNKRIISRYLANKCSIASRIDCP SEVPTSVFGGKLREQVEERLSFYETGEIPPKNLDVMKHAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPRECE EMSRKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSPSKEBL MSDLRETAGSTSIPRRKKSTEKBSTVNDPERAGHRSGSKKKRK FSKEPVSSGPEAAGKSSSKKKKKKKHKAQED QLGTRRCLRGDKVTNAMQDFLVTINLEPRFIEPQTANLSVVFKDS NSTTPLIFVISPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RAKAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVBRANLKSYSS LGEDFLNSCHKVMEPKSLLLSLCLFHGNALBRRKFGPLGFNIPY EFFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGBINYGGRVTD DWDRRCINNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPBIFGLHDNANITFAQNBTFALLGTIIQLQPK SSSAGSQGRBBIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES NNTVLVQBVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLEIMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKWFFE APSELTQRPQVGCYHGLFLEGARWDPBAFQLAESQPKBLYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI
7120	1991	64	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSILQPQVE ESVINIGKPHSIVRLVAPCPPASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLIGVGDPKIGAAIQEBIGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQIGLGHSYSRAKVKFNVNRVD NMIQSISLLDQLDKDINTPSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLITNLAKYPASTVQIIGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAAKNKRIISRYLANKCSIASRIDCP SBVPTSVFGEKLREQVEERLSFYETGRIPRKNLDVMKHAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPECCR EMSRKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKGFSKEEL MSSDLRETAGSTSIPRKKSTPKEBTVNDPERAGHRSGSKKKRK FSKEPVSSGPEAAGKSSKKKKKFHKASQED QLGTRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVISPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RABAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMBPKSLLLSLCLFHGNALBRRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPETFGLHDNANITFAQNETFALLGTIIOLQPK SSSAGSQGREBIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLKALKGLVVMSSQLEIMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFIQAWIQDG IPAVFWISGFFFPQAFITGTLQNFARKPVISIDTISFDFKWFE APSELTORPQVGCYIHGLFLEGARWDPEAFQLAESQPKKLYFEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSILQPQVE ESVLNIGKPHSIVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKTGAAIQEBTGYNCQTGGVTAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIQSISLLDQLDKDINTPSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRREINEDKLEKLEELTMDGAKAKAIIDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALTGBAVGARLIAHAGSLITNLAXYPASTVQIIGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAAKNKGRISKYLANKCSIASRIDCF SEVPTSVFGBKLREQVBERLSFYETGRIPKNLDVMKHAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPECCE EMSRKPKKKKKQKPQBVPQENGMEDPSISFSKPKKKKFSKEEL MSSDLRETAGSTSIPRKKSTPKEBTVNDPERAGHRSGSKKKRK FSKBEPVSGSFEAAGKSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVISPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RARAMMRSSIBRGKWVFFQNCHLAPSWMPALKRLIEHINPDKVH RDFRLWLTSLPSNKPPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMBPKSLLLSLCLFHGNALBRRKFGPLGFNIPY BPTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDPYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPBIFGLHDNANITFAQNBTFALLGTIIQLQPK SSSAGSQGRBBIVEDVTQNILLKVPBPINLQWWAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLKALKGLVVMSSQLBLMA ASLYNNTYPELWSARAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPBAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTRORQRHWIKRGVALICALDY RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFFEASAK
7120	1991	64	PHCEPNPGAGAMVILHVLFEHAVGYALLALKEVEETSLLQPQVE ESVLNIGKFHSTURLVAFCPFASSQVALKRANAVSEGVVHEDLR LLLETHLPSKKKKULGVGDPKIGAALQEKIGYNCQTGGVTAET LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVRVD NMIQSISLLDQLDKDINTFSMRVRBWYGYHPPELVKI INDNAT YCRLAQFIGNRRELNEDKLEKLERLTMDGAKAKAILDASRSSMG MDISAIDLINTESFSSRVSLSRYRQSLHTYLRSKMSQVAPSLS ALIGBAVGARLIAHAGSLINLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAKNKGRISRYLANKCSIASRIDCP SEVPTSVFGEKLREQVKERLSFYETGEIPRKNLDVMKKAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPRECE EMSRKPKKKKKQEYOEVPQENGMEDPSISFSKPKKKKGFSKEEL MSSDLRETAGSTSIPKRKKSTPKEBTVNDPERAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKFHKASOED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RABAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDPLNSCHKVMBFKSLLLSLCLFHGNALBRRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPBIFGHDNANITFAQNETFALLGTIIOLQPK SSSAGSQGRBBIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES NNTVLVQBVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLEIMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWTQDG IPAVFWISGFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTGRPQVGCTHGLFLEGARWDPBAFQLAESQPKELYTEM AVIELPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTENGAGNGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADABEAFTAYLEAMRLPKNTPEBKDRRTAALQEGLRRAV
7120	1991	64	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEETSILQPQVE ESVLNIGKPHSIVRLVAFCPFASSQVALKNANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKTGAAIQEBTGYNCQTGGVTAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIQSISLLDQLDKDINTPSMRVRBWYGYHPPELVKIINDNAT YCRLAQFIGNRREINEDKLEKLEELTMDGAKAKAIIDASRSSMG MDISAIDLINIESFSSRVVSLSBYRQSLHTYLRSKMSQVAPSLS ALTGBAVGARLIAHAGSLITNLAXYPASTVQIIGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAAKNKGRISKYLANKCSIASRIDCF SEVPTSVFGBKLREQVBERLSFYETGRIPKNLDVMKHAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPECCE EMSRKPKKKKKQKPQBVPQENGMEDPSISFSKPKKKKFSKEEL MSSDLRETAGSTSIPRKKSTPKEBTVNDPERAGHRSGSKKKRK FSKBEPVSGSFEAAGKSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVISPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RARAMMRSSIBRGKWVFFQNCHLAPSWMPALKRLIEHINPDKVH RDFRLWLTSLPSNKPPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMBPKSLLLSLCLFHGNALBRRKFGPLGFNIPY BPTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDPYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPBIFGLHDNANITFAQNBTFALLGTIIQLQPK SSSAGSQGRBBIVEDVTQNILLKVPBPINLQWWAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLKALKGLVVMSSQLBLMA ASLYNNTYPELWSARAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPBAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTRORQRHWIKRGVALICALDY RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFFEASAK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, P=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence	Cogucato	\=possible nucleotide insertion)
<u> </u>	Dequence		ETROB
7122	2	546	RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPPREASAK
/122		540	LTTLVDADAEAFTAYLEAMRLPKNTPEBKDRRTAALQEGLRRAV
ļ			SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF
l	ľ	ļ	GAYFNVLINLRDITDBAFKDQIHHRVSSLLQEAKTQAALVLDCL
1	1	1	ETRQE
7123	1	1092	KPAVPEARSAGTSEAGRSGAEEVSCGSVSGDGAAMRLTPRALCS
ŧ.	1	[	AAQAAWRENFPLOGROVARWPPGHMAKGLKKMQSSLKLVDCIIE
		}	VHDARIPLSGRNPLFQETLGLKPHLLVLNKMDLADLTEQQKIMQ
ŀ	,		HLEGEGLKNVIFTNCVKDENVKQIIPMVTELIGRSHRYHRKENL
Ì			BYCIMVIGVPNVGKSSLINGLRRQHLRKGKATRVGGBPGITRAV
1	J.	j	MSKIQVSERPLMFLLDTPGVLAPRIESVETGLKLALCGTVLDHL
1	1	1	VGRETMADYLLYTLNKHQRFGYVQHYGLGSACDNVKRVLKSVAV
ł	'		KLGKTQKVKVLTGTGNVNVIQPNYPAAARDFLQTFRRGLLGSVM
<b>.</b>	1	[	LDLDVLRGHPRV
7124	2	382	LPLTLLLAAPFAHLLLPPGHDQSPCWHPGPALSPGTLGPLSWAM
i	İ	Į.	ANSGLQLLGYFLALGGWVGIIASTALPQWKQSSYAGDASIQLR8
		1	KVFVLESENGGDSLGLPRDCGMSCLLHSAVRSBKGFWS
7125	166	1127	NCISEKRNYSFSMQKGKGRTSRIRRRKLCGSSESRGVNESHKSE
1	}		FIELRKWLKARKPQDSNLAPACFPGTGRGLMSQTSLQEGQMIIS
			LPESCLLT\RDTVIRSYLGAYITKWKPPPSPLLALCTFLVSEKH
i	1		AGHRSLLRA\YLEILPKAYTCPVCLEPEVVNLLPKSLKAKAEEQ
l .		ļ .	RAHVQEFFASSRDFFSSLQPLFAEAVDSIFSYSALLWAWCTVNT
		•	RAVYL\SPGSGNAFLQSRTPVQLAPYLDLLNHSPHVQVKAAFNE
	1		ETHSYBIRTTSRWRKHEEVFICYGPHDNQRLFLEYGFVSVHNPH
	İ		ACVYVSRGWNQLCS
7126	1	733	CRDMAAFIVPSPARRCSQKGSLGHLPTQPWLWAAMSPRGQERGT
ł	1		SHSQARBPQRPGRWLLGSLQSSPGTLGQAGTASRRRGCMVQRWV
1			QVATGRRAVQVPKGALGLALGETSPGASRGMSGGAGGCWALGWA
			PSPVLPSWLLEGPPPWLSIISDSGTQRPSPRRCPARPSPWGPQC
[	!		WRGGRIASAEASST*TPGSGSRARSGRRSPGSRRRSASAPSPTP
			PTDACA*SCVARPAGSRSSRPAAA
7127	1311	277	GLPAMCST*KAGYYERTEGDCIPKDR*IEKRPFKEI*RRIPRIF
1	Ì		AKQKQI+9+NSQKIGASEIDRGRKEADCSDAPAAARIGAVSVFR
	1		rstqbarvsprsnaksanlravrad+wehfvllfhtpbqflabc
	ţ .	•	ICRST**K*WHQLC*PLSSL*TGLKRKLLL*VLFRI*WLKDCDV
1	I		*FCQKIFATNFCNWQNLIQ*EE*KPVEYSVEN*HIMNLLLPM*L
1	1		CQSSLRDQTIVTWRM+RNYSMFRINMISSL+DGSIHIPLKLHFY
[	1		PALIFTLTVPINSCCQRPLPLFAHQSIKTLASSGSPMLACLRFL
			LVKKRAPIHTPRSPGCSV*CKHVLVKDNKNNCVGSEV
7128	2	5228	GRVDLWTILLGRSALRBLSQIRABLNKHWRRLLBGLSYYKPPSP
[	1 .		SSAEKVKANKOVASPLKELGLRISKFLGLDEEQSVQLLQCYLQE
l	<u> </u>		DYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHL
I	1		LTYFQDERHPYRVEYADCVDKLEKELVSKYRQQFEBLYKTBAPT
ĺ	<b>{</b>		wethgnlmterqvsrwfvqclreqsmlleiiflyyayfemapsd
	1		LLVLTKMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVE
1			GMDIESLHKCALDDRRELHQPAQDGLICQDMDCLMLTFGDIPHH
}	1		APVLLAWALLRHTINPERTSSVVRKIGGTAIQLNVFQYLTRLLQ
			SLASGGNDCTTSTACMCVXGLLSFVLTSLELHTLGNQQDIIDTA
	<b>,</b>		CEVILADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLL
	1		RALVSGRSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWR
	Į l		RQTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSW
	· '		TLFTCBIEMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIA
	1		DCLLPITSRIYMLLQRLTTVISPPVDVIASCVNCLTVLAARNPA
]	1	,	KVWTDLRHTGPLPFVAHPVSSLSQMISAEGMNAGGYGNLLMNSE
}			QPQGEYGVTIAFLRLITTLVKGQLGSTQSQGLVPCVMFVLKEML
	l		

No:	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No:   nucleotide   corresponding to first mains acid residue of size tamins acid residue of amins acid residue of amins acid sequence   Secrime, T-Threenine, N-Naparagine, mains acid sequence   Secrime, T-Threenine, V-Valine, amins acid sequence   Secrime, T-Threenine, V-Valine, amins acid sequence   Secrime, T-Threenine, V-Valine, amins acid sequence   Secrime, T-Threenine, V-Valine, amins acid sequence   Secrime, T-Threenine, V-Valine, V-Valine, amins acid sequence   Secrime, T-Threenine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine	1 -			(A-A) aning C-Contains D-Aspartic Acid R=
Location   Corresponding   Lofirst   Standard   Lofirst   Standard   Lofirst   Standard   Corresponding   Lofirst   Standard   Corresponding   Lofirst   Standard   Corresponding   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofirst   Lofi				
corresponding to first amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen	, NO:			
to first amino acid residue of amino acid residue of amino acid amino acid sequence  ##Tryptophan, Y=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide deletid Codon, /=possible muclectide insertion)  ##Tryptophan, Y=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, Y=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, Y=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, Y=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, Y=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, Y=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, Y=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, Y=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, Y=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, Y=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, Y=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, Y=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, Y=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, V=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, V=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, V=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, V=Tytosine, X=Unknown, *=Stc Codon, /=possible muclectide insertion)  ##Tryptophan, V=Tytosine, X=Unknown, V=Tytosine, X=Unknown, V=Tytosine, X=Unknown, V=Tytosine, X=Unknown, V=Tytosine, X=Unknown, V=Tytosine, X=Unknown, V=Tytosi			,	1
amino acid residue of amino acid sequence solventy for the form of the sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequ				
xestdme of amino acid sequence Codon, /-possible mucleotide deletion, sequence Codon, /-possible mucleotide disertion)  PSTHEMERNSHYREGICCLILELHEATHECHETOLISHET LQRICCISLATEMENSTYREGICCLILELHEATHECHETOLISHET LQRICCISLATEMENSTYREGICCLILELHEATHECHETOLISHET LQRICCISLATEMENSTYREGICCHILELHEATHECHETOLISHET LQRICCISLATEMENSTYRUNG GOOGGELLKTVKIAPSUTTAVIRLERPSNYVSELEOALSGEE GENELLAVIARSTTAVIRLERPSNYVSELEOALSGEE GENELLAVIARSTTAVIRLERPSNYVSELEOALSGEE GENELLAVIARSTTAVIRLERPSNYVSELEOALSGEE GENELLAVIARSTERSTENDIRTCHAUPSNYVAGELES GURTHLAVIARSTTAVIRLERPSNYVSELEOALSGEE GENELLAVIARSTERSTENDIRTCHAUPSNYVAGELES GURTHLAVIARSTERSTENDIRTCHAUPSNYVAGELES GURTHLAVIARSTERSTERSTENDIRTCHAUKTICLERTYVVAGSLE LXDTLKKSIERRAVISSGYVESLAVHVARSTERSSCTSILKS PLATENCHWISTOLIAUKTICLER TYVVAGSLE LXDTLKKSIERRAVISSGYVESLAVHVARSTERSSCTSILKS VAGANGAURTHAUKTICLER TYVVAGSLE LXDTLKSIERRAVISSGYVESLAVHVARSTERSSCTSILKS VAGANGAURTHAUKTICLER TYVVAGSLE LXDTLKSIERRAVISSGYVESLAVHVARSTERSSCTSILKS VAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAUKTICLER TYVAGANGAURTHAU	1			
amino acid sequence   Sequence   Sequence   Sequence   Sequence	[			
sequence				
PSYMERYENGIGGLIELHATIMICHETULISES  LOPICIC CLANTEROGYTH BUIGLOYDITUMANAQPESDOR  QGQQLLIKTVKLAPSVTNNVIRLKPPSNVVSPLEQALSCHE  GRNLIAVLAKYITHEUDPALPRIAJQLLKREATVAPRISVYAVA  MDAAARIRARITHEUGKI IR MORKIKVMIL MEPITVALVAT  GIATELIALEVKOQSDOSKRESIGNIN SCHARV VWELLING  QDRYMCPPLIARRATAFHARIAUDDRISAMINISTREKTMEN  SPLEGTISEPSETSERSILBTCALIMKI ICLESTYVVVKEL  LKOTHKREST ERKRATWAGGVISCLAVUVARETUSTIVALVET  LKOTHKREST ERKRATWAGGVISCLAVUVARETUSTIVALVET  LVSAMMILITATTIRDIMHITOSVVRRQLEDUJOLOTICAT  LVSAMMILITATTIRDIMHITOSVVRRQLEDUJOLOTICAT  VAQAQQUMEKTKAKVFSAPITVLQMKEMEVSDIPQYSQLVI  CETIGBEVTALFTQTRIBIALGSATEDROSMSTDICSSRESILBEV  VAQAQQUMEKTKAKVFSAPITVLQMKEMEVSDIPQYSQLVI  CETIGBEVTALFTQTRIBIALGSATEDROSMSTDICSSRESILBEV  VAQAQQUMEKTKAKVFSAPITVLQMKEMEVSDIPQYSQLVI  CETIGBEVTALFTQATERISALASSATEDROSMSTDICSSRESILBEV  RUDGVOLVISHTARECECOVEDOSONILQVTERDILIPTLATITI  SLAMKGUNLHFTEATHILLILARTQQGATAVAGGATTQSICCI  LSVVQLSTNOTATOFSAPIRSISLAPSWGGVILLIPTLATITI  SLAMKGUNLHFTEATHILLILARTQCGATAVAGGATTQSICCI  LKYNGLISTATOFSAPIRSISLAPSWGGVILLIPTLATITUTALINGUNGHAMADESSRESONIA  ASBQQALHTUQVGLIKLIGKTLAARRHFTDVQTLLLOSARVI  PATIFLALSFTTFTODSVAPEGGTILLATUNVALIMIGBEN  PITLOLSINGUNGUNGUNGUNGUTULISLOSARVI  BYNGLALSTYPTTTDSSVAPEGGTILLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOARSTELLATUNVALIMIGBEN  BEPLTQAVGLISTOA	1		sequence	
IQPICICSLAYTRAGOTVINIMGIGUPTINMWAQRPSIAGALSCHE GROULIKTYKLARSYNTMYKILKPENNYMYDELGOALSCHE GROULIKTYKLARSYNTMYKILKPENTYMYDELGOALSCHE GROUNTARTITELGSKIRK OMERIK VMILLBERITAVA VIA MAAAIRDAYTITELGSKIRK OMERIK VMILLBERITAVA VIA GLIELFILLBERGKURG SLOSKERSLOMN SCELHAV VMELDE GDRYMCPPLHERAAIAFHALMGDERDSAMINLETEREMEN SPLEGTISEPPESTSEPSIERIKACHANIV VARELDE GDRYMCPPLHERAAIAFHALMGDERDSAMINLETEREMEN SPLEGTISEPPESTSEPSIERIKACHANIVARTESSSCTSLISTYVKRISLE LKOTILKKYSIEKREPAWSGVYKSLAVIVARTESSSCTSLISTYVKRISLE LKOTILKKYSIEKREPAWSGVYKSLAVIVARTESSSCTSLISTYVKRISLE LKOTILKKYSIEKREPAWSGVYKSLAVIVARTESSSCTSLISTYVKRISLE LKOTILKKYSIEKREPAWSGVYKSLAVIVARTESSSCTSLISTYVKRISLISTYVKRISLE LKOTILKKYSIEKREPAWSGVYKSLAVIVARTESSSCTSLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYSTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYVKRISLISTYKKRISLISTYKKRISLISTYKKRISLISTYKRISLISTYKKRISLISTYKKRISLISTYKKRISLISTANIA KANTINIA TYPEDVARIATIOTISTISTYKKRISLISTISLISTYKKRISLISTI		sequence		
OGGGGLILTETVIKLABSTYTÄNVIRLIKPESIVAPENSVARA GRNLIAVIAKYI YHRIDDALPIALOLLIKENLAVPARSYYAA MDAAAIRDAYTITELQSK\IR\ DMRIK\VMIIL\EPLITVA\VET GLIELIELIEUKUNG\SOGSKERSIGNIN\SCERAV\VMELIA GLIELIELIEUKUNG\SOGSKERSIGNIN\SCERAV\VMELIA ODRYNCPPLIERAATAFIELIAUODRISAAHULETKEKEMER SPLEGTISEPSETSERSILETCALIMKI ICLETYYVVORGI LKOTILKERSIEKRAYMIGGVYKSLAJVINARTEKSISCTSILER LKOTILKERSIEKRAYMIGGVYKSLAJVINARTEKSISCTSILER LKOTILKERSIEKRAYMIGGVYKSLAJVINARTEKSISCTSILER LVSARMILLI LATTIEDIMHLTOSVVIRRQLEIJUNGTETLI PASVINCELIGRAKTALLILIGKOMREHIGSDVSTLIGELTSTI VIQADQOLMERTRAKVISAFTYULQMKEMKVSDIPOYGGUIL CETTLOERVITALARTEQGATAVAGGSITQGIT CITTLOERVITALARTEQGATAVAGGSITQGIT SLAMKRINIHPTRATIHLILITARTQGATAVAGGSITQGIT SLAMKRINIHPTRATIHLILITARTQGATAVAGGSITQGIT LLSVYQLSINGTATPESARRELDAPSWGYVIRLISMINRQLI LRYNEPPRALDPVGVUGRETLACCIMAVRTVQSLACLERBING LLIKYNEPPRALDPVGVUGRETLACCIMAVRTVQSLACLERBING LIKYNEPPRALDPVGVUGRETLACCIMAVRTVQSLACLERBING ASSOQALITTVGVIGLIKLIEKTLAARRIFTEDVGCILLOSILISR QHTLQIKKRIGGLESAV\AQRV\QRPPSAASAAPSSSKOATI FILLIALISPTTTTPISEVAPRGTILLATUNVALMMIGSIT FILLIALISPTTTTPISEVAPRGTILLATUNVALMMIGSTEL REPHITAVASLTSORARTITUSALISHATYMENCHILLISQARRYI PAVEPBUKQRMKQELSSELSTLISSLISRYPRRGASSPATGV SPOGRITSISKARPSSQEPLIQUVQAPVRIMOR REPHITAVASLTSORARTITUSARIPTOTEXMILLIGRISAAVVBINT GCHATTYRTTPAVLFHQHINGSPRASVAVNITRISGGABLTVINK GTAYVASTTGAVATALGIALIKTHYSELIGRYPYPAAVAAAN NIPHMIGRELKVGIPVTDENGINLGESANAKQATTOVALAMA NIPHMIGRELKVGIPVTDENGINLGESANAKQATTOVALAMA NIPHMIGRELKVGIPVTDENGINLGESANAKQATTOVALAMA NIPHMIGRELKVGIPVTDENGINLGESANAKQATTOVALAMA NIPHMIGRELKVGIPVTDENGINLGESANAKQATTOVALAMA NIPHMIGRELKVGIPVTDENGINLGESANAKQATTOVALAMA NIPHMIGRELKVGIPVTDENGINLGESANAKQATTOVALAMA NIPHMIGRELKGVGPPTLENGTHISTORAGATATORAGATTOPARAMA NIPHMIGRELKGVGIPVTDENGINLGESANAKQATTOVALAMA NIPHMIGRELKGVGIPVTDENGINLGESANAKGATALISTO GATTATATTORAGATATICHATIKHTSPLICHRETUKSAGATATALIST TIDOTSGUNGATATILISTARTYKPYNISKICLEPTY NINDENLADVINGESTANGATALISTORAGATATALISTORAGATATALISTORAGATATALISTORAGATATALISTORAGATATALISTORAGATATALISTORAGATATALISTORAGATATALISTORAGATATALISTORAGATATALISTORAGATATALISTORAGATA	1			<u> </u>
CNNLTAVIAKTIYHKIDPALPRIAIQLEKRIATVAPHSVYAC     NDAAAIRDAYITRUGSK\IE\DMRIKQLUKIL\ERITAV\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETICA\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\Uetica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UETica\UEtica\UEtica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Uetica\Ueti	1		·	
NDAAAIRDAPILFELQSK\IR\DMNIK\WHIL\BERLIVA\Vee   GLIKLPINLEVKDS\SDSKBFSLGNW\SCLIMAY\VeeLIDE   ODRYWCPPILHRAAIAFLIRIMODRRDSAMIVLETERPHYBEE   SPLEGTLESPSKTSESTLETCALINKII CLEXIYYVKSLL   LKOTLKKES EKRPAWSCYVKSLAVHVENSELSSCTSLLKEI   LKOTLKKES EKRPAWSCYVKSLAVHVENSELSSCTSLLKEI   LVSAMMILLII LATHIADIMHLITOSVURGLEILDULDITAAL   PASVNICHLEGSMKKTILLILLILKOKRERELSPELIDVILOGITAAL   PASVNICHLEGSMKTILLILLILKOKRERELSPELIDVILOGITAAL   PASVNICHLEGSMKTILLILLILKOKRERELSPELIDVILOGITAAL   PASVNICHLEGSMKTILLILLILKOKRERELSPELIDPILOGISTAL   PASVNICHLEGSMKTILLILLILKOKRERELSPELIDGISTAGE   VIQADQOIMEKTKAKVYSAPITVUQMERNKVODIDCSTRSHE   REDGVCVLGIHLAKKLECEVDROGISMILQVTRILDITCHTILTI   SLEMKKONLHPTERTIHLLILTLARTQGATAVAGAGITQSICL   LSYVOISTIGRTOTPSSRSKSLDAPSMFCVLSMSIMSQSIL   LRYNFLPERALDPVUVIGURETLQCLANVETVQSLACLERDHI   PILLOLANPREWHHLDQCHEDIOVNICHCTSMILISMS   GHYLQANSIGLETLAGICHATURVACAGGITQSILCS   CHYLQANSIGLETLAGICHATURVACAGGITQSILCS   CHYLQANSIGLETLAGICHATURVACAGGITQSILCS   CHYLQANSIGLETLAGICHATURVACAGGITCHAGE   CHYLQANSIGLETLAGICHATURVACAGGITCHAGE   PEULISTAGE PASVAGAGATAVAGAGATURVACAGGITCHAGE   PAUPPADKGRINGCISSARSTILGSISASSISTAGSGESPASSERDPNINIG   PAUPPADKGRINGCISSARSTILGSISASSISTAGSGESPASSERDPNINIG   PAUPPADKGRINGCISSARSTILGSISASQOYBANA   TOROMTY STETTYPAUFWON HINGSPANVYNTINGGBAPLIVU   STANDAYATATAGINAALTKUSPLIGFPUPAANAAN   NIPLMRORELBY ADPASSARSTILGSISASQOYBANA   STANDAYATAGINAALTKUSPLIGFPUPAANAAN   NIPLMRORELBY TYPLOLANPORKHIGESNAAKQATTQVVOXS   MAARGHIPPINTERKAATIRGATATAGINAALTKUSPLIGFPUPAANAAN   NIPLMRORELBY TYPLOLANPORKHIGESNAAKQATTQVVOXS   MAARGHIPPINTERKAATIRGARAARQATTQVVOXS   MAARGHIPPINTERKUSUPPITURGKHIGHAANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA				
GLIKLTIANEVKOG SIGSKRFSIGMW\SCIRIAV\VEKLING ODRYWCPLIRRANIAPIELIAMODRREDSAMIVILETKPHYMES SPLEGTISPPSETSEPSILETCALIMKIICLEIYYVVKGSLL LKOTLKKFSIEKRRAVMSGYVKSLAVHVABTEGSSCTSLIKEY LVSAMKMILITATHADIMHITDSVVRRGULFUVDOTTAALI PASWNCLRIGSMKCTILLILLIKOMKBELGSVDRILGPITSII VIQADQOLMBETKIKAVYSAFTIVUQMKREDLGSVDRILGPITSII VIQADQOLMBETKIKAVYSAFTIVUQMKREDLGSVDRILGPITSII VIQADQOLMBETKIKAVYSAFTIVUQMKREDLGSVDRILGPITSII VIQADQOLMBETKIKAVYSAFTIVUQMKREDLGSVDRILGPITSII VIQADQOLMBETKIKAVYSAFTIVUQMKREDLGSVDRILGPITSII UNDADOLMBETKIKAVYSAFTIVUGMKREDLGSVDRILGPITSII SLAMKONLHIPTERTIHLILTIATROQGARTAVAGAGITQSICL LSVYQLSTMGTAOTPSASKISLADPSMEOVYRLSMSIMRQLL LKYNFLPBALDPVUVSIGRETLQCIANAVTAVAGARITQSI LKYNFLPBALDPVUVSIGRETLQCIANAVTAVAGARITQSI LKYNFLPBALDPVUVSIGRETLQCIANAVTAVAGARITQSI PILGLSNPMKSWHEHLPQUMRDIQVSIGGLGCIBADH PILGLSNPMKSWHEHLPQUMRDIQVSIGGLGCIBADH PILGLSNPAVARTHOPVOCQULSCUCKATERS QHYLQNVGSTORGGTRIKSILMPTHRECTYLLISQAMKYI PAVHPRUKQRHKQSISTASSISSISHYPRRGAPSSPATG SPQCKSTSISISKSPSGSGPELIQUVAQAPVUNTAVAGARITAVA PAVHPRUKQRHKQSISTASSISSISHYPRRGAPSSPATG SPQCKSTSISISKASPSGSGPELIQUVAQAPVUNTAVAGARITAVA TGCMMFYKTTPAVIFONINGSTAVAVYITNRSGDAPLIVAV GCTAVYSATTGAVATAIGINALTHAVSPLICESSARIVIDDOC PPGITEREMRAXYITOSAPHPITORSKULLGIMSAQVYMM TGCMMFYKTTTPAVIFONINGSPAVAVYTNRSGDAPLIVAV GTAVYSATTGAVATAIGINALTHAVSPLICESSARIVIDDOC PPGITSREMRAXYITOSARIPIPOTGSKULLIGMSAQVYMNA NIPLMRQRELKVGIPVTDENGNILGSBANAAKQAITOVVSK MAAPGRAIPPFIMTSIEKKAPLKREPWMSAPLIVVUSCOPLIV GTAVYSATTGAVATAIGINALTHAVSPLICESSARIVIDAVOS MAAPGRAIPPFIMTSIEKKAPLKREPWMSAPLIVVUSCOPLIV TILCCALFPGKSSMSVISLABALQAKIGSSHPELRRYPTAVA NIPLMRQRELKVGIPVTDENGNICGSSIPBERRYPTKAV NISDRIADVILMRGSPPNQAIVUNSHERKPCCLSSSPA AARGIIEVVKPILBEACKVAPPARDRRANICALSPTI NISDRIADVILMRGSPPNQAIVUNSHERKPCCLSSSPA AARGIIEVVKPILBEACKVAPPARDRRANICALSPTI NISDRIADVILMRGSPPNQAIVINSHERKPICORPTITYSLE REBLIKLHVQOHPGBCCGPLOGGALEILERRIRVGVHNGLG RPDVVVLVPRMDVALTRSASPSRKVVSSSKTSGSQALVURS REBLIKLHVQOHPGBCCGPLOGGALEILERRIRVGVHNGLG RPDVVLIVPRMDVALTRSASPSRKVVSSSKTSGSQALVURS REBLIKLHVQOHPGBCCGPLOGGALGILERRIRVGVHNGLG RPSVVLVIPSADAVARDPSINVTSRSBERHIDAPTSVGKVKVPSAS	(			
ODRYWCPPLHERALAPLERALMODREDSAMIVLETER KPMEN SPLEGTIS PPSETSEPS ILETCALIMK I CLEITYVVKOSLI LKOTLKKES I EKKRAWSGYWELAWIVASTESSECTSLISLE LVSAMMILLI LATTIHAD IMHLIDSVVERQLEIDVLOTTALI PASVNICHLEGMKETLLI LILEKOMKERLISGADE TLOPIJETLI VIQADQIMEKTKAKVESAPTIVUKOKMIKVES I PUSUSUM CERTQERVI TALFODTHELALGASATEDKOSMETDOCSBERIE RDGYCVLGIHLAKELCEVDEDGDSWLQVTRILD PLIPTILITI SLAMKQNIHIPTERATLALILITLATYQGATAVARAGITQS I CLEVQUSTRIAD PLAPTLATTI SLAMKQNIHIPTERATLALILITLATYQGATAVARAGITQS I CLEVQUSTRIAD PLAPTLATTI SLAMKQNIHIPTERATLALILITLATYQGATAVARAGITQS I CLEVQUSTRIAD PLAPTLATTI SLAMKQNIHIPTERATLALILITLATYQGATAVARAGITQS I CLEVQUSTRIAD PLAPTLATTI SLAMKQNIHIPTERATLALILITLATYQGATAVARAGITQS I CLEVQUSTRIAD PLAPTLATY SLAMKQNIHIPTERATLALILITLATYQGATAVARAGITQS I CLEVQUSTRIAD PLAPTLATY COMPANIAN ASROQLAHTYQTGLICHLISK I CLARVATYQGATAVARATICALTSHIAMS I CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK OHTU CHEVALOT SPHISK O				
SPLEGTIS.PPSETSEPS ILETCALIMKIICLEITYVVKKSILL LKOTLKKFSIEKREAYMSGYVKSLAVHUABTEGSSCTSILEN LVSAMMILLIIATTIHADIMHILTDSVURGUFLUVLOGTRALI PASVNCIRIGSMKCTLLILLILGMUREHGSVUS LIPPITEII VIQADQQHEKTKAKVEAFITYUQMKEMKVSDIPQYSGLVI CETLQKSVIALEDGYRISLALGSATEDKOMETDOCSBRIRE RQSVVVLGIHLAKELCEVDEDGDSWLQVTRLPILPITETII SLEMKGNLHPTEATIHLLILTLARTQQGATAVAGAGITQSICL LSVVQLSTMGTAQTESASKKSLDAPSWGGYVRLSMLMOGLI LRYNFLPEALDPVGVHQERTLQCLANAVTVQSLACLERADHI PILQLSNPMKEMHFILDQLMRDIQVALGVLGACTSFHIBSK QHTLQNKINGGLIPSAVAQSVQADEVARSAAPSSSKOPAAR ASEQQALHTVQYGLKILGKTLAALRHFTPDVCQILLDQSLD EYNELFALSFTTPTFDSEVAPSFGTILATVNVALMBIGELDBY PAUPEDKQRMKQELSSENSTILJSSLSKYPRRGAPSSPATGV SPQGKSTSILSSFTIKKSLIMPTIMSNCCYLLLISQMGXI PAVHPEDKQRMKQELSSENSTILJSSLSKYPRRGAPSSPATGV SPQGKSTSILSKAPSGEPLIQLOVQAFVRIMOR  7129 1 1054 PREFEWRERLH-AGPASSAGGSFGRASGTMSGELPPNINICK WDDSTFIGRANHFFTVTDFRNILINEQLESAKILHDYRQG PGGITEREMMRKXI LYNDSPHDTICEKKALIGKMSAQVYMMN TGCMMTFYRTTSAVLFMQHINGSPAAVVNYTNISGBAPLTVW GTAVVSATTGAVATALIALINLTHKHSEAPLITURGPVPPAAVAAAN NIPLMRGRILKUGIPVTDBNGNRLGESANAKQATTQVVVSK MAAPGMAIPPPIMNTLEKKAPLKRPPWMSAPIQVGTUKYTNK SARGPYRRGSGSSVILINKSMOBINGFPVPRAVAANA NIPLMRGRILKUGIPVTDBNGNRLGESANAKQATTQVVVSK MAAPGMAIPPPIMNTLEKKAPLKRPPWMSAPIQVGTUKYTNK  TRACGAPTRSGSVTSLINKSMOBINFSVOKOQULSLIH RCSHQDLLPDIADSHQQATEKISDLTIQDSQVVVVNNINL AQIATQNYFSNPKETDGDBDVYBIKSEBESBLEISHNRR DSKFVDADPSDNVCSGNTLIISINSPRTPKRPVMSKILLSSPIT NINSDKIANTLMRGFSFNQQNTUVQSLREKGCLSSSSFA NARGHEVWYRFILGREVVYRFILGRACKVMPPARAMENIPLDDAVQFHILE RLHKELSCPGSATGDQVPPKEQ  7132 1420 1087 IDMILLSGALVSGPYTLITTAVSADLCTRKELKGNAHALSTV IIDDTGSVGAALGPLLAGLLSPEGSKNVPYMLMPADACALLE RLHKELSCPGSATGDQVPPKEQ  7133 2 3648 OQFGLLBAHGESGDALKRPHIQKFYTTGHDDDLPFTLYPSLE RBBLLRHVQOHPGGCCGPLOGGALEILERRLERQUMOGIGE RPQVVVLVPBMDVALTRSSPSPRVVSSKTSSGQALVLRS SEBKVGVSGSTLRFOPSLASSENLADAPTEVSGRAVKRRPSR PTSSSSPPAPVBRANAVIQLERGLGGALEILERLERGURVGNRIGGE PTSSSSPPAPVBRANAVIQLERGLGGALEILERLERGRERGERGERFSSPPORAPTGRANAVIALGSSGALAGRASSPSPOD ARPTSQLPRGSQASPQAAGSPFPLAGGISCHLAGRASRSPTDG ARPTSQLPRGSGASPAAGAPFPCVSGRKRRPSR	1			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
ILKOTLKKP SIERRAYMSGYVKSLAVHVABTEGSSCTSILLSV LVSAMRMILI I IATHAD IMBILTDSVVRRQLFLUVLDGTKALI PASVNCLRIGSMKCTLLLI LLRQMRREIGSVDETLSPILTSTI VIQADQQLMERTKAKVSSAFITVLQMKEMKUSDIPQYSGLVIV CETLQBEVTALFDOTRISLLGSAFDEDDSMETDDCSSRSRE RDGVCVLGIHLAKRLCEVDEDGDSMLQVTRLPILLTTI SLAMKQNLHPTEATHHLLITLARTQQGATAVAGAGITQS ICI LSVYQLSTMGTAQTPSSARKSLDAPSWGVYRLSMSLMMQLI LRYMPLPBALDPUGVHQBRTLQCIAAVATVQSLACERADHT PILQLSMMKMHHEIDLAMRDIOVANGYLCOACTSPILISRA QHYLQNKMGDGLPSAV\AQRV\QRPPSAASAPSSKQDANA ASRQQALHTVQYGGLKILGKTLAARRHTEDUCQILLQSLL EXYMPLPBALDPUGVHQBRTLACTIAATVNVALIMLIGELDS RPHOQAVGLSTDABSTRTIKSSLMFTMENCFYLLISQAMRYL PAVPRPKDKQRMXQGLSSESTLISSLSTLISSLYFRGGAPSSPATG SPQGKSTSLSKASPESQEDLIQVQAPVRIMOR PAUPRBKQRMXQLESSESTLISSLSTHYSGELPPNINIK RPHOQAVGLSTDABSTRTIKSSLMFTMSGELPPNINIK PAVPRPKDKQRMXQGLSSESTLISSLSTHYSGELPPNINIK GCHMETVETTPALVERQWINQSPRAVVNYTNINSGGAPLTVN GCHMETVETTPALVERQWINQSPRAVVNYTNINSGGAPLTVN GCHMETVETTPALVERQWINQSPRAVVNYTNINSGGAPLTVN GCTAYVSATTGAVATALGLNALTKHVSPLIGRFUPPAAVAAAN NIPHMRQRBLKVGIPVTDRNGRRLGESANAAKQATQNVVS MAAPGMAI PPFIMTLEKKAPLKFPPMSAPIOVGLVGPCLU TPLCCALFPQKSSMSVTSLERBLQAKIQSSEPELRRVYTNK GTAYVSATTGAVATALGLNALTKHVSPLIGRFUPPAAVAAAN NIPHMRQRBLKVGIPVTDRNGRRLGESANAAKQATQNVVS MAAPGMAI PPFIMTLEKKAPLKFPPMSAPIOVGLVGPCLU TPLCCALFPQKSSMSVTSLERBLQAKIQSSEPELRRVYTNK RCSHQDLLPPLADSHQQFTEKKAPLKFPMSAPIOVGPCLUPCLU TPLCCALFPQKSSMSVTSLERBLQAKIQSSEPELRRVYTNK RCSHQDLLPPLADSHQQFTEKKSPLTLTQDSQKVVVNNNIL RCSHQDLLPPLADSHQQFTEKKSPLTLTQDSQKVVVNNNIL RCSHQDLLPPLADSHQQFTEKKSPLTLTQDSQKVVVNNNIL RCSHQDLVYNSWKETGDEDDVYG KKSEDESSELBLSHRRR DSRVDADPSDNVCSGTTIHISINSPRTPKRFVUNSKIGLSPYT VNDSDKLNDYLMRGGSDEDVYGTKSECGLSSSSPA  7131 805 573 AARGHIEVVFFLIERCKVMPFAKDRWGNIPLDDAVQFMLE RLIAGRAVSGATGPLTTTAVSADLGTHKSLKGNAHALISTT IDGTGSVGAALGPLLAGLLSPGSMSVFYMLMFADACALLE RLIHKELSCPSSATGQVPPKEQ  7132 1420 1087 IDMILESCALSSGASGALGRENSTEDU RBBLLKHVQDHPGGCCOPLOGGALEILERILKQVHNOLGE RPQVVLVPBMDVALTRSASPSRVVSSKYSSGSGALVLRS RBBLLKHVQDHPGGCCOPLOGGALEILERILKQVHNOLGE RPQVVLVPBMDVALTRSASPSRVDYSSSKYSGSGGALVLRS SEEKVQNESGSTLRFOPSLGSEKHLOAPTEVTSGPKVRRSR PTSSSSPAPUPRVLAAPQASPYCHGLISQLAAR	J			<u> </u>
I JVSAMEMILITATTEADIMENTOSVURRQLELDVILOCTRAIL PASVNCLPILGSMKCTLLITILALCKRENGSVOBTIGPILTSTIL VIQADQQLMEKTKAKVESAF TYVLQMKEMKVSDIPQYSQLVI CETTQEEVITALFDQTREISLALGSATEDDDSMETDCSRSREN RDGVCVLGHILAKRICSVDEDGSHLQVTRRLEPILFTLITTT SLRMKQNLHPTEATHHLIATLARTQQGATAVAGGATIQSICI LSVYQLSTNGTAQTFSASKKSLDAPSWFGVYRLSMSIMEQLI LRYMFLPEALDPVGVHOERTLQCLARVETVQSLACLERADHT PILQLSNFMKEMHFHLDQLMRDIQVALGYLCQACTSFHISKR QHYLQNKNGGGLFSAV, AQEV\QRPSASAAPSSSKOPAAL ASBQQALHTVQYGLKKLEKTLAARRHFTPDVCQTLLOQSLC RYNFLPALSFTTPTTEDSEVAPSFGTLATVWALIMLIGELDB RPLTQAVGLSTQABGTRTLKSLLMPTMENCFYLLISQAMRYI PAVHPRDKQRMKQELSSENSTILISSLSKYPRRAGPSPARTOF SPQGKSTSISLSKAPSESQEPLIQUVQAFVRIMQR RPLTQAVGLSTQABGTRTLKSLLMPTMENCFYLLISQAMRYI PAVHPRDKQRMKQELSSENSTILISSLSKYPRRAGPSPARTOF SPQGKSTSISLKAPSESQEPLIQUVQAFVRIMQR RPLTQAVGLSTQABGTRTLKSLLMPTMENCFYLLISQAMRYI PAVHPRDKQRMKQELSSENSTILISSLSKYPRRAGPSPARTOF SPQGKSTSISLKAPSESQEPLIQUVQAFVRIMQR RPLTQAVGLSTQABGTRTLKSLLMPTMENCFYLLISQAMRYI PAVHPRDKQRMKQELSSENSTILISSLSKYPRRAGPSPARTOF SPQGKSTSISLKAPSESQEPLIQUVQAFVRIMQR TGCMMTFYRTTPAVLFRQMINQSPRAVVNYNINKSGDAPLTVW GTAYVSATTGAVATALGLNALTHENPLIGEFVPPAAVAAAN NIFLMRQRELKVGIPVTDENIGNILGESARAKQATTQVVVSR MAAPGMAI PPTMYTLEKKAFLKRPWAPLIGEFVPPAAVAAAN NIFLMRQRELKVGIPVTDENIGNILGESANAKQATTQVVVSR MAAPGMAI PPTMYTLEKKAFLKRPWAPLIGEFVPPAAVAAAN NIFLMRQRELKVGIPVTDENIGNILGESANAKQATTQVVVSR MAAPGMAI PPTMYTLEKKAFLKRPWAPIOLGGAPTQVVVXNINKL RCSSHQDLLPDTADSHQQGTEKKSDLTTQDSQCMPUNDKHLGLSHR RCSSHQDLLPDTADSHQQGTEKLSDLTTQDSQCKVVVNNINL AQAIATOMYSHVKSTTGDEBDDYVET KEEDESBLEISHBRIRG DSKPVDADPSDNVCSGNTLISINSPRTPKRVNSKLGLSPYT NINSDKINNYLMRGPSNQCOTIVQSLERKFQCLSSSFR  TJ131 805 573 AARGHEVVKFILEBCKWPPAROKRITELDDAVQFMILE  TLINGTGSVGAALGPLLAGLLSPSGNSNVFYMLMFADACALLE RLIHKELSCPGSSATGQVPFKEQ  TJDGTGSVGAALGPLLAGLLSPSGNSNVFYMLMFADACALLE RLIHKELSCPGSATGQCVPTREQ  THE SESPLAVENGRAAFSPSTCH WYRRAWMPLLEADSGRVTLPLQGGLQVNSHCHLERNLAVQUMICHG RPQVVVLVPRMDVALTRSASPSSPCOGRAWALGASRSPTDH ARPTSGLPRGSQASPAQAGFPLEAGISLEADLAGSSFNOM- ARPTSGLPRGSQASPAQAGFPLEAGISLEADLAGSSSVTALAGRSGSPSTOM- ARPTSGLPRGSQASPAQAGFPLEAGISLEADLAGSSSVTALAGGGSASMVLLGSSS				
PASVNCIRICSMECTILLILIROWEREIGSUDEILGPITBIL  VIQADQQIMEKTKAKVFSAFITVIQMEKRIVSDIPQYSQLVI  CETIQBEVIALFEQTEMBLAIGSATEDKDSMETDDCSRSRIER RDGVCVIGHLAREICEUDERGDSMLQVTEREPILPTLITTI  SLRMKGNLHFTERTHELLILTARTQGATAVAGAGETTQSICI  LSVVQLSTNGTAQTPSASRKSLDAPSWFGVYRLSMSLMSQLL  LRYMPIPBRALDFVGVHQRETLQCLNAVRTVQSLACLERADHI  PILGLSMFMEMBHEHLPQLMEDILQVNIGYLCQACTSFHBSR QHYLQNGNGGLSPAV\QRVV\QRPSAARAPSSSKOPAAN  ASSQQALHTVQYGLKILISKTLAMFTDVCQTLLQSLD  EYNFLFALSFTTPTDSEVAPSFGTLLATVNVALIMIGSLDS  EPHTQAVGLSTGASSRISTLSSLSRYPRRGAPSSPATGV SPQGKSTSLSKASPESQEPLIQLVQAFVERIMOR  PEPEFREWRRICH*PGASSSGGSFGRSGTMSGELPDNINIG SPQGKSTSLSKASPESQEPLIQLVQAFVERIMOR  7129  1 1054 PEPEFREWRRICH*PGASSAGGSFGRSGASGTMSGELPDNINIG SPQGKSTSLSKASPESQEPLIQLVQAFVERIMOR  7129  1 1054 PEPEFREWRRICH*PGASSAGGSFGRSGASTMSGELPDNINIG SPQGKSTSLSKASPESQEPLIQLVQAFVERIMOR  7129  1 1054 PEPEFREWRRICH*PGASSAGGSFGRSGASTMSGELPDNINIG SPGGKTSLSKASPESQESSASTMSGELPDNINIG SPGGLTEREEWRRAXIYDSABFIEDTGEKMILIGMSAQVPHIN  NIPIMRQRELKVGIPVTDENGRILGSENANAKQAITQVVSR GTAVVSATTGAVATALGLNALTKHVSPLIGRMSQPPLTVW GTAVVSATTGAVATALGLNALTKHVSPLIGRMSQPPLTVW GTAVVSATTGAVATALGLNALTKHVSPLIGRMSQPPLTVW GTAVVSATTGAVATALGLNALTKHVSPLIGRMSPLTVVVNTN  NAPIGRBLKVGIPVTDENGRRIGGSFARGGELPDNINIG GTAVVSATTGAVATALGLNALTKHVSPLIGRMSPLTVVVNTN  NAPIGRBLKVGIPVTDENGRRIGGSFARGGELPDLRGAPLTVV  TPLCCALFPQESMSVTSLRARLQAKIQSHPELRVYFNKE GTAVVSATTGAVATALGLNALTKHVSPLIGRFYPPAVAANA  NIPIMRQRELKVGIPVTDENGRRIGGSFARGGEVVVYRNL  RCESHQDLLPDIADSHQQGTEKLSDLTLQDSQKVVVYRNL  AQIATQMYSSMVKETDGDEDDYVXIKSEEDESELBISHNRR  DSKEVDADDSDAVCSGNTLHSLINSPRTPKKPVVNSKLGLSPYT  VNSDSKLINDVLRREGSPROQNIVSEREFQCLSSSPA  7131 805 573 AAAEGHIEVVKFILEACKVNPFAKDRWSNIPLDDAVQFNHLE  LILIQDYQDSYTLSETQABAARALSKENLESSM  7132 1420 1087 IDMILISGABAVSPTQLISSSSPA  7133 2 3648 QIFGLLSGADASRASASASASASASASASATASASASASASASASASASA	1		l	
ULQADQQLMEKTKAKVFSAFTTVLQMKEMKVSDIPQYSQLVI CETLQEEVIALFDQTRHSLALGSATEDKSMETDDCSRSRHE RDGVCVLGHLAKBLCEUDERGDSWLQVTRRID ILPTLLTTI SLRMKQNLHFTRATHILLITLARTQQGATAVAGAGTTQSICI LSVVQLSTNGTAQTPSAFKSLDAPSHGVGYLSMSLMEQLI LSVVQLSTNGTAQTPSAFKSLDAPSHGVGYLSMSLMEQLI LSVVQLSTNGTAQTPSAFKSLDAPSHGVGYLSMSLMEQLI LSVVQLSTNGTAGTPSAFKSLDAPSHGVGYLSMSLMEQLI LSVVQLSTNGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG				
CETLQEEVIALFDOTRIBLAGSATEDROSMETDOCSRSRER RUGYCVIGIHLAKELCEUDROSMUQVTRIADILTILITI  SLRWKQNIHFTERTIHLILTILARTQQQATAVAGAGITQSICI LSVVQLSTNGTAQTESAGRKSLDAPSWEGVYRLSMSIMBOLI LRYNFLPBALDPVGVHQBRTLQCIANAVRTVQSLACLERADHT FILQLSNFMKBMHFHLPQLMBBILQVNLGYLCQACTSFHISR QHYLQNNNGGLPSAV\QRVV\QRPSAASAPSSKOPANH ASRQQAHTYQYGLKKILKIKTLAALRHFTPDVCQTLLQSLD EYNFLFALSFTTPTDSEVAPSFGTLLATVNVALNMLGELDM RPHLQAVGLSTQAEGTRTIKSLLMFTMENCFYLLLGQAMRYL PAVIPRDKQBMKQESSRISTLISLSERYPRGAPSSPATG SPQGKSTSLSKASPBSQBPLIQLVQAPVRHMQR PAVIPRDKQBMKQESSRISTLISLSLSKYPRGAPSSPATG SPQGKSTSLSKASPBSQBPLIQLVQAPVRHMQR WQGSTFIGRANHFFYTVDFRNILLINSQLESARKLVHDYRQC PPGLTEMEUMRAYYTDGSRHIPDTGEKMILLGRMSAOVPMNM TGCMMTFYRTTPAVLFWQHINQSPNAVVNYTNRSGDAPLTVM GTAVVSATTGAVATALGLINALTKUSSLLIGRFVPPAAVAAN NIPLMRGRBLKVGIPVTDENGNRLGSSANAKQATGVULVGPCLV MAAGMAIPPFHNTIEKKAPLKFWSPLIGRFVPPAAVAAN NIPLMRGRBLKVGIPVTDENGNRLGSSANAKQATGVULVGPCLV MAAGMAIPPFHNTIEKKAPLKFPMSAPLOVGLUGPCLV MAAGMAIPPFHNTIEKKAPLKFPMSAPLOVGLUGPCLV MAAGMAIPPFHNTIEKKAPLKFMSAPLAGULGUGPCLV TPLCCALFPQKSSMSVTSLRABLQAKIQESHPELRRVYFNKC 130 2 780 HEVPSLQTGSPJLPGGSVQRCSVVVSQPNKENWCQDHLYNSLGS MAAGMAIPPFHNTIEKKAPLKFMSAPLAGULGUGPCLV NGSGVFHISQGSSVVLINKSMPTSPDVKRQDLISLHE RCESHQDLLPDLADSHQQSTEKLSDLTLQDGQKVVVVNRNLE AQIATGNYFSNYKETDGDEDDYVSIKSBEDSEBLBISHNRR BCKFVDADFSDNVCSSNYLINGSPTPKFVPNSKLGLSPYT VNDSDKLNDYLMRGPSPDQOKIVOSLBERFQCLSSSSPA  7131 805 573 AAAEGHEVVKFFLIGRCKVMPFAKÖRMGNIPLDDAVQFNHLE KLLQDYQDSYTLSETQARAARALSKENLESMV 7132 1420 1087 IDMLLGGAVSGPYTLITTAVSADLGTHKSLKGLSPYT VNDSDKLNDYLMRGGSPOARAARALSKENLESMV 7133 2 3648 QQIPGLLBAGIGSGDALRKPRIQMFYMMMFADACALLE RLHKKESCPGSATGDQVPFKEQ  7133 2 3648 QQIPGLLBAGIGSGDALRKPRIQMFYMMMFADACALLE RLHKKESCPGSATGDQVPFKEQ  7133 2 3648 QQIPGLLBAGIGSGDALRKPRIQMFYMMMFADACALLE RLHKELSCPGSATGDQVPFKEQ  7136 REBLILBLHVQDHFQGGTGPLDGALEITLERRLRVGVHNGLG RPQVVVVLVEMDVALTKSASFSRRVVSSSKTSSGSQALNLISS RLPBMVGHPAFAVITQLESVYSSSPAGDGNASVTSLSNLAG MVRNAVMPLLEADSGRVTLPLQGGIGVPPSHCLVYKVPSAS SEKVKQYESGTLRFQFSISGSERHLDAPTEVSGFKVERRPSR PTSPSSPAPVRVLAAPQNSPVGPGLSISQLAASFRSFTQG ARPTSQLDPHGSQASPAQAQEPPLEAGISLBLAGLLSVLISULAL	}	1	ł	■ The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of th
RUGUCVIGHHARECEUUREGESMIQVTREBILETLLTILS SLEMKKONLHPTERATHHILITLARTQGEATAVAGAGITQSICI LSVVQLSTNGTAQTESAGRKELDAPSWFGVYRLSMSIMEQLI LRYMFLPEALDFUGVGUGRETLQCLMANTYOSLACLERADHT FILQLSHMKEWHFHLPQLMRDIQVNIGTYGSLACLERADHT FILQLSHMKEWHFHLPQLMRDIQVNIGTYGSLACLERADHT FILQLSHMKEWHFHLPQLMRDIQVNIGTYGSLACLERADHT FILQLSHMKEWHFHLPQLMRDIQVNIGTYGSLACLERADHT FILQLSHMKEWHFHLPQLMRDIQVNIGTYGSLACLERADHT FILQLSHMKEWHFHLPQLMRDIQVNIGTYGLACTSHLBSR RSPQAGLHTYQYGLLKILSKTLAALRHFTPUQCILLDQSLL RSPHLPASSTSLKASPESGEPLIQUAVERNOR RPLTQAVGLSTQABGTRTLKSLLMFTMENCFYLLISQAMRYI PAVHPRDKQRMKQELSSRISTILSSLSRYFRRGAPSSPATGV SPQKKSTSLSKASPESGEPLIQUAPVERNOR SPQKKSTSLSKASPESGEPLIQUAPVERNOR TOCHMTSTRTTPAVLEGAFHPUGAPVERNOR TGCMTSTYRTTPAVLEGAFHPUGAPVERNOR TGCMTSTYRTTPAVLEGAFHPUGESARLIJGRMARAQVFMNN TGCMTSTYRTTPAVLEGAFHPUGESARLIJGRWARAQVFMNN TGCMTSTYRTTPAVLEGAFHPUGESARLIJGRWARAQVFMNN TGCMTSTYRTTPAVLEGAFHPUGESARLIJGRWARAQVFMNN TGCMTSTYRTTPAVLEGAFHPUGESARLIJGRWARAQVFMNN TGCMTSTYRTTPAVLEGAFHPUSSCHILJGRWARAQVFMNN TGCMTSTYRTTPAVLEGAFHPUSSCHILJGRWARAQVFMNN TGCMTSTYRTTPAVLEGAFHPUSSCHILJGRWARAQVFMNN TGCMTSTYRTALGLAURTSSPLOWLOGEHPELRRVYFNK TALASSPLOWLOGENTISLISLEADATIQUALOGEN TPLCCALFPQKSSMSTYSLEARLAGAKIQBEHPELRRVYFNK AQIATQNYFSNKETIGGEDDYVSIKSBEDESBLEISHNRRR BCSSHQDLEPTIADSQQGTEKLEADLILQDSQRVVVVVRNILE AQIATQNYFSNKETIGGEDDYVSIKSBEDESBLEISHNRRR DSKRVDADPSDNVCSGTNILISLISLEADLILQDSQRVVVVVNRNLE AQIATQNYFSNKETIGGEDDYVSIKSBEDESBLEISHNRRL DSKRVDADPSDNVCSGTNILSLISLERDLILQDSQRVVVVVNRNLE AQIATQNYFSNKETIGGEPTPLARADAGARLESTY TIDDTGSVGAALSPLLAGLLSPSGWSNVFVMLMFADACALLE KLIGHTQDHPGSTGDFLAGGLISPSGWSNVFVMLMFADACALLE RIHKELSCGSAFTARQVFNKERS TIDDTGSVGAALSPLLAGLLSPSGWSNVFVMLMFADACALLE RIHKELSCGSAFTARQVFNKERS REPUVVLVPBMDDALTRSASFSRFVVSSGKSTSSGSGALVLES RLPEMVCHPAFAVIFQLEGUFTSGLOADLFFTTSLSALAL MVRNAVMPLLEADSGRVTLARGAFSFTQG PTSPSSPPAPVRVLAAPQNSPVGGGLSISQLAASPSFTCB PTSPSSPPAPVRVLAAPQNSPVGGGLSISQLAASPSFTCB ARPTSQLPHGSQASPAQAQEPPLEAGISHLBADLSGTSLVLE ARPTSQLPHGSQASPAQAQEPPLEAGISHLBADLSGTSLVLE ARPTSQLPHGSQASPAQAQEPPLEAGISHLBADLSGTSLVLE	1		ļ	= -
SIRMKONLHPTERATLHILLTLARTQQARTAVAGAGITQSICI LSVVQLSTINGTAQTPSASKKSLDAPSWFGVYRLSMSLMEQLI LSVVQLSTINGTAQTPSASKKSLDAPSWFGVYRLSMSLMEQLI LRYMPLPERALDPVQVHQERITQCANAVRTVQSLACLBERDHT FILQLSMMKWHEHLPQLMRDIQVMIGTLQACTSFIHSRR QHYLQNKNGDGLPSAV\AQRV\QRPPSARASAPSSSKQPAD ASEQQALHTVQYGLLKILEKTLAARRHFTPDVCQILLQGSLD BYNFLFALSFTTPTPDSVAPFGGTLLATAVWALMMLGELDN BPLTQAVGLSTQAEGTRTLKSLIMPTWENCPYLLTGQAMRYI PAVHPRDKQRMKQELSSRISTILSSLSRYFRGAPSSPATGV SPQGKSTSLSKASPESQBELIQLVQAFVRHMQR PAVHPRDKQRMKQELSSRISTILSSLSRYFRGAPSSPATGV SPQGKSTSLSKASPESQBELIQLVQAFVRHMQR PREFRWRRELH*AGPASSAGGESGASGTMSGELPPNINIK WDQSTFIGRANHFFTVTDPRNILLTMEQLESARKIVHDYRQG PPGLTEMELWRAXYIYDSAPHDDTGEKMLLGRMSAQVPMN TGCMMFFYRTTPAVLWWWINDSPNAVVNYTMRSGDAPLTVW GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPPAAVAAAN NIPLMRGRBLKVGIPVTDENGANLGESARAKQAITQVVSTG MAAPEMAIPPFINNTLEKKRPLKRFPWMSAPIQVGLVGPGLU TPLCCALFPQKSSMSVTSLRARLQAKIQSHPELRRVYFNK GTAYVSATTGAVATALGLNALTKHVSPLIGRFVUPPAAVAAAN NIPLMRGRBLKVGIPVTDENGANLGESARAKQAITQVVSTG MAAPEMAIPPFINNTLEKKRPLKRFWMSAPIQVSLVGPGLU TPLCCALFPQKSSMSVTSLRARLQAKIQSHPELRRVYFNK GTAYVSATTGAVATALGLNALTKHVSPLIGRFVUPPAAVAAAN NIPLMRGRBLKVGIPVTDENGANLGESHPELRRVYFNK GTAYVSATTGAVATALGLNALTKHVSPLIGRFVUPPAAVAAAN NIPLMRGRBLKVGIPVTDENGANLGESHPUPPAAVAAAN NIPLMRGRBLKVGIPVTDENGANLGESHPELRRVYFNK GTAYVSATTGAVATALGLNALTKHVSPLIGRFVUPPAAVAAAN NIPLMRGRBLKVGIPVTDENGANLGESHPERRVCOPHLYNSLG  TPLCCALFPQKSSMSVTSLRARLQAKIQOSHPKRCOPHLYNSLG BCKPUDADFSDNVCSGNTLHISINSPRTFKKPVNSKIGLSPTIV YNDSDKLNDYLMRGPSFNQQOTTVGSLREFRQCLSSSSFA  AAAEGHIEVVKFFLIBACKVMPFAKDRWGNIPLDDAVQFNHLE LLDDYQDSTLISETQARAARALSKERLESHW TIDGTGSVGAALGPLLAGLLSPGKMRFRIQLESHY KLLQDYQDSTLISETQARAARALSKERLESHW TIDGTGSVGAALGPLLAGLLSPGKMVFYMLMFADACALLF RLHKELSCGSSATGDQVPFREQ  T133 2 3648 QIPCLLAGLSPGGCCPLDGGALFLERGLDLFFTLYPSLE BEBLLELHVQDHFQEGCCPLDGGALFLERDLSVTSLSNLAC MVFMAVMPLLEADSGRVTLDFTGGPRVRSPGR RPGVVVLVPEMDVALTRSASFSRKVSSSKYSSGSGALVLRS RLPEMVGHPAFAVITQLEYFSSPAGUPGRASVTSLSNLAC MVFMAVMPLLEADSGRVTLPLQGGTGDPHSHCLVYKVPSAS SEBVKQVSGTLRFQFSQASGPPGGGISHLEADLSQTISVLE SEBVKQVGGTLRFQFSQASGPPGGGISHLEADLSQTISVLE ARPTSQLPHGSQASPAQAQPPPLEAGISHL	1		}	· · · · · · · · · · · · · · · · · · ·
LSVYQLSTNGTAQTPSASRKSLDAPSWPGVYKLSMSLMEQLI LRYMPLPEALDPYUVIQURTLCCLANVETVQSLACLBEADIT PILQLSMMRKSMHHLPQLMRTUQCHAVTTVQSLACLBEADIT PILQLSMMRKSMHHLPQLMRTUQVIAGYLOQCTSPHISKS OHYLQNKNGGGLPSAV\AQRV\QRPPSASAAPSSSKQPADA ASRQQALHTUQYGLLKILEKTLAALRHFTPDVCQTLLLQSLL EYNFLPALSYTTPTPDSEVAPSFGTILATVNVALMMLGELDN EPLTQAVGLSTOABGTRTLKSLIMPTMRRCFYLLISQAMRYI PAVHPRKQRMKQELSSELSTLLSELSHYFRGAPSSPATGV SPQGKSTSLSKASPESQPELLQLVQAFVRHMQR 7129 1 1054 PRRFRWRRLH*AGPASSAGGSPGRASGTWSGELPPNINIKE PPGGTEBELWRRAKYITDSAFHPDTGEKMILLGRMSAQVPMNN GCMMTFYRTTPAVLFWQMINQSPNAVWYTNRSGDAPLTVN GCMMTFYRTTPAVLFWQMINQSPNAVWYTNRSGDAPLTVN GTAYVSATTGAVATALGLMALTKVSPLIGRFVPPAAVAAN NIPLMRGRELKVGIPVTDRNGNRLGESNAAKQATTQVVVSR MAAPGMAIPPPINNTLEKKAPLKRFPWMSAPLOVGLVGPCLV TPLCCALFPQKSSMVTSLEABLQAKIQBSHPELRRVFFNKC TALCCALFPQKSSMVTSLEABLQAKIQBSHPELRRVFFNKC SAGQPYHBSQSSSVLINKSMDSINYPSDVGKQQLLSLHE RCSSHQDLLPDIADSHQQTEKLSDLTLQDSQKVVVVNRNLE AQIATQNYPSNPKETDGBDDVVEKSBEDBSELBISHNRR DSKKVDADPSDNVCSGNTLHSLNSPRTFKKPVNSKLGLSPYI VNDSDKLNDVLWRGPSPNQONIVQSLBKFGCLSSSFA AAARGHIEVVKFLJEACKVMPPAKDRGNIPLDDAVQFNHLS- TJ32 1420 1087 IDMILLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTV LILDDYQDSYTLSGTOABAARALSKENLESMV 7132 1420 1087 IDMILLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTV LILDDYGGSVGALGFLAGLLSFGMSNVFYMLMFADACALLF RLIHKELSCPGSATGDQVPFKEQ 7133 2 3648 QQIPGLPAGGSGSDALRKPRLQKFTTGHLDDLFFTLYPSLE RBILLEHVQDHPGGGCOPLOGGALETLERRLRVGVHNSLIGE RPLIKHLBLSCPGSATGDQVPFKEQ QVVVLVPEMDVALTRSASPSRKVVSSKTSSGSQALVLRS RLPEMVGHPAFAVIFQLEVFSSPAGVDGNASVTSLSNLAC MYRMAVNPLLEADSGRVTILPGGGQDFPLEAGISQLAASPRSPTQE PSPSSPPAPPRVLAAPQNSPVGGGLISQLAASPRSPTGE PSPSSPPAPPRVLAAPQNSPVGGGLISQLAASPRSPTGE ARPTSQLPHGSQAPAQAQEPPLEAGISHLEADLSQTSLVLKS LARQLQBLPFTPHHAPITVGTGTRSSAGGPSRASMVLLQSSG	i		j	-
IRYMPI-PRALDPVGVHORRTI-QCLMAVRTVQS-LACLERADHT PILQLSNPMKBWHFHLPQLMRDIQVNLGYLCQACTSFLHERR QHYLQNKWGGGLPSAV\AQRY\QRPPSAASAPSSKQPAAL ASBQQALHTVQYGLLKILSKTLAALRHFTPDVCQTLLLQSLL EYNFLFALSFTTPTPSEVAPSFGTLLATVNVALMILGSLD EPLTQAVCLSTQABGTRTI-KSLLMFTMENCFYLLLSQAMRYI PAVIPRDKQRMKQELSSRI-STILSSLBYPRRGAPSSPATG SQGKSTSLSKASPBSQEPLIQLVQAFVRHMOR  7129 1 1054 PRIFRWRRELH-AGPASSAGGSFGRASGTMGELPPNINIKE WDQSTF1GRANHFFYVTDPRNILLVNEQLESARIKYHDYRQC PPGLTENELWRAKY1YDBAPHPDTGEKMILLGRMSAQVPMIN TGCMMTFYRTTPAVLFMGWINQSPNAVVNYINRSGDAPLTVN GTAYVSATTGAVATALGLAALTKHVSPLIGEFVPPAAVAAN NIPLMRQRELKUG1PVTDBCNRILGESANAKQATTQVVVSS MAAPGMAIPPFIMNTLEKKAPLKRFPWMSAPIQVGLVGPCLV TPLCCALFPQKSSMSVTSLRAELQAKIQESHPELRRVFNKK RCSHQDLLPDIADSHQQGTEKLSDLTTQDSGKVVVVSRNLE RCSHQDLLPDIADSHQQGTEKLSDLTTQDSGKVVVVSRNLE RCSHQDLLPDIADSHQQGTEKLSDLTTQDSGKVVVVSRNLE DSKPVDADFSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYT YNDSDKLNDYLMRGFSPNQONIVOSLERKFQCLSSSFRA AARGHIEVVSPLIRACKVNPPAKORWINDFIDDAVQPNHLE LLQDYQDSYTLSETQARAARALSKENLESMV 7131 805 573 AARGHIEVVSPLIRACKVNPPAKORWINDFIDDAVQPNHLE LLQDYQDSYTLSETQARAARALSKENLESMV 7132 1420 1087 IDMILESGALVSGPYTLTTAVSADLGTHKSLKGRAHLESTV LIDGTGSWGAALGPLLAGLLSPSGWSNVFYMIMFADACALLF RLIHKELSCPGSATGDQVPFKEQ 7133 2 3648 QQIPGLEFAHGESGBALRKRPRIQFTTGHLDDLFFTLYPSLE REBLIELHUQDHFQSGCOPITCHDLDFFTLYPSLE REBLIELHUQDHFQSGCOPITCHDLDFFTLYPSLE REBLIELHUQDHFQSGCOPITCHDLDFFTLYPSLS REPLICHHVQDHFQSGCOPITCHDDARSTSSAGQALVRS RLPEWGHPAPAVIFQLEFYVSSSRAGDGALASVTSLSINLAC VNWAVMNPLLEADSGRYTLPLQGGIQDNPBHCLVYKVPSAS SEEVKQVESGTLRRQGSTGSGERHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPUGGGLSISQLAASSPSPTQU PTSPSSPPAPVPRVLAAPQNSPUGGGSISLCLARSPRSPTQE PTSPSSPPAPVPRVLAAPQNSPUGGRASITSLGLAASPRSPTQE PTSPSSPPAPVPRVLAAPQNSPUGGGSISLCLARSPRSPTQE PTSPSSPPAPVPRVLAAPQNSPUGGRASITSLEALLGSSTLVLE LARQUGUSLPYTPLHAPIVGTQTRSSAGOPSRASWULLQSSG	Į			
PILQLSNPMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSRK QHYLQNINGGLEPSAV\LQKRV\QRPQSAASAPSSSKQPAAH ASEQQALHTVQYGLLKIKETLAALRHFTPDVCQTLLQSLD EYNFLFALSFTTPTDSEVAPSFGTLLATVNVALNMLGBLDK EPLTQAVGLSTQABGSTRTIKSLLMFHTPNCTYLLISQARRYL PAVNFPRDKQRMKQELSSRLSTILSSLSHYFMENCTYLLISQARRYL PAVNFPRDKQRMKQELSSRLSTILSSLSHYFMENCTYLLISQARRYL SPQGKSTSLSKASPBSQEPLIQLVQAFVRHMQR 7129 1 1054 FRFFRWRRFLH*AGPASSAGGSFGRASTMSGELPNINIK WDQSTFJGRANHFFFVTDPRILLTNBGLESARKIVHDYRQC PPGLTENELWRAKYIYDSAFHPDTGEKMILLGRMSAQVPMN TGCMMTFYRTTPAVLFMQWINQSRNAVVNYTNRSGDAPLTVW GTAYVSATTGAVATALGLINALTKHVSPLIGFFVPFAAVAAAN NIPLMRQRELKVGIPVTDBNGNRLGESANAAKQAITQVVVSK MAAPGMAIPPFIMMTLEKKAFLKRFPMMSAPIQVLJOFCLV TPLCCALFPQKSSMSVTSLRACQAKIOSSHPELRRVYFNK TGLAKSQPYHRSQSSSSVLINKSMDSINTYSDVGRQLISLIH RCESHQDLLPDIADSHQQGTEKLSDLTLQDSGKVVVVMRNLE AQIATQNYSNFKETDGDEDDYVEIKSEEDESELELSHNRR DSKFVDADFSDNVCSGNTLHISLNSSFTFKKRPVNSRLGLSFYT YNDSDKLNDYLWRGPSPNQQHIVQSLRKERQLSSSSFST 7131 805 573 AAABGHIKVVKFILBACKVNFFAKDRWGNIFLDDAVQFNHLE KLLQDYQDSYTISSTQABAAARALSKENLESMV 7132 1420 1087 IDMILLSGALVSGFYTLITTAVSADLGTHKSLKGNAHALSTV IIDDTGSVGAALGFILAGLSPSGWSNVYYMLMFADACALLE RLIHKBLSCPGSATIGQVPFKEQ 7133 2 3648 QQIPGLLFAHGESGDALKKPRLQKTTGHLDDLFFTLYPSLE RBBLIKLHVQDHFQBGCGPJLDGGALEILERRLRVGVHRGLGE RPQVVVLVPBMDVALTRSASFSRKVSSSKTSSGSQALVLRS RLIPENVGHPRRAVIFQLEYVFSSFAGVDGNAASVTSLSINLAG WYRRWNMPLLBADSGRVTLPLQGGLGPHCLLYRVVPSAS SEEVKQVESCTLRPQFSLGSEEHLDAPTEPVSGPKVERPSR PTSPSSPPAPVPRVLAAPQNSPVCPGLSISJQLAASPRSPTQB PTSPSSPPAPVPRVLAAPQNSPVCPGLSISJQLAASPRSPTQB PTSPSSPPAPVPRVLAAPQNSPVCPGLSISJQLAASPRSPTQB PTSPSSPPAPVPRVLAAPQNSPVCPGLSISJQLAASPRSPTQB ARPTSQLPHGSQASPAQAEPPLEAGISHLEADLGGTSLVLK ARPTSQLPHGSQASPAAQAEPPLEAGISHLEADLGGTSLVLK ILBGLQGLUPTTHAPLTVVCTQTRSSAGQOSRASMVLLQGSG	<u> </u>		ļ	
OHYLONKNGGLPSAV\AQRV\QRPSAASAAPSSKOPAAL	1			
ASBQQALHTVQYGLLKILSKTLAALRHFTDDVCQILLDQSLD BYNFLFALSFTTPTDSBVAPSFGTILATVNVALIMLGBLDB BPLTQAVGLSTQABGTFTLKSLLMFTMENCFYLLISQAMRYI PAVHPRDKQRMKQELSSBLSTLJSSLSRYPRRGAPSSPATGV SPQGKSTSLSKASPBSQBPLIQLVQAFVRHMQR  7129 1 1054 PRFPRWRRHL+AGPASAGSPGRASGTMSGELDPNINIG WDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRQG PPGLTENELWRAKYIYDSAFHPTDEKMILLGRMSAOVPMN TGCMMTFYRTTPAVJEWGHUDQSFNAVWYTNRSGDAPLTVN GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPPAAVAAN NIPLMRQRELKVGIPVTDENGNELGBANAAKQAITQVVVSR MAAPGMAIPPFIMNTLEKKAFLKRPFWMSAPLQVGYCLV TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNKC GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPPAAVAAN NIPLMRQRELKVGIPVTDENGNELGBANAAKQAITQVVVSR MAAPGMAIPPFIMNTLEKKAFLKRFFWMSAPLQVGYCLV TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNKC GTAYVSATTGAVATALGLNALTKHVSPLIGRFVVPPAAVAAN NIPLMRQRELKVGIPVTDENGNILGBANAAKQAITQVVVSR MAAPGMAIPPFIMNTLEKKAFLKRFFWMSAPLQVGYCLV TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNKC TPLCCALFPQKSSMSVTSLEAELQAKIAGSITANSELGSPAT AQIATQNYFSNFKETDGDEDDYVEIKSBEDESBLELSHNRRR BCKFVDADFSDNVCSGNTLISLNSSPTPKKPVNSKLCLSPYT YNDSDKLNDYLWRGPSPHOQNIVQSLEERGQLSSSSFA  7131 805 573 AAAEGHIEVVKFILBACKVNFFAKDRWGNIPLDDAVQFNHLE KLLDDYQDSYTLSETQARAARALSKENLESMV  7132 1420 1067 IDMLLISGALVSGPYTLITTAVSADLGTHKSLKGNBIALSTV IDDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLF RLIHKELSCPGSATGDQVPFKEQ  7133 2 3648 QQIPGLLPAHGESGDALRFPLQKPTTGHLDDLFFTLYPSLE BEBLLELHVQDHFQSGCGPLDGGALEILERRLRVGVINGLGE RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLKS RLIPEMVGHPAFAVIFQLEYVFSSAFSVDCNAASVTSLSNLAC MYRWAVMPLLEADSGRVTLIPLQGGIQPNPSHCLVYKYPSAS SEEVKQVESGTLRFQFSLGSEERLDAPTEPVSGFKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQL ARPTSQLPHGSQASPAQAQEPPLEAGISHLEADLSGTSLVIK LABQLQEUPFFTIHAPIVVGTQTRSSAGQPSRASMVLLQSSG	}			
BYNFLFALSFTTPTDSEVAPSFGTILATVNVALNMIGBLDH BPLTQAVGLSTQABGTRTIKSLIMFTMENCFYLLISQAMRYL PAVHERDKORMKQELSSERSTLISSLSSTYPERGAPSSPATGV SPQGKSTSLSKASPBSQEPLIQLVQAFVRHMQR 7129 1 1054 PRFFWRRRLH+AGPASSAGGSFGRASGTNSGELPPNINIK WDQSTFIGRANHFFTVTDPRINILLTNEQLESARKIVHDYRQG PPGGTENELWRRKYITDSASHPDTGEKMILIGRMSAOVPMSM TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTVW GTAYVSATTGAVATALGLINALTTHVSPLIGRFVPFAAVAAAN NIPLMRQRSHKVGIPVTDENGNLIGESANAAKQAITQVVVSS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGPCLV TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNKC 1SAKSQPYHRSQSSSVYLINKSMDSINYPSDVCKQQLISLHE RCESHQDLLPDTADSHQQGTEKLSDLTLQDSQKVVVVMRNLE BREVDADPSDNVCSGNTLHSLNSPRTPKRFVNSKLGLSFYI YNDSDKLNDYLWRGPSPNQQOTIVLSKEEDESBLELSHNRR DSKFVDADPSDNVCSGNTLHSLNSPRTPKKFVNSKLGLSFYI YNDSDKLNDYLWRGPSPNQQNIVQSLREKFQCLSSSSFA 7131 805 573 AAABGHIEVVKFIJEACKVNPFAKDRWGNIPLDDAVQFNHLE KLLQDYQDSYTLSETQABAAARALSKELESMV 7132 1420 1087 IDMILISGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTV ILDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLE RLIHKELSCPGSATDQVPFKPLGTHEDLFTHYPSLE BEBLLELHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGF RPQVVVLVPBMDVALTRSASFSRKVVSSSKTSSGSQALVLKS RLIPEMVGHPAFAVIFQLEYVFSSPAGDVDCHAASVTSLSNLAC MVRWAVMPLLEADSGRVTLPLQGGLQPNSHCLVXKVPSAS SEEVKQVESGTLRFQFSLGSERKLDAPTEPVSGPKVERRPSR PTSPSSPPAPVBRVLAAPQNSTVEGGLISIGLAASPRSPTQBE PTSPSSPPAPVBRVLAAPQNSTVEGGLISIGLAASPRSPTQBE PTSPSSPPAPVBRVLAAPQNSTVEGGLISIGLAASPRSPTQBE ARPTSQLPBFTLHAPIVVGTQTTRSSAGQPSRASMVLLQSSG				
RPLTQAVGLSTQABGTRTLKSLLMFTMENCPYLLISQAMRYI PAVHPRDKQRMKQELSSELSTLJSSLSKYFRGAPSSPATOV SPQGKSTSLSKASPESQPLIQLVQAFVRHMOR  7129 1 1054 PRFFWRRRLH+AGPASSAGGSFGRASGTMSGELPPNINIKE WDQSTPIGRANHFTVTDPRNILLTMEQLESARKIVHDYRQG PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMNN GTGMTFYRTTPAVLFMQWINQSPRAVVMYTMSGDAPLTVM GTAYVSATTGAVATALGLMALTKHVSPLIGRFVPPAAVAAAN NIPLMRQRELKVGIPVTDENCHRLGESANAAKQAITQVVVSR MAAPGMAIPPFIMNTLEKKAFLKRPPWMSAPIQVGLVGPCLV TPLCCALFPQKSSMSVTSLRALQAKIQSSHPELRRVYFNKC  7130 2 780 HEVPSLQTSDPLPGSVQRCSVVVSQPNKENWCQDHLYNSLGF ISAKSQPYHRSQSSSVLINKSMDSINYPSDVGKQQLLSLHR RCESHQDLLPDIADSHQQGTEKLSDLTLQDSQKVVVVNRNLE AQIATQNYSNYKETDGDEDDYVEIKSEEDEEELEISHNRLE DSKPVDADPSDNVCSGRTLHSLNSPRTPKKPVMSKLGLSPYI YNDSDKLNDYLWRGPSPNQQNIVQSLREKFQCLSSSFA  7131 805 573 AAAEGHIEVVKFILEACKVNPPAKORWGYIPLDDAVQFNHLE LLQDYQDSYTLSETQARAARALSKENLESMV  7132 1420 1087 IDMLLISGALVSGPYTLITTAVSADLGTHKSLGGNAHALSTV IDGTGSVGAALGPLLAGLLSPSGWNYYMMMFADACALLF RLHKELSCPGSATEDQVPFKEQ  7133 2 3648 QQIPGLLPAHGESGDALKKPRLQKPITGHLDDLFFTLYPSLE BEBLLELHVQDHEPQEGCSPLDGGALEILBRRLRVGVNRGLGF RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRS RLPEMVGHPAFAVIPQLEYVFSPRXVVSSKTSSGSQALVLRS RLPEMVGHPAFAVIPQLEYVFSPRXVVSSKTSSGSQALVLRS SEEVKQVBSGTLRFQFSLGSEEHLDAPTEPVSGPKVRRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAGPFPLEAGISHLEADLSGTSLVILAB RRTSQLPHGSQASPAQAGPFPLEAGISHLEADLSGTSLVILAS ARPTSQLPHGSQASPAQAGPFPLEAGISHLEADLSGTSLVILAS	1			
PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATCY SPQGRSTSLSKASPESQEPLIQUVQAFVRHMQR 7129 1 1054 FRFFRWRRFLH*AGPASSAGGSFGRAGGMSGELPPNINIKE WDQSTFIGRANHFTVTDPRNILLTNEQLESARKIVHDYRQG PPGLTENELWRAKYIYDSAFHPTGEKMILIGRMSAQVPMM TGCMMTFYRTTPAVLFWQHINDSPNAVVNYTNRSGDAPLTVN GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPPAAVAAN NIPLMRQRELKVGIPVTDENGNRLGESANAKQAITQVVVSF MAAPGMAIPPFINNTLEKKAPLKRFPWMSAPIQVGLVGPCLV TPLCCALFPQKSSMSVTSLERBLQAKIQSSHPELRRYFPNK AQARYQNYSNFKETDSDPLPGSVQRCSVVVSQPNKENWCQDHLYNSLGF RCESHQDLLPDIADSHQQGTEKLSDLTLQDSQRVVVVNRNLE AQARYQNYSNFKETDGDEDDYVEIKSEBDESLBLSHNRRR PSKFVDADPSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYL YNDSDKLNDYLWRGPSENQONIVQSLREKFQCLSSSSFA 7131 805 573 AAAEGHIEVVKFILBACKVNPFAKDRWNIPLDDAVQFNHLE KILODYQDSYTISETQABAARALSKENLESMV 7132 1420 1087 IDMLLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTV IIDGTGSVGAALGPLLAGLSPSGWSNVFYMLMFADACALLE RLIHKELSCPGSATGDQVPKEQ 7133 2 3648 QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTDYPSLE REBLIELHVQDHFQEGCGPLDGGALEILERRLRVGVENGLGE RPQVVVLVERMDVALTRSASFSRKVVSSSKTSSGSQALVLRS RLPEMVGHPAFAVIFQLBYVFSSPASVDCNAASVTSLSNLAG WYRNAVMPLLEADSGRVTLPLQGGIQPPSHCLVYKVPSAS SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVFRVLAAPQNSPVGFGLSISQLAASPRSPQB ARPTSQLPRISGSQASPAQAQBFPLERGISHLEADLSGTSLIVLE ARPTSQLPRISGSQASPAQAQBFPLERGISHLEADLSGTSLIVLE LABQLQELPFTFLHAPIVVGTQTRSSAGQPSRASMVLLQSSG				
SPQGKSTSLSKAS PESQEPLIQLVQAFVRHMQR  7129 1 1054 PRRFRWRREH **AGPASSAGSFGRASGTMSGELPPNINIK* WDQSTFIGRANHFFTVTDRNILLTNEQLESARKIVHDYRQG PPGLITENELWRAKYIYDSAFHPDTGEKMILLGRMSAQVPMMM TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTVM GTAYVSATTGAVATALGLNALTHRVSPLIGRFVPPAAVAAAN NIPLMRQREHKVGIPVTDENGRRLGESANAKQAITQVVSK MAAPGMAIPPFIMMTLEKKAFLKRFPWMSAPLQVGLVGPCLV TPLCCALFPQKSSMSVTSLBABLQAKIQESHPELRRVYFNKC  7130 2 780 HEVPSLQTSDPLPGGSVQRCSVVSQPMKENWCQDHLYNSLGR RCESHQDLLPDIADSHQQGTEKLSDLTLQDSGKVVVVNRNLE AQIATQNYFSNFKETDGDEDDYVEIKSBEDESBLBLSHNRRR DSKFVDADFSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYI YNDSDKLNDYLWRGPSPNQQNIVQSLREKFQCLSSSSFA  7131 805 573 AAAEGHIEVVKFLIBACKVWPFAKDRWGNIPLDDAVQFNKLE SKLLQDYQDSYTLSETQABAAARALSKENLESMV  7132 1420 1087 IDMLLSGALVSGPYTLTTTAVSADLGTHKSLKGNAHALSTV ILDGTGSVGAALGPLLAGALLSPSGWSNVFYMLMFADACALLF RLIHKELSCRSSATGDQVFFKEQ  7133 2 3648 QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLE RBBLLEHVQDHFQBGCGFLDGGALETLERRLRVGVHNGLGE RPQVVVLVPEMDVALTRSAFSRRVVSSSKTSSGSQALVLRS RBPUVVLVPEMDVALTRSAFSRRVVSSSKTSSGSQALVLRS RBPUVVLVPEMDVALTRSAFSRRVVSSSKTSSGSQALVLRS RLPEWWGHPAFAVIFQLEVYFSSPAGVDGNAASVTSLSNLAC MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSAS SEEVKQVESGTLRFGFSLSSERHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVCPGLSISQLAASPRSPTQH ARPTSQLPHGSQAGSPQAQAFPLEAGTSHLEADLSGTSLVLE LABQLQGLPFTPLHAPIVVGTQTRSSAGQPSRASWVLLQSSG	l .			· ·
7129 1 1054 PRRFRWRRLH+AGPASSAGGSPGBASGTMSGELPPNINIKE WDOSTFIGRANHFFTVTDPRNILLITNEGLBSARKIVHDYRGG PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMNM TGCMMTFYRTTPAVLFWOMINQSPNAVVNYTNRSGDAPLTVN GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPPAAVAAAN NIPLMRQRBLKVGIPVTDENGRILGESANAAKQAITQVVVSR MAAPGMAIPPFINNTLEKKAFLKRFFWMSAPIQVGLVGFCLVV TPLCCALFPQKSSMSVTSLBABLQAKIQESHPELRRVYFNKC 130 2 780 HEVPSLQTSDPLPGSVQRCSVVVSQPMKENWCQDHLYNSLGF RCESHQDLLPDIADSHQQTTEKLSDLTLQDSQKVVVVNRNLE RCESHQDLLPDIADSHQQTTEKLSDLTLQDSQKVVVVNRNLE AQIATQNYFSNFKETDGDEDDYVEIKSBEDESBLBLSHNRRR DSKFVDADFSDNVCSGNTLHSLNSPRTFKKPVNSKLGLSPYI YNDSDKLNDYLWRGPSPNQQNIVQSLRBKFQCLSSSSFA 7131 805 573 AAAEGHIEVVKFLIBACKVWPFARDRWGNIPLDDAVQFNHLE KLLQDYQDSYTLSETQABAARALSKENLESMV 7132 1420 1087 IDMLLISGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTV IDGTGSVGAALGFLLAGLLSPSGWSNFYMLMFADACALLE RLIHKELSCPGSATGDQVPFKEQ 11DGTGSVGAALGFLLAGLLSPSGWSNFYMLMFADACALLE RLIHKELSCPGSATGDQVPFKEQ RPGVVVLVPEMDVALTRSASFSRRVVSSSKTSSGSQALVLRS REBLLEHVQDHFQEGCGPLGGALEILERRLRVGVHNGLGF RPQVVVLVPEMDVALTRSASFSRRVVSSSKTSSGSQALVLRS RLPEMVGHPAFAVIFQLEYVFSSPAJDGNAASVTSLSNLAG MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVVKVPSAS SEEVKQVESGTLRFQFSLGSEBKLDAFTEPVSGPKVRRPBRR PTSPSSPPAPVPRVLAAPQNSPVCPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAGFFLEAGTSHLBADLSGTSLVLE LBBQLQELPFTPLHAPIVVGTQTRSSAGQPSRASWVLQSSG	ł		ŧ	
### WDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRQG  #### PPGLTEMELWRAKYIVDSAFHPDTTGEKMILIGRMSAQVPMM TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTVM GTAYVSATTGAVATAIGLNALTKHVSPLIGRFVPPAAVAAN NIPLMRQRELKVGIPVTDENGNRLGESANAAKQAITQVVVSR MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCLU  #### TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNKC  7130 2 780 HEVPSLQTSDPLDGSVQRCSVVVSQPNKENWCODHLYNSLGF ### CESHQDLLPDIADSWQQGTEKLSDLTLQDSQKVVVVNRNLE RCESHQDLLPDIADSWQQGTEKLSDLTLQDSQKVVVVNRNLE AQIATQNYFSNFKETDGEDDYVEIKSEEDESELBLSHNRS DSKFVDADFSDNVCSGNTLHELNSPRTPKKPVNSKLGLSFYI YNDSDKLNDTUWRGPSPNQQNIVQSLREKFQCLSSSSFA  7131 805 573 AAAEGHIEVVKFLIEACKVNPFAKDRWGNIPLDDAVQFNHLE KILQDYQDSYTLSETQARAARALSKENLESMV  7132 1420 1087 IDMLLSGALVSGFYTLITTAVSADLGTHKSLKGNAHALSTV IIDGTGSVGAALGPLLAGLLSPSGMSNVFYMLMFADACALLE RLIHKELSCPGSATGDQVPFKEQ  7133 2 3648 QQIPGLLPAHGESGDALRKPRLQKFTTGHLDDLFFTLYPSLE BEBLLEILHVQDHFQESGPLDGGALEILERRLRVGVHNGLGE RPGVVVLVPPMDVALTRSASFSRKVVSSKTSSGSQALVLES RLPEMVGHPRAVIFQLEYVFSSPASVDGRAASVTSLSNLAG MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSAS SEEVKQVESGTLRFQFSLGSEEHLDAPTEVVSGPKVERRPSR PTSPSSPPAPVFRVLAGGISEKHLDAPTEVVSGPKVERRPSR PTSPSSPPAPVFRVLAGGISEKHLDAPTEVVSGPKVERRPSR PTSPSSPPAPVFRVLAGGISEKHLDAPTEVVSGPKVERRPSR ARPTSQLPHGSQASPAQAGPFLEAGISHLEADLSGTSLVLE IABQLQELPFTFLHAPIVVGTQTRSSAGQPSRASWULLQSSG	7166		1054	
PPGLTENELWRAKYIYDSAPHPDTGEKMILIGRMSAQVPMNM TGCMMTFYRTTPAVLFWQWINQSPNAVVNYTNRSGDAPLTW GTAYVSATTGAVATALGINALTKHVSPLIGRFVPPAAVAAAAN NIPLMRQRELKVGIPVTDENGMRLGESANAAKQATTQVVVSR MAAPGMAIPPFIMNTLEKKAPLKRFPWMSAPIQVGUVGFCLV TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNKG TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNKG TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNKG RCSHQDLLPDIADSHQQGTEKISDLTLQDSQKVVVVNRNLE RCSSHQDLLPDIADSHQQGTEKISDLTLQDSQKVVVVNRNLE AQIATQNYFSHFKETDGDEDDYVEIKSBEDESELBLSHNRRR DSKFVDADFSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYI YNDSDKINDYLWRGPSPNQNIVQSLREKFQCLSSSSFA  T131 805 573 AAAEGHIEVVKFLIEACKVNPFAKDRWGNIPLDDAVQFNHLE KLLQDYQDSYTLSETQABAAARALSKENLESMV  T132 1420 1087 IDMLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTV IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLF RLIHKELSCPGSATGDQVPKEQ  T133 2 3648 QQIPGLLPAHGESGDALKPRLQKPITGHLDDLFFTLYPSLE REBLLKHVQDHFQEGCGPLDGGALEILERRLRVGFHNGLGE RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLKS RLPEMVGHPAFAVIPQLEGVFSPASVDCHAASVTSLSNLAC MYRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSAS SEEVKQVESGTLRPQFSLSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNS PVGFGLSISQLAASPRSPTQE ARPTSQLPHGSQASPAQASPPLEAGISHLEADLSGTSLVLE IABQLQELPPTPLHAPIVVGTQTRSSAGQPSRASWULLQSSG	/129	1	1054	
TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTVM GTAYVSATTGAVATALGLINALTKHVSPLIGRFVPFAAVAAAN NIPLMRQRELKVGIPVTDENGRRLGESANAAKQAITQVVVSR MAAPGMAIPPFINNTLEKKAFLKRFPWMSAPIQVGLVGFCTLV TPLCCALFPQKSSMSVTSLBAELQAKIQESHPELRRVYFNKG TPLCCALFPQKSSMSVTSLBAELQAKIQESHPELRRVYFNKG TPLCCALFPQKSSMSVTSLBAELQAKIQESHPELRRVYFNKG TPLCCALFPQKSSMSVTSLBAELQAKIQESHPELRRVYFNKG TPLCCALFPQKSSMSVTSLBAELQAKIQESHPELRRVYFNKG TPLCCALFPQKSSMSVTSLBAELQAKIQESHPELRRVYFNKG TPLCCALFPQKSSMSVTSLBAELQAKIQESHPELRRVYFNKG TPLCCALFPQKSSMSVTSLBAELQAKIQESHPELRRVYFNKG TPLCCALFPQKSSMSVVSQPKKENGQDHLYNSLGF TPLCCALFPQKSSMSVLSBAAKIQESHPELRRVYFNKG RECSHQDLLPPIABHGQGTEKLSDLTLQDSQKVVVVNRILF AQIATONYFNKETDGBEDDYVEIKSEBERGLSHNRILF RCESHQDLLPPIABHGVGGTEKLSDLTLQDSQKVVVVNRILF AQIATONYFNKETDGBEDDYVEIKSEBERGLSHSHNRILF BSKFVDADFSDNVCSGNTLHSLNSPTPKKPVNSKLGLSPYI YNDSDKLNDYLWRGPSPNQQNIVQSLRERFQCLSSSSFA TLDYNDSDKLNDYLWRGPSPNQQNIVQSLRERFQCLSSSSFA TLDYNDSDKLNDYLWRGPSPNQDFTHABLDSGTSKLSDLSGKSKTSSGSQALVLRS REBLLBLHVQDHFQEGCGPLDGGALEILERRLRVGVVHNGLGF RPQVVVLVPMDVALTRSASFSRKVVSSSKTSSGSQALVLRS RLPEMVGHPAFAVIFQLBYVFSSPAGVDGNASVTSLSNLAC MVRWAVWNPLLEADSGRVTLPLQGGIQPMPSHCLVYKVPSAS SEEVKQVESGTLRFQFSLGSEBHLLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAFQNS PVGFGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSGTSLVLE LBEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASWLLQSSG	٠.		'	
GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAAN NIPLMRQRBLKVGIPVTDENGNRLGESANAKQAITQVVVSR MAAPGMAIPPFINNTLEKKAPLKRFPWMSAPIQVGUGPCLIV TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNKC TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNKC TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNKC TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNKC TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNKC TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNKSLGS TSAKSQPYHRSQSSSSVLINKSMDSINYPSDVGKQQLLSLHR RCESHQDLLPDIADSHQQGTEKLSDLTLQDSQKVVVVNRNLE AQIATQNYFSNFKETDGDEDDYVBIKSEEDESELBLSHNRRR DSKFVDADFSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYI YNDSDKLNDYLWRGPSPNQQNIVQSLRBKFQCLSSSSFA AAABGHIEVVKFLIEACKVMPFAKDRWGNIPLDDAVQFNHLE KLLQDYQDSYTLSETQABAABAALSKENLESMV TJ32 1420 1067 IDMLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTV IIDGTGSVGAALGPILAGLLSPSGWSNVFYMLMFADACALLF RLIHKBLSCPGSATGDQVPFKEQ TJGGTGSVGAALGPILAGLLSPSGWSNVFYMLMFADACALLF RLIHKBLSCPGSATGDQVPFKEQ TLHKBLSCPGSATGDQVPFKEQ RPQVVVLVPBMDVALTRSASFSRKVVSSSKTSSGSQALVLRS RPQVVVLVPBMDVALTRSASFSRKVVSSSKTSSGSQALVLRS RLPEMVGHPAFAVIFQLEYVFSSPAGVDGNAASVTSLSNLAC MVRWAVMNPLLEADSGRVTLPLQGGTQPNPSHCLVYKVPSAS SEEVKQVESGTLRFQPSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAGSPPLEAGTSHLEADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	1		Ì	) - · · · · · · · · · · · · · · · · · ·
NIPLMRQRELKVGIPVTDENGNRLGESANAAKQAITQVVVSK MAAPGMAIPPFIMNTLEKKAFLKRFPMMSAPIQVGLVGPCLV TPLCCALFPQKSSMSVTSLERAELQAKIQESHPELRRVYFMKG TPLCCALFPQKSSMSVTSLERAELQAKIQESHPELRRVYFMKG TPLCCALFPQKSSMSVTSLERAELQAKIQESHPELRRVYFMKG TPLCCALFPQKSSMSVTSLERAELQAKIQESHPELRRVYFMKG TPLCCALFPQKSSMSVTSLERAELQAKIQESHPELRRVYFMKG TPLCCALFPQKSSMSVTSLERAELQAKIQESHPELRRVYFMKG TPLCCALFPQKSSMSVTSLERAELQAKIQESHPELRRVVYFMKG TISAKSQPYHESQSSSVLINKSMDSINYPSDVGKQQLLSLHR RCESHQDLLPDIADSHQQFTEKLSDLTLQDSQKVVVVNRNLE AQIATQNYFSNFKETDGDEDDYVEIKSBEDESBLBLSHNRRR DSKFVDADFSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYI YNDSDKLNDYLMRGGSPNQQNIVQSLREKFQCLSSSSFA AAABGHIEVVKFLIEACKVMPFAKDWGNIPLDDAVQFNHLE KLLQDYQDSYTLSTQAKAAAKALSKENLESMV TIDALLSGALVSGPYTLITTAVSÄDLGTHKSLKGNAHALSTV IIDGTGSUGAALGPILAGLLSPSGWSNVFYMLMFADACALLE RLIHKBLSCPGSATGDQVPFKEQ RLIHKBLSCPGSATGDQVPFKEQ TLIHKBLSCPGSATGDQVPFKEQ RLIHKBLSCPGSATGDQVPFKEQ RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRS RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRS RLPEMVGHPAFAVIFQLEYVFSSPAGVDGANASVTSLSNLAG MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSAS SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAGEPPLEAGISHLEADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	ł			
MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGPCLV TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNKG TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNKG TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNKG TSAKSQPYHESQSSSVLINKSMDSINYPSDVGKQLLSLEH RCESHQDLLPDIADSHQQGTEKLSDLTLQDSQKVVVVNRNLE AQIATQNVYSNFKETDGDEDDVVEIKSBEDESBLELSHNRRR DSKPVDADPSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYL YNDSDKLNDYLWRGPSPNQQNIVQSLREKFQCLSSSSFA  7131 805 573 AAABGHIEVVKFLIBACKVNPFARDRWGNIPLDDAVQFNHLE KILQDYQDSYTLSETQABAABKALSKENLESMV  7132 1420 1087 IDMLLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTV IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLF RLIHKBLSCPGSATGDQVPFKEQ  7133 2 3648 QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLE BEBLLBLHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGF RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRS RLPEMVGHPAFAVIFQLEYVFSSPASVDGNAASVTSLSNLAG MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSAS SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	} ·			I .
TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNKG  7130 2 780 HEVPSLQTSDPLPGSVQRCSVVVSQPNKENWCQDHLYNSLGR ISAKSQPYRRSQSSSSULINKSMDSINYPSDVGKQQLLSLING RCESHQDLLPDIADSHQQGTEKLSDLTLQDSQKVVVVNRHLE AQIATQNYPSNPKETDGDEDDYVEIKSBEDESBLBLSHNRRB DSKFVDADPSDNVCSGNTLHSLINSPRTPKKPVNSKLGLSFYI YNDSDKLNDYLWRGPSPNQQNIVQSLREKFQCLSSSSFA  7131 805 573 AAAEGHIEVVKFLIEACKVNPFAKDRWGNIPLDDAVQFNHLE KILODYQDSYTLSETQABAAARALSKENLESMV  7132 1420 1087 IDMLLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTV IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLF RLIHKELSCPGSATGDQVPFKEQ  7133 2 3648 QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLE REBLLELHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGF RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRS RLPEMVGHPAFAVIFQLEYVFSSPASVDGNAASVTSLSNLAC MVRWAVWNPLLEADSGRVTLPLQGGIQPNSHCLVYKKPSAG SEEVKQVESGTLRFQPSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGFGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSGTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	Į	,	}	
7130 2 780 HEVPSLØTSDPLPGSVQRCSVVVSQPNKENWCQDHLYNSLGR ISAKSQPYHRSQSSSSVLINKSMDSINYPSDVGKQQLLSLHR RCESHQDLLPDIADSHQQGTEKLSDLTLQDSQKVVVVNRNLE AQIATQNYPSNYKETDGDEDDYVBIKSBEDESBLBSHRIRR DSKPVDADPSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYI YNDSDKLNDYLWRGPSPNQQNIVQSLREKFQCLSSSSFA  7131 805 573 AAAEGHIEVVKFLIEACKVNPFAKDRWGNIPLDDAVQFNHLE KLLODYQDSYTLSETQARAAARALSKENLESMV  7132 1420 1087 IDMLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTV IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLF RLIHKELSCPGSATGDQVPFKEQ  7133 2 3648 QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLE BEBLLELHVQDHFQEGCSPLDGGALEILERRIRVGVHNGLGF RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVIR RLPEMVGHPAFAVIPQLBYVFSSPASVDCNAASVTSLSNLAG MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSAS SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	Į.			
ISAKSQPYHRSQSSSVLINKSMDSINYPSDVGKQQLLSLHER RCESHQDLLPDIADSHQQGTEKLSDLTLQDSQKVVVVNRNLE AQIATQNYPSNFKETDGDEDDYVBIKSBEDBSBLBISHNRRR DSKFVDADPSDNVCSGNTLHSLNSPRTFKKFVNSKLGLSPYI YNDSDKLNDYLWRGPSPNQQNIVQSLREKFQCLSSSSFA AAAEGHIEVVKFLIEACKVNPFAKDWGNIPLDDAVQFNHLE KLLQDYQDSYTLSETQABAAARALSKENLESMV 7132 1420 1087 IDMILLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTV ILDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLF RLIHKBLSCPGSATGDQVPFKEQ 7133 2 3648 QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLE BEBLLBLHVQDHFQEGCSPLDGGALEILERRLRVGVHNGLGE RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLSG RLPEMVGHPAFAVIPQLBYVFSSPASVDGNAASVTSLSNLAG MVRMAVMPLLEADSGRVTLPLQGGIQPNPSHCLVVKVPSAS SEBVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQEFPLEAGISHLBADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	L-7230		700	
RCESHQDLLPDIADSHQQGTEKLSDLTLQDSQKVVVVNRNLE AQIATQNYPSNPKETDGDEDDYVEIKSBEDESBLBLSHNRRR DSKPVDADPSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYT YNDSDKLMDYLWRGPSPNQQDIVQSLREKFQCLSSSSFA  7131 805 573 AAAEGHIBVVKFLJEACKVNPFAKDRWGNIPLDDAVQFNHLE KLLQDYQDSYTLSETQABAAARALSKENLESMV  7132 1420 1087 IDMLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTV IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLF RLIHKELSCPGSATGDQVPFKEQ  7133 2 3648 QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLE BEBLLBLHVQDHFQEGCSPLDGGALEILERRLRVGVHNGLGF RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRS RLPEMVGHPAFAVIFQLEYVFSSPASVDCNAASVTSLSNLAG MVRWAVWNPLLEADSGRVTLPLQGGIQPNSHCLVYKVPSAS SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQEFPLEAGISHLBADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	/130	<del>'</del>	/80	
AQIATQNYPSNPKETDGDEDDYVEIKSBEDESELBLSHNRRR DSKPVDADPSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYI YNDSDKLMDYLWRGPSPNQQNIVQSLRBKFQCLSSSSFA  7131 805 573 AAAEGHIEVVKFLIEACKVNPFAKDRWGNIPLDDAVQFNHLE KLLQDYQDSYTLSETQABAARALSKENLESMV  7132 1420 1087 IDMLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTV IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLF RLIHKBLSCPGSATGDQVPFKEQ  7133 2 3648 QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLE BEBLLRLHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGF RPQVVVLVPEMDVALTRSASFSRRVVSSSKTSSGGQALVLRS RLPEMVGHPAFAVIFQLEYVFSSPASVDCNAASVTSLSNLAG MVRWAVWNPLLEADSGRVTLPLQGGIQPNSHCLVYKVPSAS SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSFTQH ARPTSQLPHGSQASPAQAQEFPLEAGISHLBADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG			1	• · · · · · · · · · · · · · · · · · · ·
DSKFVDADFSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYLYNDSDKLNDYLWRGPSPNQONIVQSLRBKFQCLSSSSFA  7131 805 573 AAABGHIEVVKFLIBACKVNPFARDRWGNIPLDDAVQFNHLE KLLQDYQDSYTLSETQARAARALSKENLESMV  7132 1420 1087 IDMLLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTV IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLF RLIHKBLSCPGSATGDQVPFKEQ  7133 2 3648 QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLE BEBLLBLHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGF RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGGALVLRS RLPEMVGHPAFAVIFQLEYVFSSPASVDGNAASVTSLSNLAG MVRWAVWNPLLEADGRVTLPLQGGIQPNPSHCLVYKVPSAS SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQEFPLEAGISHLBADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG		ŀ	1	
YNDSDKLNDYLWRGPSPNQQNIVQSLREKFQCLSSSSFA  7131 805 573 AAAEGHIEVVKFLIEACKVNPFAKDRWGNIPLDDAVQFNHLE KILODYQDSYTLSETQABAAAKALSKENLESMV  7132 1420 1087 IDMLLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTV IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLF RLIHKELSCPGSATGDQVPFKEQ  7133 2 3648 QQIPGLLPAHGESGDALRKPRLOKPITGHLDDLFFTLYPSLE EBELLELHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGF RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRS RLPEMVGHPAFAVIFQLEYVFSSPASVDGNAASVTSLSNLAC MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKKPSAS SEEVKQVESGTLRFQPSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGFGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG				
7131 805 573 AAAEGHIEVVKFLIEACKVNPFAKDRWGNIPLDDAVQFNHLE KLLQDYQDSYTLSETQAEAAARALSKENLESMV 7132 1420 1087 IDMLLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTV IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLF RLIHKELSCPGSATGDQVPFKEQ 7133 2 3648 QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLE REBLLEHHVQDHFQECGSPLDGGALEILERRLRVGVHNGLGF RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGGQALVLRS RLPEMVGHPAFAVIPQLBYVFSSPASVDGNAASVTSLSNLAC MVRWAVWHPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSAS SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQEPPLEAGISHLEADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	1	i		
KLLQDYQDSYTLSETQARAARALSKENLESMV  7132 1420 1087 IDMLLLSGALVSGPYTLITTAVSÄDLGTHKSLKGNAHALSTV 11DGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLF RLIHKELSCPGSATGDQVPFKEQ  7133 2 3648 QQIPGLLPAHGESGDALIKPRLOKPITGHLDDLFFTLYPSLE REBLIRLHVQDHFQECCGPLDGGALEILERRIRVGVHNGLGF RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGGQALVLRS RLPEMVGHPAFAVIPQLBYVFSSPASVDGNAASVTSLSNLAC MVRWAVMPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSAS SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQEFPLEAGISHLBADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	77.53	905		
7132 1420 1087 IDMLLLSGALVSGPYTLITTAVSÄDLGTHKSLKGNAHALSTV IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLF RLIHKELSCPGSATGDQVPFKEQ 7133 2 3648 QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLE REBILIKLKUQDHFQEGCSPLDGGALEILERRLRVGVHNGLGF RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVIK RLPEMVGHPAFAVIPQLBYVFSSPASVDGNAASVTSLSNLAG MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSAS SEEVKQVESGTLRFQPSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	1737	805	573	· ·
IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLF RLIHKELSCPGSATGDQVPFKEQ  7133 2 3648 QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLE REBLIRLAUQDHFQEGCSPLDGGALEILERRLRVGVHNGLGF RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVIRS RLPEMVGHPAFAVIPQLBYVFSSPASVDGNAASVTSLSNLAC MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSAS SEEVKQVESGTLRFQPSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	- mark	<del></del>		
RLIHKBLSCPGSATGDQVPFKEQ  7133 2 3648 QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLE BEBLLBLHVQDHFQEGCGPLDGGALBILERRILRVGVHNGLGF RPQVVVLVPEMDVALTRSASFSRRVVSSSKTSSGSQALVLRS RLPEMVGHPAFAVIFQLBYVFSSPAGVDGNAASVTSLSNLAG MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSAS SEBVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSFTQH ARPTSQLPHGSQASPAQAQEFPLEAGISHLBADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	7132	1420	1087	
7133 2 3648 QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLE  BEBLLBLHVQDHFQEGCGPLDGGALBILERRILRVGVHNGLGF  RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRS  RLPEMVGHPAFAVIPQLEYVFSSPAGVDGNAASVTSLSNLAG  MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSAS  SEBVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR  PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH  ARPTSQLPHGSQASPAQAQEFPLEAGISHLBADLSQTSLVLE  IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG			}	(
BEBLLELHVQDHFQEGCGPLDGGALEILERRIRVGVHNGLGF RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRS RLPEMVGHPAFAVIPQLEYVFSSPASVDGNAASVTSLSNLAC MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSAS SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	-			
RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRS RLPEMVGHPAFAVIFQLEYVFSSPAGVDGNAASVTSLSNLAC MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSAS SEEVKQVBSGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQBFPLEAGISHLEADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	7133	2	3648	
RLPEMVCHPAFAVIFQLBYVFSSPAGVDCHAASVTSLSNLAC MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSAS SEEVKQVBSGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQBFPLEAGISHLEADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	ł .			
MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSAS SEEVKQVBSGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQBFPLEAGISHLEADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	1			1
SEBVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSR PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQEPPLEAGISHLEADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG				4
PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQH ARPTSQLPHGSQASPAQAQEPPLEAGISHLEADLSQTSLVLE IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG	·			
Arptsolphgsoaspaoaoeppleagishleadlsotslule Iaboloelpptplhapivugtotrssagopsrasmullossg	1	}		
IABQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSG				PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQHCL
	}			
,			]	BILDANKQPARAVSATEPVTFNPQKEESDCLQSNEMVLQFLAFS
	1		ł	RVAQDCRGTSWPKTVYFTFQFYRFPPATTPRLQLVQLDBAGQPS
		•		SGALTHILVPVSRDGTFDAGSPGFQLRYMVGPGFLKPGRRRCFA
RYLAVQTLQIDVWDGDSLLLIGSAAVQMKHLLRQGRPAVQAS	L			RYLAVQTLQIDVWDGDSLLLIGSAAVQMKHLLRQGRPAVQASHE

CEO	Predicted	Predicted end	I haire agid gogment goals in the glome! montide
SEQ	ſ	L .	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i .	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į.	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
I	amino acid	sequence	Codon, /=possible nucleotide deletion,
)	1 '	sequence	
	sequence		\=possible nucleotide insertion)
Į.	ļ.	(	LEVVATEYEQDNMVVSGDMLGFGRVKPIGVHSVVKGRLHLTLAN
		ļ.	VGHPCEQKVRGCSTLPPSRSRVISNDGASRFSGGSLLTTGSSRR
1		]	KHVVQAQKLADVDSELAAMLLTHARQGKGPQDVSRBSDATRRRK
1	ł	1	LERMRSVRLQRAGGDLGRRGTSVLAQQSVRTQHLRDLQVIAAYR
1	}		ERTKAESIASLLSLAITTEHTLHATLGVAEFFEFVLKNPHNTQH
ĺ		[	TYTYBIONPELSVIVDSQEWRDFKGAAGLHTPVBBDMFHLRGSL
	ł		APOLYLRPHETAHVPFKPOSFSAGOLAMVOASPGLSNEKGMDAV
ł	1	ł	
į.	<b>,</b>	<b>{</b>	SPWKSSAVPTKHAKVLFRASGGKPIAVLCLTVELQPHVVDQVFR
ļ	}		FYHPELSFLKKAIRLPPWHTFPGAPVGMLGEDPPVHVRCSDPNV
l'	1	1	ICETONVGPGEPRDIFLKVASGPSPEIKDFFVIIYSDRWLATPT
1	]		QTWQVYLHSLQRVDVSCVAGQLTRLSLVLRGTQTVRKVRAFTSH
ł .	I	1	PQELKTDPKGVFVLPPRGVQDLHVGVRPLRAGSRFVHLNLVDVD
1	1		CHOLVASWLVCLCCROPLISKAFBIMLAAGBGKGVNKRITYTNP
1		İ	YPSRRTFHLHSDHPBLLRFREDSFQVGGGETYTIGLQFAPSQRV
I	1	ĺ	GEBEILIYINDHEDKNBEAFCVKVIYQ
7134	2115	1111	GGEGFSYPPHVGLSLGTPLDPHYVLLEVHYDNPTYEEGLIDNSG
1 '134	2113	1	
1	i	ł	LRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFQSEGHCTL
1	1	1	ECLERALRARKPSGIHVPAVLLHAHLAGRGIRLRHFRKGKEMKL
1	}		LAYDDDFDFNFQEFQYLKEEQTILPGDNLITECRYNTKDRAEMT
ſ			wgglstrsemclsyllyyprinltrcasipdimeqlqfigvkbi
1			YRPVTTWPFIIKSPKQYKNISFMDAMNKFKWTKKEGLSFNKLVL
[	}	l	SLPVNVRCSKTDNABWSIQGMTALPPDIERPYKAEPLVCGTSSS
1	1	1	SSLHRDFSINLLVCLLLLSCTLSTKSL
7135	2	2072	FVPRVTPRSLSLOGPKGESVGSITQPLPSSYLIFRAASESDGRC
, 233			WLDALELALRCSSLLRLGTCKPGRDGEPGTSPDASPSSLCGLPA
1 .	'		SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR
	ŀ		-
1	ì		KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE
ł	ŀ		ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH
ļ	Į	l i	ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG
}	ļ.	i ·	ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAPHVSNRKDGFCIS
1	j	1	GSITAKSRPYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG
ì		1	ILYGTMTLELGGKVTIBCAKNNFQAQLEFKLKPFFGGSTSINQI
1	1	ĺ	SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR
1	l	(	QRLRQHTVPLEEQTELESHRLWQHVTRAISKGDQHRATQEKFAL
I	1	]	REAGRORARERGESLMPWKPQLFHLDPITGEWHYRYEDHSPWDP
Į.	l .	ł	LKDIAOFEODGILRTLOORAVAROTTFLGSPGPRHERSGPDORL
1	1	ì	RKASDOPSGHSOATESSGSTPESCPELSDEBODGDFVPGGESPC
1	1		PRCRKEARRIGALHEALLSIREAGORLHRHLSAMLSSTARAAGA
l	l	l	
H 773.2-	<del></del>	<del> </del>	PTPGLLQSPRSWFLLCVFLACQLFINHILK
7136	2	418	DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK
}	1	1	SQQRKVRQMIBQLQNSKAVIQSKDATIQELKBKIAYLBABNLEM
	1	ļ	HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV
	I	ł	IRVVET
7137	2	466	WASGMSTVPGGSRHSLGIQVRGGWGVTGGEERSLTVPVADTWQA
I	1 -	]	GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI
ł	1	ł	PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKEVTYFT
	[	1	
J	<del> </del>	L	RMEQLSDKESYKLSCQLEPENP
7138	2	466	WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA
1	i	i	GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI
I	Į.	<b>.</b>	PDDLDGNTNKRSKBVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT
J	1	1	RMEQLSDKESYKLSCQLEPENP
7139	1	357	SLRNSARGLKMAASAARGAAALRRSINOPVAFVRRIPWTAASSO
1	1 -	}	LKEHFAQFGHVRRCILPPDKETGFHRGLGWVQFSSEEGLRNALQ
ĺ	J	[	
1 3246	<del></del>	ļ	QENHI I DGVKVQVHTRRPKLPQTSDDEKKDF
7140	1401	1957	RASSLQVLKANGGLIPSSFQQQHTGQXALBKLFDLKVYDCFCSF
ł .	<u> </u>	l	NMNVSLEKQLRPSQPWPRGKCRKTPGWRKARPKAQDLRGDLGKT
L			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide	
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G≈Glycine,	
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,	
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,	
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,	
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,	
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop	
	amino acid	sequence	Codon, /=possible nucleotide deletion,	
)	sequence	}	\=possible nucleotide insertion)	
			QAGPAEAHTRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLQSQ	
ì	ì	1	WTPKGQDPPLMFSEDYQKSLLEQYHLGLDQKLRKYVVGELIWNF	
1	[	1	ADFMINQCG	
7141	124	1073	LDSRSCWLDMEDLBEDVRFIVDETLDFGGLSPSDSREEEDITVL	
Ì			VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEE1LD	
l	)	ì	BANKLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP	
1			VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK	
}			EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA	
			AASPETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP	
ĺ			GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM	
[ .		{	GATRSNLQPP	
7142	658	839	LIPLMLHMBLKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL	
ļ		1	KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT	
	ļ	1	LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP	
	<b>{</b>		ECFRFIEEAKRKDGVVLVHCNA	
7143	3	773	SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ	
<b>,</b>	ţ	<b>(</b>	GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG	
ļ			VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA	
}		1	SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR	
			KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG	
}	}	<b>j</b>	HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI	
7144	1	988	FRVNMODGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR	
1	1	}	RCPAPRPAGVSYVIRDBVEKYNRNGVNALQLDPALNRLFTAGRD	
1		ł	SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS	
1	<b>{</b>	1	DTTVKVWNAHKGFCMSTLRTHKDYVKALAYAKDKELVASAGLDR	
	[		QIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNQLGTII	
1	l	}	VSGSTBKVLRVWDPRTCAKLMKLKGHTDNVKALLLINRDGTQCLS	
1	1	1	GSSDGTIRLWSLGQQRCIATYRVHDEGVWALQVNDAFTHVYSGG	
<b>\</b>	1	}	RDRKIYCTDLRNPDIRVLICE	
	L	<del></del>		

TRADOCS:1416260.1(%CSK011.DOC)

## WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- 7. An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

- (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 12. An antibody directed against the polypeptide of claim 10.
- ·13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex;
   and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

 a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and
  - b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.

- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computerreadable format.
- 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

International application No.

PCT/US00/34263

A. CLASSIFICATION OF SUBJECT MATTER						
IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; C07K 14/00 US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 350						
According to International Patent Classification (IPC) or to both national classification and IPC						
B. FIELUS SEARCHED						
Minimum documentation searched (classification system followed by classification symbols) U.S.: 536/23.1; 435/320.1, 455, 468, 530/300, 350						
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched						
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) MEDLINE, EAST						
C. DOC	UMENTS CONSIDERED TO BE RELEVANT					
Category *	Citation of document, with indication, where a		Relevant to claim No.			
<b>A</b> -	WAJIMA et al. The cDNA cloning and transient ex hydroxysteroid dehydrogenase of chickens. Gene. 19	999, Vol.233, pages 75-82	1-11, 13-16, and 19-26			
A	US 5,175,095 A (MARTINEAU et al) 29 December 1992 (29.12.1992), see especially columns 3-18.					
A	Database PubMed, ID No. 2393392, FREUDENSTEIN et al. mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue. Biochem. Biophys. Res. Commun. August 1990. Vol.171. No. 1. pages 250-256, see Abstract.					
A,P	Database PubMed, ID No. 10919256, HENNEBOLD et al. Ovary-selective genes I: the generation and characterization of an ovary-selective complementary deoxyribonucleic acid library. Endocrinology. August 2000, Vol.141. No.8. pages 2725-2734, see Abstract.					
A	Database PubMed, ID No. 2760883, BEIL et al. Synthe baboon (Papio anubis). J. Reprod. Fertil. July 19 Abstract.	1-11, 13-16, and 19-26				
A,P	Database PubMed, ID No. 10830289, HINSHELW( upstream of the human CYP19 (aromatase) gene me transgenic mice. Endocrinology. June 2000. Vol. 141	diates ovary-specific expression in	1-11, 13-16, and 19-26			
	·					
Further documents are listed in the continuation of Box C. See patent family annex.						
Special categories of cited documents:     "T" later document published after the international filing date or date and not in conflict with the application but cited to under						
"A" document defining the general state of the art which is not considered to be of particular relevance "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered novel or cannot be considered novel or cannot be considered to involve an inventive s						
"L" document which may throw doubts on priority claim(s) or which is cited to		when the document is taken alone				
establish the publication date of another citation or other special reason (as specified)		"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious ") a person skilled in the art				
"P" document published prior to the international filing date but later than the "&" document member of the same patent			.			
Date of the actual completion of the international search  Date of mailing of the international search  Date of mailing of the international search			ch report			
Name and mailing address of the ISA/US  Commissioner of Patents and Trademarks  Box PCT		Authorizaciofficer Asia March Michael Woodward Michael Woodward Michael Woodward				
Washington, D.C. 20231 Facsimile No. (703)305-3230 Telephone No. (703)308-0196 Form PCT/ISA/210 (second sheet) (July 1998)						

International application No.

PCT/US00/34263

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)					
This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:					
Claim Nos.:  because they relate to subject matter not required to be searched by this Authority, namely:					
Claim Nos.:  because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:					
Claim Nos.:     because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).					
Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)					
This International Searching Authority found multiple inventions in this international application, as follows: This includes 4 invention Groups and 3572 sequence species					
As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.					
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.					
As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:					
4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:					
Remark on Protest					
No protest accompanied the payment of additional search fees.					
·					

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional serch fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group IV, claim 17-18, drawn to method of indentifying a binding partner to a polypeptides. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, udner PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containg same, respectively, and methods of making as well as the first method of use of this jubject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional serch fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group IV, claim 17-18, drawn to methods of indentifying a binding partner to a polypeptides. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, udner PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containg same, respectively, and methods of making as well as the first method of use of this jubject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.